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OM nucleic - protein search using frame_plus_n2p model

Run on: March 11, 2006, 01:37:47 ; Search time 37.2 Seconds
(without alignments)
2289.022 Million cell updates/sec

Title: US-09-905-083A-30
Perfect score: 1780
Sequence: 1 9gatttccgggtccatggc.....aagaacacacaaacccctcag 969

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-O=/abes/ABSSWEB spool/US0905083/runat_10032006_152452_29654/app_query.fasta_1
-DB=A_Geneseq -OPT=fastan -SUFFIX=n2p.Tag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes02p
-USER=US0905083 @CGN 1.1 348 @runat_10032006_152452_29654 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1364	76.6	253	2	AAR67888	Human str
2	1364	76.6	253	2	AAW05383	Human amy
3	1364	76.6	253	5	ABB84421	Human SCC
4	1364	76.6	253	5	ABB84406	Human SCC
5	1364	76.6	253	5	AAU82740	Amino aci
6	1364	76.6	253	6	ABU07440	Protein d
7	1364	76.6	253	6	ABU07471	Protein d
8	1364	76.6	253	6	ABR58471	Human str
9	1364	76.6	253	7	ADB80484	Ovarian c

10	1364	76.6	253	7	ADJ68833	Human hea
11	1364	76.6	253	7	ADN39180	Cancer/an
12	1364	76.6	253	8	ADL06515	Human tum
13	1364	76.6	253	8	ADN04182	Antipgori
14	1364	76.6	253	8	ADN04182	Human ova
15	1364	76.6	253	9	ADY67588	Human kal
16	1364	76.6	253	9	ADY67588	Human kal
17	1364	76.6	253	9	AEC00353	Human kal
18	1364	76.6	253	9	AEC00353	Human kal
19	1337	75.1	257	3	ADA05732	Human NOV
20	1337	75.1	257	3	ADA05732	Human NOV
21	1252	70.3	247	6	ADA05742	Human NOV
22	1252	70.3	247	6	ADA05742	Human NOV
23	1252	70.3	247	6	ADA05734	Human NOV
24	1252	70.3	247	6	ADA05734	Human NOV
25	1235	69.4	225	8	ADN62898	Human str
26	1235	69.4	225	8	ADN62898	Human str
27	1119	62.9	224	9	ADV21100	Human str
28	1119	62.9	224	9	ADV21100	Human str
29	1085.5	61.0	249	5	ADA05744	Human NOV
30	1035.5	58.2	198	6	ADA05736	Human NOV
31	1035.5	58.2	198	6	ADA05736	Human NOV
32	996.5	56.0	243	5	ABB84419	Bovine SC
33	940.5	52.8	226	5	ABB84422	Rat SCCE
34	937.5	52.7	181	6	ADA05738	Human NOV
35	937.5	52.7	181	6	ADA05738	Human NOV
36	773	43.4	144	8	ADN62902	Stratum c
37	773	43.4	144	8	ADN62902	Stratum c
38	641.5	36.0	136	4	ADI37151	Stratum c
39	641.5	36.0	136	4	ADI37151	Stratum c
40	614	34.5	260	2	AAW10694	Human rec
41	614	34.5	260	2	AAW10694	Human rec
42	614	34.5	260	5	ABB57219	Mouse neu
43	614	34.5	260	5	ABB57219	Mouse neu
44	614	34.5	260	8	ADI39731	Murine NO
45	612.5	34.4	293	2	ADI37155	Mouse neu
					AY16777	Human ker

ALIGNMENTS

RESULT 1

AAR67888
ID AAR67888 standard; protein; 253 AA.

XX
AC AAR67888;
XX
DT 25-MAR-2003 (revised)
DT 09-AUG-1995 (first entry)
XX
DE Human stratum corneum chymotrophic recombinant enzyme (SCCS).
DE Stratum corneum chymotrophic enzyme; skin disorder; acne; psoriasis;
KW callosities; keratosis pilaris; ichthyoses; eczema.
XX
OS Homo sapiens.

XX
PN WO9500651-A1.
XX
PD 05-JAN-1995.
XX
PF 20-JUN-1994; 94WO-IB000166.
XX
PR 18-JUN-1993; 93DK-00000725.
XX
(SYMB-) SYMBICOM AB.

PA Egelrud T, Hansson L;
PI WPI; 1995-052088/07.
DR N-PSDB; AAQ81203.
XX

PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating

PT skin disorders, e.g. acne or psoriasis, and for identification of
PT specific inhibitors.

PS Disclosure; Page 97; 137pp; English.

XX The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
CC and skin care products, especially to treat and prevent acne, xeroderma,
CC or other hyperkeratotic conditions (e.g. callosities or keratosis
CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
CC recombinantly following mammal, insect, plant, or microorganism
CC transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x AAR67888 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTGCCCCCTGAGATCTTACTGCTATCTTACCTTGGAACT 75

DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20

QY 76 GCAGGAGAAGAGCCAGCGTGACAAATATTGATGGCGCCCATGTGCAAGAGCTCC 135

DB 21 AlaGlyGluGlnAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40

QY 136 CACCCATGGCAGGTGCCCTGTCTCATGTGCATACAGTCCACTGCGAGGCGTCTGTGTC 195

DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60

QY 196 AATGAGCGTGGGTGCTCATCTGCGCCCACTGCMAGATGAATGAGTACACCTGACCTG 255

DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80

QY 256 GGCAGTGATACGTGGCGCACAGGAGCTCAGAGGATCAAGGCTTCGAAGTCATTCGCG 315

DB 81 GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100

QY 316 CACCCCGGTACTCCACAGACCCCATGTATGACCTCATGCTCTGTGAAGCTCAATAGC 375

DB 101 HisProGlyTyTrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120

QY 376 CAGGCCAGGTGTCATCCATGTGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT 435

DB 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140

QY 436 GGAACACCTGTACTGTCTCCGCTGGGCGCACTTACCAGGCGCCAGATGTGACCTTTCC 495

DB 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160

QY 496 TGTGACCTCATGTGCTGATGTCAAGCTCATCTCCCTCCCGAGACTGCGACGAGGTTAC 555

DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180

QY 556 AAGGACTTACTGGAAATTCATGCTGTGGCTGGCATCCCGATCCCGATCCCAAGAAACGCC 615

DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200

QY 616 TGCATGTGTGACTCAGCGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGCTCTGGTGTC 675

DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220

QY 676 TGGGGAACTTTCCTTGGCGCCAAACCCATGAGCCAGGAGTCTTCACTCAAGTGTGCAAG 735

DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240

QY 736 TTCACCAAGTGATAAATGACACCATGAAAGAGCATCGC 774

DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 2

AAW05383

ID AAW05383 standard; protein; 253 AA.

XX AAW05383;

XX 31-DEC-1996 (first entry)

XX Human amyloid precursor protein protease.

XX Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
KW therapy.

XX Homo sapiens.

XX WO9631122-A1.

XX 10-OCT-1996.

XX 02-APR-1996; 96WO-US004294.

XX 04-APR-1995; 95US-00416257.

XX (ELIL) LILLY & CO ELI.

XX Dixon BP, Johnstone EM, Little SP;

XX WPI: 1996-464694/46.

XX N-PSDB; AAT39783.

XX New isolated human amyloid precursor protein protease - used to develop
PT prods. for the treatment or diagnosis of associated conditions, esp.
PT Alzheimer's disease.

XX Claim 1; Page 44-45; 55pp; English.

XX Human amyloid precursor protein protease (AAW05383) is involved in the
CC processing or clearance of amyloid precursor protein to form beta-amyloid
CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
CC obtd. from a human lung library. Recombinant protease can be produced in
CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
CC (partic. AV-120 host cells. It is used to develop products for the design
CC and testing of cpds. useful for treating or preventing conditions
CC associated with beta-amyloid peptide, esp. Alzheimer's disease

XX SQ Sequence 253 AA;

Alignment Scores:

Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x AAW05383 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTGCCCCCTGAGATCTTACTGCTATCTTACCTTGGAACT 75

DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20

QY 76 GCAGGAGAAGAGCCAGCGTGACAAATATTGATGGCGCCCATGTGCAAGAGCTCC 135

DB 21 AlaGlyGluGlnAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40

QY 136 CACCCATGGCAGGTGCCCTGCTCATGTGCATACGCTCCACTGCGGAGCGCTCTGGTC 195

DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60

Db 141 GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGGATGTCAGCTCATCTCCCCCAGGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValValLeuLeuSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATTCATGCTGCTGGCTGGCATCCCGACTCCCAAGAAACGCC 615
Db 181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGAATGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysIrpLeuAsnAspThrMetLysLysHisArg 253

RESULT 4

ABB84406
ID ABB84406 standard; protein; 253 AA.
XX
AC ABB84406;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human SCE protein.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.
XX
PN WO200262135-A2.
XX
PD 15-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-1B001300.
XX
PR 09-FEB-2001; 2001CA-02332655.
PR 09-FEB-2001; 2001DK-00000218.
XX
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
PI Egelrud T, Hansson L;
XX
DR WPI; 2002-643380/69.
DR N-PSDB; ABQ76226.
XX
PT Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
PS Claim 10; Page 58-59; 74pp; English.

XX This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a

CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents the human stratum
CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
CC with human kallikrein 7 (KLK7) and is used in the development of the
CC transgenic mammals described in the invention
XX

SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x ABB84406 (1-253)

QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAAAGATTATTGTATGGCGCCCATGTGTCAAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCATGCGAGTGGCCCTGCTGTCAGTGCGAATCAGTCCACTGCGGAGGCGTCTGGTTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 ANTGAGCGCTGGTGTCTCACTGCGCCCTGCAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValIleuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGTATACCTGGCGCACAGAGAGCTCAGAGGATCAAGGCTTCGAAGTCATTTCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATGACTCATGCTGTTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCCAACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCTCCGCTGGGCGACTACACAGAGCCAGATGTACCTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAGGTCATCTCTCCCCCAGGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATTCATGCTGCTGGCTGGCATCCCGACTCCCAAGAAACGCC 615
Db 181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGAATGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240

QY 736 TTCCACCAAGTGGTAATGACACCATGAAAAGCATCGC 774
 Db 241 PheThrIysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 5

AAU82740
 ID AAU82740 standard; protein; 253 AA.

AC AAU82740;
 XX

DT 23-APR-2002 (first entry)
 XX

DE Amino acid sequence of novel human protease #39.
 XX

KW Human; protease; cancer; immune-related disorder; cardiovascular disease;
 KW neuronal-associated disease; metabolic disorder; inflammatory disorder;
 KW nervous system disorder; sexual dysfunction; pain; mood disorder;
 KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
 KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
 KW ocular disease; cytostatic; enzyme.
 XX

OS Homo sapiens.
 XX

XX WO200200860-A2;
 PN

XX 03-JAN-2002.
 PD

XX 26-JUN-2001; 2001WO-US020171.
 PF

XX 26-JUN-2000; 2000US-0214047P.
 PR

XX (SUGEN-) SUGEN INC.
 PA

XX Plowman G, Whyte D, Sudarean S, Manning G, Caenepeel S;
 PI Charyczak G;
 PI

XX WPI; 2002-139913/18.
 DR

XX N-PSDB; ABK31782.
 DR

XX Nucleic acids encoding novel human proteases, useful for useful for
 PT treating diseases and disorders such as cancers, immune-related diseases
 PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
 PT disorders.
 PT

XX Claim 6; Fig 2N; 313pp; English.
 PS

XX The present invention relates to the isolation of novel human proteases,
 CC and the nucleic acids encoding them. The sequences of the invention are
 CC useful for treating diseases and disorders such as cancers (e.g. breast,
 CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
 CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
 CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
 CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
 CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
 CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
 CC disorders, cognitive disorders, hypotension, hypertension, psychotic
 CC disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease) and dyskinesias. The nucleic acids and polypeptides are also
 CC useful for treating viral infections caused by human immunodeficiency
 CC virus (HIV), and non-viral infections such as ocular disease (e.g.
 CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
 CC human proteases of the invention
 XX

SQ Sequence 253 AA;
 XX

Alignment Scores:

Pred. No.: 1.16e-134 Length: 253
 Score: 1364.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 76.6% Indels: 0
 DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x AAU82740 (1-253)

QY 16 ATGCCAAGATCCCTTCTCTGCCCCCTGCAGATCTTACTGTATCCTTAGCTTGGAAACT 75
 Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20

QY 76 GCAGGAGAAGAGCCAGGCGTGAAGATATTATGATGGCGCCCGCCATGTGCAAGAGGTCC 135
 Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40

QY 136 CACCCATGCGAGTGGCCCTGCTCAGTGGCAATCAGCTCCACATGCGAGCGCTCTCGTC 195
 Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60

QY 196 AATGAGCGTGGTGTCTACTGCGGCCCTCATGCAAGATGAATGAGTACACCGTCACCTG 255
 Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80

QY 256 GGCAGTGATACGCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGC 315
 Db 81 GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100

QY 316 CACCCCGGCTACTCCACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
 Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120

QY 376 CAGGCCAGGCTGTCCATCCATGGTGAAGAGTCAAGTGGCTGCCCTCCCGCTCGCAACCCCT 435
 Db 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140

QY 436 GGAACACCTGTACTCTCCGCTGGGGCAGTACCAAGAGCCAGATGACCTTTTCCC 495
 Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160

QY 496 TCTGACCTCATGCGTGGATGTCAGCTCATCTCCCGCCAGACTGCACGAGGTTTAC 555
 Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTr 180

QY 556 AAGGACTTACTGGAATAATCCATGCTGTGGCTGGCATCCCCGACTCCCAAGAAAAGCC 615
 Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200

QY 616 TGCAATGGTGACTCAGGGGACCGTTGGTGTGAGAGGTACCTCGCAAGGTCTGGTGTCC 675
 Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220

QY 676 TGGGGAACTTCCCTTTCGCGCCCAACCAATGACCCAGAGTCTACACTCAAGTGTGCAAG 735
 Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240

QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAGCATCGC 774
 Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 6
 ABU07440
 ID ABU07440 standard; protein; 253 AA.

XX ABU07440;
 AC

XX 28-JAN-2003 (first entry)
 DT

XX Protein differentially regulated in prostate cancer #43.
 DE

XX Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.

XX Homo sapiens.
 OS

XX WO200281638-A2.
 XX

PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010824.
XX
PR 06-APR-2001; 2001US-0281731P.
PR 06-APR-2001; 2001US-0281732P.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
XX Sun Z, Jay G;
XX
XX WPI; 2003-058520/05.
DR N-PSDB; ABX10343.
XX
XX Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.
XX
XX Claim 1; Page 293-294; 416pp; English.
XX
XX The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.
CC Preferably, the expression levels of at least 10 genes are determined.
CC (I) is also useful for identifying agents that modulate a biological
CC activity of a polypeptide differentially-regulated in prostate cancer
CC cells, which involves contacting a polypeptide differentially-regulated
CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.
CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer
XX
XX Sequence 253 AA;
SQ
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 6 Gaps: 0
US-09-905-083A-30 (1-969) x ABU07440 (1-253)
QY 16 ATGGCAAGATCCCTCTCTCGCCCTGCGAGATCTTACTGCTATCTTAGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGCAAGATTATTGATGGCGCCCTCATGTGCAAGAGCTCC 135
|||||

Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCTGCTCAGTGGCAATCAGTCCACTGGCGAGCGCTGCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAenGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGTGTCTCAGTCCGCCCTCAAGATGAATGAGTACACCGTGACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGGACAGGAGAGCTCAGAGATCAAGGCTCGAAGTCATTCGCG 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTTATGACCTCATCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGCTGTCATCCATGCTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAAACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAAACACCTGACTGCTCTCGGCTGGGCGACTACACAGAGCCAGATGTGACCTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGATGTCAGGCTCATCTCCCCCAGGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAAAAATTCATGCTGCTGCGCTGGCATCCCCGACTCCAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TCAATGTGTACTAGGGGACCGTGTGTGTGTCAGAGTACCTCGAAGTCTGGTGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGGCCCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 7
ABU07471
ID ABU07471 standard; protein; 253 AA.
XX
AC ABU07471;
XX
DT 28-JAN-2003 (first entry)
XX
DE Protein differentially regulated in prostate cancer #74.
XX
KW Prostate cancer; gene expression; differential regulation;
KW molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
XX
OS Homo sapiens.
XX
PN WO200281638-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010824.
XX
PR 06-APR-2001; 2001US-0281731P.
PR 06-APR-2001; 2001US-0281732P.
XX
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
PA
XX

PI Sun Z, Jay G;
XX WPI; 2003-058520/05.
DR N-PSDB; ABX10375.
XX
XX Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.
XX
XX Claim 1; Page 351; 416pp; English.
XX
XX The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.
CC Preferably, the expression levels of at least 10 genes are determined.
CC (I) is also useful for identifying agents that modulate a biological
CC activity of a polypeptide differentially-regulated in prostate cancer
CC cells, which involves contacting a polypeptide differentially-regulated
CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.
CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer
XX
XX Sequence 253 AA;
SQ
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 6 Gaps: 0
US-09-905-083A-30 (1-969) x ABU07471 (1-253)
QY 16 ATGGGAGAGATCCCTCTCCCTGGCCCTGCAGATCTTACTGCTATCTTACCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
Db 21 AlaGlyGluGluAlaGlnGlyAspGlyIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGTGCCCTCTGCTCAGTGGCAATCAGCTCCACCTGCGGAGGCGTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGTGGGTGCTCTGCTGCGCCCTGCAAGTGAATGAGTACACCGTGACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80

QY 256 GGCAAGTATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGCCCTCGAAGTCAATTCGCG 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLeuGlyAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTATAGCTCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTCTATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCCGAACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCCGCTGGGCGACTACACAGGAGCCAGATGTGACTTTCCTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGGTGGATGTCAGGCTCATCTCCCTCCCGCTGCCGAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTrp 180
QY 556 AAGGACTTACTGGAATAATTCATGCTGTGGCTGGCATCCCGACTCCCAAGAAAAAGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGTGTGACTCAGGGGAGACGTTGGTGTGCAGAGGTACCTGCAAGTCTGGTGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAGACTTTCCTTGGCGGCAACCAATGAGCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240
QY 736 TTCACCAAGTGAATAATGACACCACTGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 8
ABR58471
ID ABR58471 standard; protein; 253 AA.
XX
AC ABR58471;
XX
DT 07-JUL-2003 (first entry)
XX
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
XX
KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX
OS Homo sapiens.
XX
PN WO2003029468-A1.
XX
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031467.
XX
XX 02-OCT-2001; 2001US-0327135P.
PR 30-MAY-2002; 2002US-0384531P.
XX
XX (CORI-) CORIXA CORP.
XX
PI Algate PA, Mannion J;
XX
DR WPI; 2003-372001/35.
XX
XX New polynucleotide and polypeptide useful for diagnosing and/or treating
PT cancer, particularly ovarian cancer, and as a vaccine.
XX
XX Claim 2; Page 157-158; 169pp; English.
XX
XX The invention relates to a novel isolated polynucleotide. The
CC polynucleotides of the invention have cytostatic activity, and may have a

CC use in gene therapy, and in a vaccine. The composition and methods are
CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
CC The composition may also be used as a vaccine to prevent cancer. The
CC present sequence is used in the exemplification of the invention

XX SQ Sequence 253 AA;

Alignment Scores:
Pred. No.: 1,16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 6 Gaps: 0

US-09-905-083A-30 (1-969) x ABR58471 (1-253)

QY 16 ATGGCAAGATCCCTCTCTCGCCCTGCAGATCTTACTGCTTCTAGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGCCAGGTCACAGATTATTGATGGCGCCCATGTGCAAGAGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCTCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGTGTCTACTGCGGCCCTCAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGGACAGGAGCTCAGAGGATCAAGCCCTCGAAGTCATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACAGAGCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTCATCCATGTGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCCAACCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GMAACACCTGACTGCTCTCCGCTGGGCACTACACAGAGCCAGATGTGACCTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAGGCTCATCTCCCGCCAGACTGCACGAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValThr 180
QY 556 AAGGACTTACTGGAAATTCATGCTGTGCGCTGGCATCCCGACTCCCAAGAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGTGTGACTCAGGGGACCGTTGGTGTGAGAGGTACCTCGAAGGTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCAACCAATGACCCAGGAGTCTACACTCAAGTGTCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240
QY 736 TTCACCAAGTGAATAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 9

ID ADB80484

XX ADB80484 standard; protein; 253 AA.

AC ADB80484;
XX 04-DEC-2003 (first entry)
XX Ovarian cancer-associated protein #24.

DE KW cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW post-operative chemotherapy; radiation therapy; tumour prognosis;
XX pre-cancerous lesion detection.

XX OS Homo sapiens.

XX PN WO2002102235-A2.

XX PD 27-DEC-2002.

XX PF 18-JUN-2002; 2002WO-US019297.

XX PR 18-JUN-2001; 2001US-0299234P.

XX PR 27-AUG-2001; 2001US-0315287P.

XX PR 05-SEP-2001; 2001US-0317544P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Mack DH, Gish KC;

XX PI WPI; 2003-167431/16.

XX DR N-PSDB; ADB80483.

XX PT Detecting an ovarian cancer-associated transcript in a cell from a

XX PT patient, comprises contacting a biological sample from the patient with a

XX XX polynucleotide that hybridizes to an ovarian cancer gene.

XX PS Claim 13; Page 291; 332pp; English.

XX CC The invention relates to a method of detecting an ovarian cancer-

XX CC associated transcript in a cell from a patient, by contacting a

XX CC biological sample from the patient with a polynucleotide that selectively

XX CC hybridizes to a sequence at least 80% identical to any of one of 80

XX CC nucleic acid sequences given in the specification. The method is useful

XX CC in diagnosing ovarian cancer and in identifying and using agents and/or

XX CC targets that inhibit ovarian cancer. The nucleic acid molecule,

XX CC polypeptide and the antibody may also be used in detecting ovarian

XX CC cancers, monitoring and early detection of relapse following treatment,

XX CC monitoring response to therapy, selecting patients for post-operative

XX CC chemotherapy or radiation therapy, in selection of pre-cancerous lesions,

XX CC determining tumour prognosis, early detection of pre-cancerous lesions,

XX CC and as vaccines. This sequence corresponds to one of the proteins used

XX CC for the detection method of the invention.

XX SQ Sequence 253 AA;

XX Alignment Scores:

XX Pred. No.: 1,16e-134 Length: 253

XX Score: 1364.00 Matches: 253

XX Percent Similarity: 100.0% Conservative: 0

XX Best Local Similarity: 100.0% Mismatches: 0

XX Query Match: 76.6% Indels: 0

XX DB: 6 Gaps: 0

XX US-09-905-083A-30 (1-969) x ADB80484 (1-253)

XX QY 16 ATGGCAAGATCCCTCTCTCGCCCTGCAGATCTTACTGCTTCTAGCTTGGAACT 75

XX Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20

XX QY 76 GCAGGAGAGAGCCAGGTCACAGATTATTGATGGCGCCCATGTGCAAGAGCTCC 135

XX Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40

XX QY 136 CACCCATGCGAGTGGCTCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195

XX Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60

XX QY 196 AATGAGCGTGGTGTCTACTGCGGCCCTCAGATGAATGAGTACACCGTGCACTG 255

XX Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80

XX QY 256 GGCAGTGATACGCTGGCGGACAGGAGCTCAGAGGATCAAGCCCTCGAAGTCATCCGC 315

XX Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100

XX QY 316 CACCCCGGTACTCCACAGAGCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375

XX Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120

XX QY 376 CAGGCCAGGCTGTCATCCATGTGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCCAACCCT 435

XX Db 121 GlnAlaArgLeuSerSerMetValLysValLysValArgLeuProSerArgCysGluProPro 140

XX QY 436 GMAACACCTGACTGCTCTCCGCTGGGCACTACACAGAGCCAGATGTGACCTTTCC 495

XX Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160

XX QY 496 TCTGACCTCATGTGCGTGGATGTCAGGCTCATCTCCCGCCAGACTGCACGAAGGTTTAC 555

XX Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValThr 180

XX QY 556 AAGGACTTACTGGAAATTCATGCTGTGCGCTGGCATCCCGACTCCCAAGAAACGCC 615

XX Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200

XX QY 616 TGCATGTGTGACTCAGGGGACCGTTGGTGTGAGAGGTACCTCGAAGGTCTGGTGTC 675

XX Db 201 CysAsnGlyAspSerGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220

XX QY 676 TGGGGAACCTTCCCTTGGCGCAACCAATGACCCAGGAGTCTACACTCAAGTGTCAAG 735

XX Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240

XX QY 736 TTCACCAAGTGAATAATGACACCATGAAAAAGCATCGC 774

XX Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

XX RESULT 9

XX ID ADB80484

XX ADB80484 standard; protein; 253 AA.

Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
Qy 196 AATGAGCGCTGGGTGCTCACTGCGCCCACTGCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGlnTyrThrValHisLeu 80
Qy 256 GGCAGTATACGCTGGCGGCGAGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
Qy 316 CACCCCGCTACTCCACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
Qy 376 CAGGCCAGCTGTCATCCATGGTGAAGAGTCAAGTCTCCCGCTCGAACCCTT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
Qy 436 GGAACACCTGTTACTGCTCGGCTGGGGCACTACAGAGCCAGATGTGACCTTCCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
Qy 496 TCTGACCTCATGTGCGGGATGTCAGCTCATCTCTCCCGCCAGACTGCACGAAGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
Qy 556 AAGGACTTACTGGAATAATTCATGCTGCGCTGGCATCCCGCACTCCAGAAAAAGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
Qy 616 TGAATGGTGACTCAGGGGACCGTGGTGTGAGAGTACCTCGCAAGCTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
Qy 676 TGGGGAACTTTCCTTGGCGGCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
Qy 736 TTCACCAAGTGGATTAATCACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpLeuAsnAspThrMetLysLysHisArg 253

RESULT 10
ADJ68833
ID ADJ68833 standard; protein; 253 AA.
XX
AC ADJ68833;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID639.
XX
DE mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX

PA (MITO-) MITOKOR.
XX (BUCK-) BUCK INST AGE RES.
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 639; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nontropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 253 AA;
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 7 Gaps: 0
US-09-905-083A-30 (1-969) x ADJ68833 (1-253)
Qy 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTGTAGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr 20
Qy 76 GCAGGAGAGNAGCCCGGAGTACAGATATTATGATGGCGCCCGCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
Qy 136 CACCCATGCGAGGTGGCGCCCTGCTCAGTGGCAATCAGCTCCAGTGGGAGGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
Qy 196 AATGAGCGCTGGGTGCTCACTGCGCCCACTGCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGlnTyrThrValHisLeu 80
Qy 256 GGCAGTATACGCTGGCGGCGAGAGCTCAGAGGATCAGAGCTCGAAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
Qy 316 CACCCCGCTACTCCACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
Qy 376 CAGGCCAGCTGTCATCCATGGTGAAGAGTCAAGTCTCCCGCTCGAACCCTT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
Qy 436 GGAACACCTGTTACTGCTCGGCTGGGGCACTACAGAGCCAGATGTGACCTTCCC 495

Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAAATTCATGCTGTGCTGGCATCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeProAspSerLysLysAsnAla 200
QY 616 TCGAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGTACCTCGCAAGGTCGTGGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACTTCCCTTGGCGCCNACCATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAATGACACCATGAAAGCAATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 11
ID ADN39180
XX ADN39180 standard; protein; 253 AA.
AC ADN39180;
XX
XX
DT 17-JUN-2004 (first entry)
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
DE Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; lechemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnarary; gene therapy; vaccine.
XX Homo sapiens.
XX WO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002WO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX 21-NOV-2001; 2001US-0332464P.
XX 29-NOV-2001; 2001US-0334393P.
XX 03-DEC-2001; 2001US-0335394P.
XX 14-DEC-2001; 2001US-0340376P.
XX 08-JAN-2002; 2002US-0347211P.
XX 10-JAN-2002; 2002US-0347349P.
XX 08-FEB-2002; 2002US-0355250P.
XX 13-FEB-2002; 2002US-0356714P.
XX 20-FEB-2002; 2002US-0359077P.
XX 29-MAR-2002; 2002US-0368809P.
XX 04-APR-2002; 2002US-0370110P.
XX 12-APR-2002; 2002US-0372246P.
XX 05-JUN-2002; 2002US-0386614P.
XX 16-JUL-2002; 2002US-0396839P.
XX 22-JUL-2002; 2002US-0397775P.
XX 22-JUL-2002; 2002US-0397845P.
XX 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KB, Zlotnik A;
XX WPI; 2003-468649/44.
XX

DR N-PSDB; ADN39179.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO 498; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 253 AA;
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 7 Gaps: 0
US-09-905-083A-30 (1-969) x ADN39180 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTTGCTATCTCTAGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuThr 20
QY 76 GCAGGAGAAGAGCCAGGCGTGCACAGATTATTGATGGCGCCCATGTGCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGTGTCTCACTGCGCCCTGCAGATGAATGAGTACACCGCTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCAGAGAGCTCAGAGGATCAAGGCTCGAAGTCATTCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheAsg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATGACTCATCTGCTGTAAGTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTCACTCCATGTTGAAGAAAGTCAGGCTGCGCTCCCGCTGCCAACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAAACCACTGTACTGTCTCCGGCTGGGGGCATCTACCAGAGCCAGATGTACCTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180

QY	556	ARGGACTTACTGGAAAAATTCATGCTGTGCGCTGGCATGCCCTCAAGAAAAACGCC	615
Db	181	LysAspLeuLeuGluAsnSerMetLeuCyAlaGlyIleProAspSerLysLysAsnAla	200
QY	616	TSCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCCCTGCCAAGGCTCTGGTGTCC	675
Db	201	CysAsnGlyAspSerGlyGlyProLeuValCysargGlyThrLeuGlnGlyLeuValSer	220
QY	676	TGGGGAACCTTTCCCTTGGGGCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG	735
Db	221	TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys	240
QY	736	TTCCACCAAGTGGATTAATGACACCATGAAAAAGCATCGC	774
Db	241	PheThrLysTrpIleAsnAspThrMetLysLysHisArg	253
RESULT 12			
ID	ADL06515	ADL06515 standard; protein; 253 AA.	
AC	ADL06515;		
XX	ADL06515;		
DT	20-MAY-2004	(first entry)	
XX			
DE	Human tumour-associated antigenic target (TAT) polypeptide #14.		
XX			
KW	Human; tumour-associated antigenic target; TAT; cell death; tumour;		
KW	cancer; cytostatic.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004016225-A2.		
XX			
PD	26-FEB-2004.		
XX			
PF	19-AUG-2003; 2003WO-US025892.		
XX			
PR	19-AUG-2002; 2002US-0404809P.		
PR	21-AUG-2002; 2002US-0405645P.		
PR	23-SEP-2002; 2002US-0413192P.		
PR	15-OCT-2002; 2002US-0413008P.		
PR	15-NOV-2002; 2002US-0426847P.		
PR	02-JUL-2003; 2003US-0484959P.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;		
PI	Spencer SD, Wu TD, Zhang Z;		
XX			
DR	WPI; 2004-257144/24.		
DR	N-PSDB; ADL06435.		
XX			
PT	New antibody that binds to a tumor-associated antigenic target (TAT)		
PT	polypeptide, useful for preparing a composition for diagnosing or		
PT	treating cancer.		
XX			
PS	Claim 2; SEQ ID NO 95; 319pp; English.		
XX			
CC	The present invention relates to the isolation of human tumour-associated		
CC	antigenic target (TAT) polynucleotide and polypeptide sequences. Also		
CC	disclosed is an antibody that binds to a TAT polypeptide. The antibody is		
CC	a monoclonal antibody, an antibody fragment, a chimeric antibody or a		
CC	humanised antibody. It is conjugated to a growth inhibitory agent. It is		
CC	produced in bacteria or in CHO cells and induces death of a cell to which		
CC	it binds. The antibody is useful for preparing a composition for		
CC	diagnosing or treating tumours and cancer. The present sequence		
CC	represents a human TAT polypeptide of the invention.		
XX			
SQ	Sequence 253 AA;		
Alignment Scores:			
Pred. No.:	1.16e-134	Length:	253

Score:	1364.00	Matches:	253
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	76.6%	Indels:	0
DB:	8	Gaps:	0
US-09-905-083A-30 (1-1969) x ADL06515 (1-253)			
Qy	16	ATGCCAAGATCCCTCTCTCTCCCTCGAGATCTTACTGCTATCTTACGCTTGGAAATC	75
Db	1	MetaAlaArgSerLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr	20
Qy	76	GCAGGAGAAGAGCCAGGTGACAGATTATTGATGGGCCCCATGTGCAGAGAGGCTCC	135
Db	21	AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer	40
Qy	136	CACCATGGCAGGTGGCCCTCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCTCTGGTC	195
Db	41	HisProIrrGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal	60
Qy	196	AATGAGCGCTGGGTGTCACCTGCCGCCACCTGCAAGATGAATAGTACACCGTGCACCTG	255
Db	61	AsnGluArgIrrValLeuThrAlaAlaHisCysLysMetAsnGluTyrrThrValHisLeu	80
Qy	256	GGCAGTGAATACGCTGGGGCAGAGAGCTCAGAGGATCAAGGCTCGAAGTCATCTCCGC	315
Db	81	GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg	100
Qy	316	CACCCCGCTACTCCACAGACCCATGTTAATGACCTCAGCTCGTGAAGCTCAATAGC	375
Db	101	HisProGlyTyrrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer	120
Qy	376	CAGGCCAGGTGTTCATCATGGTGAAGAAATCAAGCTGCGCTCCCGCTGCCAACCCTCT	435
Db	121	GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro	140
Qy	436	GGAAACACCTGTACTGTCTCCGGCTGGGGCACTACACAGAGCCAGATGTGACCTTTCCC	495
Db	141	GlyThrThrCysThrValSerGlyTyrrpGlyThrThrThrSerProAspValThrPhePro	160
Qy	496	TCTGACCTCATGTCGGTGGATGTCAGCTCATCTCCCCCAGGACTGCACGAAGGTTTAC	555
Db	161	SerAspLeuMetCysValAspValLysLeuLysSerProGlnAspCysThrLysValTyrr	180
Qy	556	AAGGACTTACTTGGAAATTCATGCTGTGCGCTGGCATCCCGACTCCAAGAAAAACGCC	615
Db	181	LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla	200
Qy	616	TGCAATGGTGACTCAGGGGGACCGTGGTGTGCAGAGGTACCTCCAAGGCTGTGTGTC	675
Db	201	CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer	220
Qy	676	TGGGGAATTTCCCTTGGGGCAACCCATGACCAGGAGTCTACACTCAAGTGTGCAG	735
Db	221	TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrrThrGlnValCysLys	240
Qy	736	TTCAACCAAGTGGATAAATGCACCATGAAAAAGCATCGC	774
Db	241	PheThrLysIrrIleAsnAspThrMetLysLysHisArg	253
RESULT 13			
ID	ADN04182		
XX	ADN04182 standard; protein; 253 AA.		
AC	ADN04182;		
XX	XX		
DT	01-JUL-2004 (first entry)		
XX	XX		
DE	Antipsoriatic protein sequence #286.		
XX	antipsoriatic; gene therapy; psoriasis; diagnosis.		
OS	Homo sapiens.		

XX WO2004028479-A2.
XX
XX
XX PD 08-APR-2004.
XX PF 25-SEP-2003; 2003WO-US030907.
XX PR 25-SEP-2002; 2002US-0414006P.
XX (GETH) GENENTECH INC.
XX PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX WPI; 2004-305105/28.
DR N-PSDB; ADN04181.
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX
XX Claim 9; SEQ ID NO 576; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.
XX
XX Sequence 253 AA;
XX
Alignment Scores:
Pred. No.: 1.16e-134 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 8 Gaps: 0
US-09-905-083A-30 (1-969) x ADN04182 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTCTTACCTTGGAACCT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGACCCAGGTCACAGATTATGATGGCGCCCATGTCACAGAGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCCCTGCTCAGTGGCAATCAGCTCCAGTGGAGGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGGTGCTCACTGCGGCCCTCAAGATGAATGAGTACACCGCTGCACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysAlaMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGGCGACAGGAGCTCAGAGGATCAAGGCTCGAAGTCATTCGCG 315
DB 81 GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTTATGACCTCATGCTCGTGAAGCTCAATAGC 375
DB 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGCTGTATCCATCTGTGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAAACCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTGTCTCCGGCTGGGGCAGCTACACGAGGCCGAGATGTGACCTTTCC 495
DB 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160

QY 496 TCTGACCTCATGTGCGTGGATGTCAGGCTCAAGCTCTCTCCCGGAGCTGCACGAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATAATTCATGCTGTGCGTGGCATCCCGGACTCCAGAAACGCGC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGTGCTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTCCAGGCTGTGGTGCC 675
DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTTCCCTTGGCGCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAGCATCGC 774
DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 14
ADR72880
ID ADR72880 standard; protein; 253 AA.
XX
AC ADR72880;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human ovarian cancer-related tumour marker kallikrein 7 (hk7) protein.
XX
KW kallikrein 7; tumour marker; ovarian cancer;
KW epithelial ovarian carcinoma; human; serine protease; enzyme; KLK7.
XX Homo sapiens.
XX
PN WO2004075713-A2.
XX
PD 10-SEP-2004.
XX
PF 26-FEB-2004; 2004WO-CA000281.
XX
PR 26-FEB-2003; 2003US-0450406P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Diamandis EP;
XX
DR WPI; 2004-661815/64.
DR N-PSDB; ADR72881, ADR72882.
XX
XX Kallikrein markers detection method for detecting ovarian cancer in
PT patient, involves detecting kallikrein markers and CA125 in sample
PT amounts.
XX
PS Example 2; SEQ ID NO 10; 102pp; English.
XX
CC The invention relates to a novel method for detecting a plurality of
CC kallikrein markers associated with ovarian cancer. The method comprises
CC obtaining a sample from a patient and detecting in the sample a plurality
CC of kallikrein markers, and optionally carbohydrate antigen CA125, wherein
CC the kallikrein markers are selected from the group consisting of
CC kallikrein 5, kallikrein 6, kallikrein 7, kallikrein 8, kallikrein 10 and
CC kallikrein 11. The detected amounts of the kallikrein markers are
CC compared with standard amounts. The method of the invention may be useful
CC for detecting kallikrein markers associated with ovarian cancer in a
CC patient and thus for detecting ovarian cancer, particularly epithelial
CC ovarian carcinoma. The current sequence is that of the human ovarian
CC cancer-related tumour marker kallikrein 7 (hk7) protein of the invention
CC which is a secreted serine protease and is encoded by DNA located at
CC chromosome 19q13.4.
XX
SQ Sequence 253 AA;

Alignment Scores:			
Pred. No.:	1.16e-134	Length:	253
Score:	1364.00	Matches:	253
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	76.6%	Indels:	0
DB:	8	Gaps:	0
US-09-905-083A-30 (1-969) x ADR72880 (1-253)			
Qy	16	ATGCGCAAGATCCCTTCTCTCGCCCTGCGAGATCTTACTGCTATCTCTAGCTTGCGAAACT	75
Db	1	MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr	20
Qy	76	GCAGGAGAAAGACCCAGGGTGACAGATTATTGATGGCGCCCCCATGTGCAAGAGGCTCC	135
Db	21	AlaGlyGluGluAlaGlnGlyAspLysIleLeuAspGlyAlaProCysAlaAaGlySer	40
Qy	136	CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGGGAGGCGTCTGGTC	195
Db	41	HisProTrrpGlnValAlaLeuLeuSerGlyAenGlnLeuHisCysGlyGlyValLeuVal	60
Qy	196	AATGACGCGTGGGTGCTCTACTCCGCCCACTGCAAGATGAATAGTAGTACACCGTGCACCTG	255
Db	61	AsnGluArgTrrpValLeuThrAlaAlaHisCysLysMetAsnGluTrrpThrValHisLeu	80
Qy	256	GGCAGTGATACCTGGCGACAGGAGAGCTCAGAGGATCAAGGCTCGAAGTCATTCCGC	315
Db	81	GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg	100
Qy	316	CACCCCGGTACTCCACACAGACCCATGTTAATGACCTCAGCTCGTGAAGCTCAATAGC	375
Db	101	HisProGlyTrrSerThrGlnThrHisValAenAspLeuMetLeuValLysLeuAsnSer	120
Qy	376	CAGGCCAGGCTGTCTATCCATGCTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAAACCCCT	435
Db	121	GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro	140
Qy	436	GGAAACCACTGTACTGTCTCCGGCTGGGGCACTACACAGAGCCAGATGTGACTTTTCCC	495
Db	141	GlyThrThrCysThrValSerGlyTrrpGlyThrThrThrSerProAspValThrPhePro	160
Qy	496	TCAGCTCATGTGGGTGATGTCATGACTCATCTCCCGCCAGGACTGCACGAGGTTTAC	555
Db	161	SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr	180
Qy	556	AAGGACTTACTGAAAAATTCATGTGTGGCTGGCATCCCCGACTCCAAAGAAAACGCC	615
Db	181	LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla	200
Qy	616	TGCATGTGTGACTCAGGGGGACCGTGTGTGTGCAGAGGTACCCCTGCAAGTCTGGTGTCC	675
Db	201	CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer	220
Qy	676	TGGGGAACTTCCTTTGCGGGCCAAACCAATGACCCAGGAGTACACTCAAGTGTGCAAG	735
Db	221	TrrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrrThrGlnValCysLys	240
Qy	736	TTCCACCAAGTGGATAATGACACCATGAAAAAGCATCCG	774
Db	241	PheThrLysTrrpIleAsnAspThrMetLysLysHisArg	253
RESULT 15			
ADY67588			
ID	ADY67588 standard; protein; 253 AA.		
XX	ADY67588;		
AC			
XX			
DT	19-MAY-2005 (first entry)		
XX			
DE	Human kallikrein 7 protein SEQ ID NO:1.		
XX			

KW	kallikrein; serine protease; neurodegenerative disease;
KW	neurological disease; nootropic; neuroprotective; Alzheimer's disease;
KW	dementia.
XX	
OS	Homo sapiens.
XX	
PN	CA2468651-A1.
XX	
PD	13-DEC-2004.
XX	
PF	14-JUN-2004; 2004CA-02468651.
XX	
PR	13-JUN-2003; 2003US-0478486P.
XX	
PA	(MOUN) MOUNT SINAI HOSPITAL.
XX	
PI	Diamandis EP;
XX	
DR	WPI; 2005-092436/11.
DR	N-ESDB; ADY67589; ADY67590.
DR	GENBANK; L33404, AFI66330.
XX	
PT	Detecting kallikrein polypeptides or their polynucleotides, associated
PT	with neurodegenerative disease in patient, by identifying kallikrein
PT	polypeptides or polynucleotides, in patient's sample, comparing detected
PT	amount with standard.
XX	
PS	Disclosure; SEQ ID NO 1; 71pp; English.
XX	
CC	The invention describes a method for detecting kallikrein polypeptides or
CC	their encoding polynucleotides, associated with neurodegenerative disease
CC	in a patient, by taking a sample from a patient, detecting/identifying
CC	one or more kallikrein polypeptides or polynucleotides encoding
CC	kallikrein polypeptides, in the sample, and comparing the detected amount
CC	with an amount detected for a standard, where kallikrein polypeptides are
CC	chosen from kallikrein 7 and kallikrein 10. Nootropic; Neuroprotective;
CC	Cerebroprotective; Antiparkinsonian. The method is useful for diagnosing,
CC	detecting and monitoring a neurodegenerative disease in a subject. The
CC	method is also useful for assessing whether a patient is afflicted with
CC	or has a pre-disposition for Alzheimer's disease or frontotemporal
CC	dementia. The present sequence represents human kallikrein 7. Human
CC	tissue kallikreins are secreted serine proteases encoded by genes that
CC	are tandemly localized on chromosome 19, more specifically to region
CC	19q13.4.
XX	
SQ	Sequence 253 AA;

Alignment Scores:					
Pred. No.:	1.16e-134	Length:	253		
Score:	1364.00	Matches:	253		
Percent Similarity:	100.0%	Conservative:	0		
Best Local Similarity:	100.0%	Mismatches:	0		
Query Match:	76.6%	Indels:	0		
DB:	9	Gaps:	0		
US-09-905-083A-30 (1-969) x ADY67588 (1-253)					
Qy	16	ATGCGACAGTCCCTTCCTGCCCTGCAGATCTTACTGTCTATCCTAGCCTTGGAAC	T 75		
Dd	1	MetAlaargSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr	I 20		
Qy	76	GCAGGAGAAGAGCCCGGGGTGACAAGATTATTGATGGCGCCCATGTGCCAAGAGGCTCG	135		
Dd	21	AlaGlydGluAlaGlnGlyAspLysIleIleIleaspGlyAlaProCysAlaargGlySer	40		
Qy	136	CACCCATGGCAGGTGGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCTGTGTC	195		
Dd	41	HisProthrGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal	60		
Qy	196	AATGAGGCTGGGTGCTCAC TGCCGCCACCAC TGCAGATGAATGAGTACACCGTGACCTG	255		
Dd	61	AsnGluargTrpValLeuThrAlaAlaHisCysLysMetAsnGluThrValHisLeu	80		

QY	256	GGCAGTGATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTTCGCG	315
Db	81	GlySerAspThrLeuGlyAspArgAlaGlnArgIleuAlaSerLysSerPheArg	100
QY	316	CACCCCGGCTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC	375
Db	101	HisProGlyTyr-SerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer	120
QY	376	CAGGCCAGGCTGTATCCATGCTGTGAAGAAAGTCAGGTCGCCCTCCCGCTGCGAACCCCT	435
Db	121	GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro	140
QY	436	GGAAACACCTGTACTGCTCCGGCTGGGGCCTTACCACGAGCCAGATGTGACCTTTGCC	495
Db	141	GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro	160
QY	496	TCTGACCTCATGTGGTGGATGTCAAGCTCATCTCCCCCAGGACTGCACGAAGGTTTAC	555
Db	161	SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr	180
QY	556	AAGGACTTACTGGAAATTCATGCTGTGGCTGGCATCCCGACTCCGAAGAAAACGCC	615
Db	181	LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla	200
QY	616	TGCAATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTCTGGTGCC	675
Db	201	CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer	220
QY	676	TGGGGAACCTTTCCCTTGGCGCCAAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG	735
Db	221	TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys	240
QY	736	TTCCACCAAGTGATAAATGACACCATGAAAAAGCATCGC	774
Db	241	PheThrLysTrpIleAsnAspThrMetLysLysHisArg	253

Search completed: March 11, 2006, 01:45:01
Job time : 191 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 11, 2006, 01:45:18 ; Search time 9 Seconds
(without alignments)
2071.868 Million cell updates/sec

Title: US-09-905-083A-30
Perfect score: 1780
Sequence: 1 Ggatttcgggtccatggc.....aagaacacaaacccctcag 969

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DRV=xlp
-O=/abs/ABSWEB/spool/US0905083/runat_10032006_152455_29708/app_query.fasta_1
-DB=PIR -QFMT=fsttan -SUFFIX=n2p.rpr -MINMATCH=0_1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bts -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US0905083 @CGN 1 1 63 @runat_10032006_152455_29708 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WAE TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1364	76.6	253	2 A53968	serine proteinase
2	614	34.5	260	2 I56559	neuropilin - mouse
3	582	32.7	261	2 A29745	tissue kallikrein
4	568	31.9	261	2 S01971	tissue kallikrein
5	563	31.6	261	1 NGMSG	7S nerve growth fa
6	563	31.6	261	2 A34079	tissue kallikrein
7	561	31.5	246	1 TRRT1	trypsin (EC 3.4.21
8	552	31.0	261	1 QKMS1	tissue kallikrein
9	552	31.0	261	2 A31136	tissue kallikrein
10	551	31.0	261	2 A25606	tissue kallikrein
11	547.5	30.8	260	2 A37938	tissue kallikrein
12	541.5	30.4	246	1 TRRT2	trypsin (EC 3.4.21
13	536	30.1	248	2 S55067	trypsin (EC 3.4.21
14	535	30.1	229	1 TRBOTR	trypsin (EC 3.4.21

15	535	30.1	265	1	KQRTP	tissue kallikrein
16	534	30.0	261	1	TRMSM5	tissue kallikrein
17	533.5	30.0	244	2	A44284	tissue kallikrein
18	533.5	30.0	247	2	A27547	trypsin (EC 3.4.21
19	533	29.9	246	2	B25528	trypsin (EC 3.4.21
20	533	29.9	259	1	KQRTTN	tonin (EC 3.4.21.-
21	533	29.9	259	2	A29746	tissue kallikrein
22	533	29.9	259	2	B31136	tissue kallikrein
23	532.5	29.9	231	2	S31778	trypsin (EC 3.4.21
24	532	29.9	242	2	S31776	trypsin (EC 3.4.21
25	532	29.9	242	2	S31775	trypsin (EC 3.4.21
26	531	29.8	261	2	A41020	tissue kallikrein
27	527.5	29.6	247	1	TRDG	trypsin (EC 3.4.21
28	527	29.6	261	2	JE0236	tissue kallikrein
29	526.5	29.6	242	2	S49489	trypsin (EC 3.4.21
30	526.5	29.6	247	2	S13813	trypsin (EC 3.4.21
31	524	29.4	231	1	TRPGTR	trypsin (EC 3.4.21
32	521	29.3	261	2	A24378	tissue kallikrein
33	519	29.2	261	1	EGMSB	tissue kallikrein
34	518.5	29.1	243	2	A35871	trypsin (EC 3.4.21
35	518.5	29.1	262	1	KQHU	tissue kallikrein
36	516.5	29.0	256	1	NGMSA	7S nerve growth fa
37	516	29.0	257	2	S33772	tissue kallikrein
38	514	28.9	232	1	KQPG	tissue kallikrein
39	513	28.8	261	2	A29586	tissue kallikrein
40	511	28.7	238	2	S31779	trypsin (EC 3.4.21
41	510.5	28.7	247	1	A25852	tissue kallikrein
42	509	28.6	263	2	S15686	tissue kallikrein
43	508	28.5	246	1	TRDGC	trypsin (EC 3.4.21
44	506	28.4	261	2	S45303	tissue kallikrein
45	503	28.3	248	2	S55066	trypsin (EC 3.4.21

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
R;Accession: A53968
R;Hansson, L.; Stromqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Alignment Scores:			
Pred. No.:	1,49e-109	Length:	253
Score:	1364.00	Matches:	253
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	76.6%	Indels:	0
DB:	2	Gaps:	0

US-09-905-083A-30 (1-969) x A53968 (1-253)

QY	16	ATGGCAAGATCCCTTCCTCGCCCTGCAGATCTTACTGCTATCCTTAGCTTGAACCT 75
DB	1	MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr 20
QY	76	GCAGGAGAGAAGACCACCGGTGCAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135

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Db      21  AlaGlyGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer  40
QY      136  CACCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAGCTCAGCTGCGGAGCGCTCTGGTTC  195
Db      41  HisProTrpGlnValAlaLeuLeuSerGlyAenGlnLeuHisCysGlyGlyValLeuVal  60
QY      196  AATGACGGTGGTGGTCTCAGTCCGCCCACTGCAAGATCAATGAGTACACCGTGACCTGG  255
Db      61  AenGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGlnTrpThrValHisLeu  80
QY      256  GGCAGTGAATACGTCGGCGCACGAGAGCTCAGAGGATCAAGGCTTCGAAGTCATTCGCG  315
Db      81  GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg  100
QY      316  CACCCCGGTACTCCACAGACCCCATGTTAATGACCTCATGCTGCTGAAGCTCAATAGC  375
Db      101  HisProGlyTy-SerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer  120
QY      376  CAGGCCAGGCTGCATCCATGGTGAAGAACGATCAGGCTGCCCTCCCGCTGCCAACCCT  435
Db      121  GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro  140
QY      436  GGAACCACTGTACTCTCCGCTGGGCGCACTTACCACGAGCCAGATGTGACCTTTCC  495
Db      141  GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro  160
QY      496  TGTGACCTCATGTGCTGATGTCAGATCATCTCCCGCCAGGATGTCAGCGAGGTTTAC  555
Db      161  SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTy  180
QY      556  AAGGACTTACTGGAATTCATGCTGGCTGGCATCCCGGATCCCGATCCCAAGAAACGCC  615
Db      181  LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla  200
QY      616  TGCATATGGTGACTCAGGGGACCGTTGGTGTGACAGAGTACCTCGCAAGTCTGGTGTC  675
Db      201  CysAenGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer  220
QY      676  TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG  735
Db      221  TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys  240
QY      736  TTCACCAAGTGGATAATGACACCATGAAAGCAATCGC  774
Db      241  PheThrLysTrpIleAsnAspThrMetLysLysHisArg  253

RESULT 2
I56559
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishin
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease gen
A:Reference number: I56559; MUID:95348817; PMID:7623137
A:Accession: I56559
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: UNIPROT:Q61955; UNIPARC:UPI00000292C5; GB:D30785; NID:g1648847; PIDN
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRI>

Alignment Scores:
Pred. No.: 7, 4e-45 Length: 260
Score: 614.00 Matches: 114
Percent Similarity: 61.9% Conservative: 39
Best Local Similarity: 46.2% Mismatches: 88
Query Match: 34.5% Indels: 6
DB: 2 Gaps: 3
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US-09-905-083A-30 (1-969) x I56559 (1-260)
QY      37  CCCCTGCAGATCTTACTGCTATCTTAGCTTGGAAACTGCAGGAGAAGAGCCAGGTT  96
Db      11  ProTrpIleLeuLeuLeuLeuPheMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGly  30
QY      97  GACAAGATTATTGATGGGCGCCCATGTGCAAGAGGCTCCACCCATGGCAGGTGGCCCTG  156
Db      31  SerLysIleLeuGluGlyArgGluCysIleProHisSerGlnProTrpGlnAlaLeu  50
QY      157  CTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTCAATGAGCGCTGGGTGCTCACT  216
Db      51  PheGlnGlyGluArgLeuIleCysGlyGlyValLeuValGlyAspArgTrpValLeuThr  70
QY      217  GCGCGCCCACTGCAAGTGAATGAGTACACCGGTGACCTGGCGAGTGATACGCTG-----  270
Db      71  AlaAlaHisCysLysGlnLysTySerValArgLeuGlyAspHisSerLeuGlnSer  90
QY      271  GCGCAGCAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCCGCCACCCCGCTACTCC  330
Db      91  ArgAspGlnProGluGlnGlnIleGlnValAlaGlnSerIleGlnHisProCysTyAsn  110
QY      331  ACA-----CAGACCCATGTTAATGACCTCATGCTGCTGAGCTCAATAGCCAGGCC  381
Db      111  AsnSerAsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAla  130
QY      382  AGGCTGTCACTCCATCGTGAAGAAAGTCAGGCTGCCCTCCCGTGGCAACCCCTCGAACC  441
Db      131  AsnLeuGlyAspLysValLysProValGlnLeuAlaAsnLeuCysProLysValGlyGln  150
QY      442  ACCTGTACTCTCTCGGCTGGGCGCACTACCAGAGCCAGATGTGACCTTTCCCTCTGAC  501
Db      151  LysCysIleIleSerGlyTrpGlyThrValThrSerProGlnGluAsnPheProAsnThr  170
QY      502  CTCATGTGCTGGATGTCAAGCTCATCTCCCGCCAGGACTGACGAGGTTTACAGGAC  561
Db      171  LeuAsnCysAlaGluValLysIleTySerGlnAsnLysCysGluAlaTyPrGly  190
QY      562  TTACTGGAAATTCATCTGCTGCGCTGCATCCCGACTCCCAAGAAAACGCTGCAAT  621
Db      191  LysIleThrGluGlyMetValCysAlaGly----SerSerAsnGlyAlaAspThrCysGln  209
QY      622  GGTGACTCAGGGGGACCGTTGGTGTGCGAGAGTACCTCCCAAGGCTGTGCTCTGGGGA  681
Db      210  GlyAspSerGlyGlyProLeuValCysAspGlyMetLeuGlnGlyIleThrSerTrpGly  229
QY      682  ACTTTCCTTGGCGCCCAACCAATGACCAGAGAGTCTACACTCAAGTGTGCAAGTTCACC  741
Db      230  SerAspProCysGlyLysProGlyLysProGlyValTyThrLysIleCysArgTyThr  249
QY      742  AAGTGGATAATGACACCATG  762
Db      250  ThrTrpIleLysLysThrMet  256

RESULT 3
A29745
tissue kallikrein (EC 3.4.21.35) mgk-9 precursor, submandibular - mouse
N:Alternate names: glandular kallikrein MGK-9; major epidermal growth factor-binding prot
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: C29746; A29745; A27120; I70015
R:Drinkwater, C.C.; Evans, B.A.; Richards, R.I.
Biochemistry 26, 6750-6756, 1987
A:Title: Mouse glandular kallikrein genes: identification and characterization of the ge
A:Reference number: A90522; MUID:88107594; PMID:3322387
A:Accession: C29746
A:Molecule type: DNA
A:Residues: 1-261 <DRI>
A:Cross-references: UNIPROT:P15949; UNIPARC:UPI00000019BA; GB:M17985; NID:g193476; PIDN:
A:Experimental source: strain BALB/c, salivary gland
R:Blaber, M.; Isackson, P.J.; Bradshaw, R.A.
Biochemistry 26, 6742-6749, 1987
A:Title: A complete cDNA sequence for the major epidermal growth factor binding protein ;
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Db	164	LysPheGlnPheThrAspAspLeuTyxCysValAsnLeuLysLeuProAsnGluAsp	183
QY	541	TGCACGAAGGTTTACAAAGGACTTACTGGAATAATTCATATGTCGTGCGCTGGCATCCCGCAC	600
Db	184	CysAlaLysAlaHisIleGluLysValThrAspAlaMetLeuCysAlaGlyGluMetAsp	203
QY	601	TCCAAGAAAAACCGCTGCATGTGTGACTCAGGGGGACCGTTGGTGTGCAGAGTACCCCTG	660
Db	204	GlyGlyLysAspThrCysLysGlyAspSerGlyGlyProLeuIleCysAspGlyValLeu	223
QY	661	CAGGTCGTGTCTCTGGGAACTTTCCTTGGCGGCAACCAATGACCCAGAGTCTTAC	720
Db	224	GlnGlyIleThrSerTrpGlyHisThrProCysGlyGluProAspMetProGlyValTy	243
QY	721	ACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGCACCAATGAAAAAGCAT	771
Db	244	ThrLysLeuAsnLysPheThrSerTrpIleLysAspThrMetAlaLysAsn	260

RESULT 6

A34079

N;Alternate names: kallikrein (EC 3.4.21.35) p1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C;Accession: A34079; S10700
R;Brady, J.M.; Wines, D.R.; MacDonald, R.J.
Biochemistry 28, 5203-5210, 1989
A;Title: Expression of two kallikrein gene family members in the rat prostate.
A;Reference number: A34079; MUID:89352606; PMID:2765531
A;Accession: A34079
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-261 <BRA>
A;Cross-references: UNIPROT:P36374; UNIPARC:UPI000012DEE7; GB:M27216; GB:M27215; GB:M27216; GB:M27215
R;Elmoujahed, A.; Gutman, N.; Brillard, M.; Gauthier, P.
FEBS Lett. 265, 137-140, 1990
A;Title: Substrate specificity of two kallikrein family gene products isolated from the
A;Reference number: S10698; MUID:90306305; PMID:2194829
A;Accession: S10700
A;Molecule type: protein
A;Residues: 25-43;112-138 <ELM>
A;Cross-references: UNIPARC:UPI0000175BEB; UNIPARC:UPI0000175BEC
A;Experimental source: submaxillary gland
A;Note: 125-Lys was also found
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;25-253/Domain: trypsin homology <TRY>
F;25-111/Product: tissue kallikrein p1 light chain #status experimental <MAT1>
F;112-261/Product: tissue kallikrein p1 heavy chain #status experimental <MAT2>
F;45,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores:

Pred. No.:	1.86e-40	Length:	261
Score:	563.00	Matches:	112
Percent Similarity:	58.3%	Conservative:	39
Best Local Similarity:	43.2%	Mismatches:	94
Query Match:	31.6%	Indels:	14
DB:	2	Gaps:	3

US-09-905-083A-30 (1-969) x A34079 (1-261)

QY	34	CTGCCCCGTCAGATCTTACTGCTATCTTAGCCCTTGGAAATGCAGAGNAGAGCCGAC	93
Db	3	LeuLeuLeuPheLeuIleLeuSerLeuGlyTrpAsnAspAlaAlaProProGlyGln	22
QY	94	GGTGACAAGATTATTGATGCGGCCCTCATGTGCAAGAGGCTCCCAACCATGGCAGGTGGCG	153
Db	23	---SerArgIleIleGlyGlyPheAsnCysGlyLysAsnSerGlnProTrpGlnValAla	41
QY	154	CTGCTCAGTGGCAATCAGCTTCCACTCGGAGGCGTCTCGTCAATGAGCGCTGGGTGCTC	213

Db 42 ValTyrHisPheAsnGluProGlnCysGlyGlyValLeuLeuHisProSerTrpValIle 61

Qy 214 ACTCGCCGCTCAAGATGAATAGTAGACACCGTCACCGTGACGTGGCAGGTATACGTCTG--- 270
|||||
Db 62 ThrAlaAlaHisCysTyrSerValAsnTyrGlnValTrpLeuGlyArgAsnAsnLeuLeu 81
|||
Qy 271 ---GGCGACAGAGACTCAGAGGATCAAGGCCTCGAAGCTCATTCGCCACCACCGGCTAC 327
|||
Db 82 GluAspGluProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProGlyPhe 101
|||
Qy 328 TCCACA-----CAGACCCCATTGTTAAATGACCTC 354
|||
Db 102 AsnLeuAspIleIleLysAsnHisThrArgLysProGlyAsnAspTyrSerAsnAspLeu 121
|||
Qy 355 ATGCTCGTGAAGCTCAATAGCACCGGCTGCTCATCCATGGTGAAGAAAGTACAGGCTG 414
|||
Db 122 MetLeuLeuHisLeuLysThrProAlaAspIleThrAspGlyValLysValIleAspLeu 141
|||
Qy 415 CCCTCCCGCTGGAAACCCCTCGAACCACTGTACTGTCTCCGGCTGGGGCAGCTACCAAG 474
|||
Db 142 ProThrGluGluProLysValGlySerThrCysLeuThrSerGlyTyrGlySerIleThr 161
|||
Qy 475 AGCCAGATGTGACCTTTCCCTCTGACCTCATGTGGTGGTGGATGTCACAGCTCATCTCCCC 534
|||
Db 162 ProLeuLysTrpGluPheProAspAspLeuGlnCysValAsnIleHisLeuLeuSerAsn 181
|||
Qy 535 CAGGACTGCACGAAGCTTTACAAAGCACTTACTGGAAAATTCACATGCTGTGGCTGGCATC 594
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Db 182 GluLysCysIleLysAlaTyrAsnAspGluValThrAspValMetLeuCysAlaGlyGlu 201
|||
Qy 595 CCCGACTCCAAGAAAAACGCTTCAATGTGTAAGTCAAGGGGACCGTTGGTGTGCAGAGT 654
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Db 202 MetAspGlyGlyLysAspIleCysLysGlyAspSerGlyGlyProLeuIleCysAspGly 221
|||
Qy 655 ACCCTGCNAGTCTGGTGTCTCTGGGAATTTCCCTTGGCGGCCAACCAATGACCCAGA 714
|||
Db 222 ValLeuGlnGlyIleThrSerTrpGlySerMetProCysGlyGluProAsnLysProSer 241
|||
Qy 715 GTCTACACTCAAGTGTGCAAGTTACCAAGTGGATAAATGACACCATGMAAAGCAT 771
|||
Db 242 VallyrThrLysLeuIleLysPheThrSerTrpMetLysLysValMetLysGluAsn 260
|||

RESULT 7

TRRT1

N; tryptsin (EC 3.4.21.4) I precursor - rat

C; Alternate names: trypsinogen I

C; Species: Rattus norvegicus (Norway rat)

C; Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004

C; Accession: B22657; A00948

J; Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984

A; Title: Structure of two related rat pancreatic trypsin genes.

A; Reference number: A22657; MUID:85054880; PMID:6094547

A; Accession: B22657

A; Molecule type: DNA

A; Residues: 1-246 <CRA>

A; Cross-references: UNIPROT:P00762; UNIPARC:UPI00001376DD; GB:J00778; NID:g206507; PIDN:I

A; Note: The authors translated the codon ATC for residue 6 as Leu and GAC for residue 17

R; MacDonald, R.J.; Stary, S.J.; Swift, G.H.

J. Biol. Chem. 257, 9724-9732, 1982

F; 1-15/Domain: signal sequence #status predicted <SIG>

F; 16-23/Domain: activation peptide #status predicted <APT>

F; 24-246/Product: trypsin I #status predicted <ENZ>

A; Reference number: A00948; MUID:82265624; PMID:6896710

A; Accession: A00948

A; Molecule type: mRNA

A; Residues: 1-246 <MAC>

A; Cross-references: UNIPARC:UPI00001376DD; GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:

C; Genetics:

A; Introns: 14/1; 67/2; 152/1; 197/3

C; Superfamily: trypsin; trypsin homology

C; Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F; 1-15/Domain: signal sequence #status predicted <SIG>

F; 16-23/Domain: activation peptide #status predicted <APT>

F; 24-246/Product: trypsin I #status predicted <ENZ>

F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Alignment Scores:
Pred. No.: 2,75e-40 Length: 246
Score: 561.00 Matches: 113
Percent Similarity: 60.1% Conservative: 39
Best Local Similarity: 44.7% Mismatches: 87
Query Match: 31.5% Indels: 14
DB: 1 Gaps: 5

US-09-905-083A-30 (1-969) x TRRT1 (1-246)

QY	16	ATGGCAAGATCCCTTCTCTGCGCCCTGCGAGATCTTACTGCTATCTCTGCTTGGAACT	75
Db	1	MetSerAlaLeuLeuLeuLeuAlaValAlaValAlaPheProLeuGlu---	19
QY	76	GCAGGAGAAGAGCCAGGCGTGAACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC	135
Db	20	-----AspAspAspIleValGlyTyrThrCysProGluHisSer	34
QY	136	CACCCATGCGAGTGCCCTGCTCAGTGCATCAGCTCCACTGCGGAGCGCTCTCGTC	195
Db	35	ValProTyrGlnValSerLeuAsnSerGlyTyrHisPhe---CysGlyGlySerLeuIle	53
QY	196	AATGACGCTGGTGTCTACTGCGCCCTGCGCAATGCAATGATGATGACCTGACCTG	255
Db	54	AsnAspGlnTrpValValSerAlaAlaHisCysTyrLysSerArgIleGlnValArgLeu	73
QY	256	GGCAGTGATACGCTG-----GGCAGCAGGAGAGCTCAGAGGATCAAGGCTCG	303
Db	74	GlyGluHisAsnIleAsnValLeuGluGlyAspGlu-----GlnPheIleAsnAlaIa	91
QY	304	AGTCTATTCGCGACCCCGCTACTCCACAGACCCATGTTAATGACCTCATGCTCGTG	363
Db	92	LysIleIleLysHisProAsnTyrSerSerTrpThrLeuAsnAsnAspIleMetLeuIle	111
QY	364	AGCTCAATAGCAGCCAGGCTGTCATCCATGCTGAAGAAAGTCAGGCTGCCCTCCGC	423
Db	112	LysLeuSerSerProValLysLeuAsnAlaArgValAlaProValAlaLeuProSerAla	131
QY	424	TGGAAACCCCTGGAACCACTGTACTGTCTCGGCTGGGCACTACACAGAGCCAGAT	483
Db	132	CysAlaProAlaGlyThrGlnCysLeuIleSerGlyTyrPGLYAsnThrLeuSerAsnGly	151
QY	484	GTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCGGACTCC	543
Db	152	ValAsnAsnProAspLeuLeuGlnCysValAspAlaProValLeuSerGlnAlaAspCys	171
QY	544	ACGAAGTTTACAGGACTTACTGGAAATTCATGCTGTGCGTGGCATCCCGACTCC	603
Db	172	GluAlaAlaTyrProGlyGluIleThrSerSerMetIleCysValGlyPheLeuGluGly	191
QY	604	AAGAAAACGCTGCAATGTGCTCAGGGGACCGTGTGTGTCAGAGGTACCTGCAA	663
Db	192	GlyLysAspSerCysGlnGlyAspSerGlyPGLYProValValCysAsnGlnLeuGln	211
QY	664	GGTCTGGTCTCTGGGGAATTTTCCCTTGGCGCCAAACCAATGACCCAGGAGTCTACACT	723
Db	212	GlyIleValSerTrpGly--TyrGlyCysAlaLeuProAspAsnProGlyValTyrThr	230
QY	724	CAAGTGTGCAAGTTTACCAAGTGGATAAATGACACCATG	762
Db	231	LysValCysAsnPheValGlyTrpIleGlnAspThrIle	243

RESULT 8

QKMS1
Tissue kallikrein (EC 3.4.21.35) mGK-1 precursor, submandibular - mouse
N:Alternate names: glandular kallikrein; kininogenin
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004

C:Accession: A00941
R:Mason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I.
Nature 303, 300-307, 1983
A:Title: Structure of mouse kallikrein gene family suggests a role in specific processing
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
A:Reference number: A00941; MUID:83219214; PMID:602295
A:Accession: A00941
A:Molecule type: DNA
A:Residues: 1-261 <MAS>
A:Cross-references: UNIPROT:P00755; UNIPARC:UPI0000001AOC; GB:V00829; NID:G52775; PIDN:CI
A:Experimental source: Quakenbush inbred strain
C:Comment: mGK-1 belongs to a family of 25 to 30 homologous kallikrein genes.
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release 1
C:Genetics:
A:Gene: mGK-1
A:Map position: 7
A:Introns: 16/1; 69/2; 165/1; 210/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland; zym
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-24/Domain: activation peptide #status predicted <APT>
F:25-261/Product: tissue kallikrein, submandibular #status predicted <MPT>
F:25-253/Domain: trypsin homology <TRY>
F:31-173,50-66,152-219,184-198,209-234/Disulfide bonds: #status predicted
F:65,120,213/Active site: His, Asp, Ser #status predicted
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1,65e-39 Length: 261
Score: 552.00 Matches: 109
Percent Similarity: 57.6% Conservative: 39
Best Local Similarity: 42.4% Mismatches: 93
Query Match: 31.0% Indels: 16
DB: 1 Gaps: 3

US-09-905-083A-30 (1-969) x QKMS1 (1-261)

QY	49	TTACTGCTATCTTACCTTGGAACTGCGAGAGAACGCCAG-----GGTGAC	99
Db	4	LeuIleLeuPheLeuAlaLeuSerLeuGlyIleAspAlaAlaProValGlnSer	23
QY	100	AGATTATTGATGGCGCCCATGTGCAAGAGCTCCACCATGGCAGGTGCCCTGCTC	159
Db	24	ArgIleValGlyGlyPheLysCysGluLysAsnSerGlnProTrpHisValAlaValTyr	43
QY	160	AGTGGCAATCAGCTCCACTGCGAGCGCTCTGTCCTCAATGAGCGCTGGGTGCTCACTGCC	219
Db	44	ArgTyrLysGluTyrIleCysGlyValLeuLeuAspAlaAsnTrpValLeuThrAla	63
QY	220	GCCCACTGCAAGATGAATGATACCGGTGACCTGGGCGAGTGATACGCTG-----GGC	273
Db	64	AlaHisCysTyrTyrGluLysAsnAsnValTrpLeuGlyLysAsnLeuTyrGlnAsp	83
QY	274	GACAGAGCTCAGAGGATCAAGCGCTCGAAGTCAATTCGGCCACCCCGCTACTCCACA	333
Db	84	GluProSerAlaGlnHisArgLeuValSerLysSerPheLeuHisProCysTyrAsnMet	103
QY	334	CAGACCCATGTTAAT-----GACCTCATGCTC	360
Db	104	SerLeuHisArgAsnArgIleGlnAsnProGlnAspAspTyrSerTyrAspLeuMetLeu	123
QY	361	GTGAAGCTCAATPAGCAGGCCAGGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCC	420
Db	124	LeuArgLeuSerLysProAlaAspIleThrAspValValLysProIleAlaLeuProThr	143
QY	421	CGCTGGAAACCCCTGGAAACCACTGTACTGCTCGGCTGGGCACTACACGAGCCCA	480
Db	144	GluGluProLysLeuGlySerThrCysLeuAlaSerGlyTrpGlySerIleIleProVal	163
QY	481	GATGTGACCTTCCCTCTGCTGCTGATGTCAAGCTCATCTATCTCCCGCCAGGAC	540
Db	164	LysPheGlnTyrAlaLysAspLeuGlnCysValAsnLeuLysLeuLeuProAsnGluAsp	183
QY	541	TGCACGAAGTTTACAAGACTTACTGGAAATTCATGCTGTGCGCTGGCATCCCGAC	600


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Db 184 CyAspLysAlaTyrValGlnLysValThrAspValMetLeuCysAlaGlyValLysGly 203
QY 601 TCAAGAAAGAAACCCCTGCAATGCTACTCAGGGGGGACCGTGTGGTGTGCAGAGGTACCCCTG 660
Db 204 GlyGlyLysAspThrCysLysGlyAspSerGlyGlyProLeuLeuCysAspGlyValLeu 223
QY 661 CAAGTCTGTGTCTCTGGGGAACCTTCCCTTGGGGGCAACCCCAATGACCCAGGAGTCTAC 720
Db 224 GlnGlyLeuThrSerTrpGlyTyrAsnProCysGlyGluProLysLysProGlyValTyr 243
QY 721 ACTCAAGTGTGCAAGTTCACCAAGTGTGATAAATGACACCATGAAAGCAT 771
Db 244 ThrLysLeuLeuLysPheThrSerTrpLysAspThrLeuAlaGlnAsn 260

RESULT 9
A31136
tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat
N:Alternate names: glandular prokallikrein 7, submandibular, proteinase A
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text change 09-Jul-2004
C:Accession: A31136; S10698; S10699; D41429; B41429; S09315
R:Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
A:Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A:Reference number: A31136; MUID:89088074; PMID:2849988
A:Accession: A31136
A:Molecule type: DNA
A:Residues: 1-261 <CHE>
A:Cross-references: UNIPROT:P36373; UNIPARC:UPI000012DEB6; GB:M19647; GB:J02837; NID:920
R:Simoujeh, A.; Gutman, N.; Brillard, M.; Gauthier, F.
FEBS Lett. 265, 137-140, 1990
A:Title: Substrate specificity of two kallikrein family gene products isolated from the
A:Reference number: S10698; MUID:90306305; PMID:2194829
A:Accession: S10698
A:Molecule type: protein
A:Residues: 25-36 <ELM>
A:Cross-references: UNIPARC:UPI0000175BB3
A:Accession: S10699
A:Molecule type: protein
A:Residues: 112-139 <EL2>
A:Cross-references: UNIPARC:UPI0000175BB3
R:Kato, H.; Nakanishi, E.; Enyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: wi
A:Reference number: A41429; MUID:88198057; PMID:3482210
A:Accession: D41429
A:Molecule type: protein
A:Residues: 112-133 <KAT>
A:Cross-references: UNIPARC:UPI0000175BB5
A:Accession: B41429
A:Molecule type: protein
A:Residues: 25-34, 'D', '36-45', 'S', '47-67', 'X', '69-75' <KA2>
A:Cross-references: UNIPARC:UPI0000175BB5
R:Brady, J.M.; MacDonald, R.J.
Arch. Biochem. Biophys. 278, 342-349, 1990
A:Title: The expression of two kallikrein gene family members in the rat kidney.
A:Reference number: S09315; MUID:90225801; PMID:2183721
A:Accession: S09315
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 43-45, 'S', '47-114', 'A', '116-261' <BRA>
A:Cross-references: UNIPARC:UPI0000175BB7
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-261/Product: tissue prokallikrein 7, submandibular #status predicted <MAT>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Alignment Scores: 1.65e-39 Length: 261
Pred. No.: 552.00 Matches: 110
Score:
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Percent Similarity: 57.8% Conservative: 38
Best Local Similarity: 43.0% Mismatches: 94
Query Match: 31.0% Indels: 14
DB: 2 Gaps: 3
US-09-905-083A-30 (1-969) x A31136 (1-261)

QY 46 ATCTTACTGCTATCCCTTAGCTTGGAACTGCAGGAGAAAGAGCCACGGGT---GACAAG 102
Db 5 IleLeuPheLeuAspLeuSerLeuGlyGlnIleAspAlaProGlyGlnSerArg 24
QY 103 ATTATTGATGGCGCCCATGTCACAGAGCTCCACCCATGGCAGGTGGCCCTGCTCAGT 162
Db 25 ValIleGlyGlyTyrLysCysGluLysAsnSerGlnProTrpGlnValAlaLeuTyrSer 44
QY 163 GGCAATCAGCTCCACTGCGGAGCGCTCTGGTCAATCAGCGCTGGGTGCTCACTGCCGCC 222
Db 45 PheThrLysTyrLeuCysGlyGlyValLeuIleAspProSerTrpValIleThrAlaAla 64
QY 223 CACTGCAAGATGAATGATGACCGGTGACCTGGCGAGTGATACGCTG-----GGCGAC 276
Db 65 HisCysSerSerAsnAsnTyrGlnValTrpLeuGlyArgAsnAsnLeuLeuGluAspGlu 84
QY 277 AGGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGCCACCCCGGCTACTCCACA--- 333
Db 85 ProPheAlaGlnHisArgLeuValSerGlnSerPheProHisProAspTyrLysProPhe 104
QY 334 -----CAGACCCACTGTTAATGACTCATCTCATCTCCCCCAGGAGTGC 363
Db 105 LeuMetArgAsnHisThrArgLysProGlyAspAspHisSerAsnAspLeuMetLeuLeu 124
QY 364 AAGCTCAATPAGCAGCCAGCGGTGTCATCCATGTGTAAGAAAGTCAAGGTGCCCTCCCGC 423
Db 125 HisLeuSerGlnProAlaAspIleThrAspGlyValLysValIleAspLeuProThrGlu 144
QY 424 TCGGAACCCCTGGACACCACTGACTGTCTCCGGTGGGGGACTACCCAGGAGCCAGAT 483
Db 145 GluProLysValGlySerThrCysLeuAlaSerGlyTrpGlySerThrLysProLeuIle 164
QY 484 GTGACCTTTCCCTCTGACCTCATGTGCTGGAGTGTCAAGCTCATCTCCCCCAGGAGTGC 543
Db 165 TrpGluPheProAspAspLeuGlnCysValAsnIleHisLeuLeuSerAsnGluLysCys 184
QY 544 ACGAAGTTTACAAGCACTTACTTGGAAATTCATCTGTGCGCTGGCATCCCGACTCC 603
Db 185 IleLysAlaTyrLysGluLysValThrAspLeuMetLeuCysAlaGlyGluLeuGluGly 204
QY 604 AAGAAAACGCTGCAATGCTGACTCAGGGGAGCCGTTGGTGTGCAGAGGTACCTGCAA 663
Db 205 GlyLysAspThrCysThrGlyAspSerGlyProLeuLeuCysAspGlyValLeuGln 224
QY 664 GGTCTGTGCTCTGGGGAACCTTTCCCTTGGGCAACCAACCCAGGAGGTACACT 723
Db 225 GlyIleThrSerTrpGlySerValProCysAlaLysThrAsnMetProAlaIleTyrThr 244
QY 724 CAAGTGTGCAAGTTCACCAAGTGGATTAATGACACCATGAAAAAGCAT 771
Db 245 LysLeuIleLysPheThrSerTrpLysGluValMetLysGluAsn 260

RESULT 10
A25606
tissue kallikrein (EC 3.4.21.35) submandibular precursor - mouse
N:Alternate names: glandular kallikrein; kininogenin
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C:Accession: A25606; S06661
R:Van Leeuwen, B.H.; Evans, B.A.; Tregear, G.W.; Richards, R.I.
J. Biol. Chem. 261, 5529-5535, 1986
A:Title: Mouse glandular kallikrein genes. Identification, structure, and expression of t
A:Reference number: A25606; MUID:86168299; PMID:3007510
A:Accession: A25606
A:Molecule type: DNA
A:Residues: 1-261 <VAN>
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A;Accession: A00944

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 11, 2006, 01:39:02 ; Search time 52.9 Seconds
(without alignments)
2584.714 Million cell updates/sec

Title: US-09-905-083A-30
Perfect score: 1780
Sequence: 1 ggaattccgggtccatggc.....aagaacacacaaacccctcag 969

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=UniProt -QFWT=fastan -SUFFIX=n2p_rup -MINMATCH=0.1 -LOORCL=0 -LOOPEXT=0
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-LOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 05.80:*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1364	76.6	253	1	KLK7 HUMAN
2	1028.5	57.8	249	1	KLK7 MOUSE
3	760	42.7	140	2	QSR567_PONPY
4	614	34.5	260	1	NRPN MOUSE
5	612.5	34.4	293	1	KLK5 HUMAN
6	612.5	34.4	293	1	Q532R3_HUMAN
7	611.5	34.4	260	1	NRPN RAT
8	609.5	34.2	276	2	O8C9E6_MOUSE
9	608.5	34.2	293	2	Q53F68_HUMAN
10	604.5	34.0	246	2	O6P320_MOUSE
11	593.5	33.3	250	2	O8CGR5_MOUSE
12	589	33.1	293	2	O9D140_MOUSE
13	586.5	32.9	242	2	O80VS4_MOUSE
14	583	32.8	251	1	KLK14_HUMAN
15	583	32.8	251	2	Q6B089_HUMAN
16	582.5	32.7	260	1	NRPN_HUMAN

17	582	32.7	261	1	KLK9_MOUSE
18	580.5	32.6	260	2	Q8IW69_HUMAN
19	578	32.5	277	1	KLK13_HUMAN
20	576.5	32.4	239	2	Q63275_RAT
21	573.5	32.2	255	1	KLK15_SAGOE
22	571.5	32.1	250	1	KLK11_HUMAN
23	568	31.9	261	1	KLK11_MOUSE
24	567.5	31.9	254	1	KLK4_HUMAN
25	567.5	31.9	254	2	Q4VB16_HUMAN
26	563	31.6	256	1	KLK15_HUMAN
27	563	31.6	261	1	KLK3_MOUSE
28	563	31.6	261	1	KLK8_RAT
29	561.5	31.5	255	2	O6IS70_HUMAN
30	561.5	31.5	276	2	Q9QN3_MOUSE
31	561	31.5	246	1	TRY1_RAT
32	560	31.5	263	1	KLK27_MOUSE
33	559.5	31.4	254	2	Q4VB17_HUMAN
34	559.5	31.4	255	2	Q96RQ0_HUMAN
35	556	31.2	275	2	Q8IXD7_HUMAN
36	555	31.2	248	1	KLK12_HUMAN
37	555	31.2	276	2	Q53YL3_HUMAN
38	554.5	31.2	234	2	Q9CV76_MOUSE
39	553.5	31.1	249	2	Q9QYN4_MOUSE
40	552.5	31.0	260	1	ESTA_CANFA
41	552	31.0	261	1	KLK1_MOUSE
42	552	31.0	261	1	KLK6_MOUSE
43	552	31.0	261	1	KLK7_RAT
44	551.5	31.0	246	2	Q6IE66_RAT
45	551	31.0	261	2	Q8C232_MOUSE

ALIGNMENTS

RESULT 1

KLK7_HUMAN STANDARD; PRT; 253 AA.

AC P49862; Q8M5N9; Q8NFV7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum
 DE chymotryptic enzyme) (hSCCE).
 GN Names=KLK7; Synonyms=PRSS6, SCCE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
 RC TISSUE=Skin;
 RX MEDLINE=94308225; PubMed=8034709;
 RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
 RA Egelrud T.;
 RT "Cloning, expression, and characterization of stratum corneum
 RT chymotryptic enzyme. A skin-specific human serine proteinase.";
 RL J. Biol. Chem. 269:19420-19426(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
 RC TISSUE=keratinocyte;
 RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
 RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
 RA Diamandis E.P.;
 RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
 RT enzyme is a new member of the human kallikrein gene family - genomic
 RT characterization, mapping, tissue expression and hormonal
 RT regulation.";
 RL Gene 254:119-128(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepier B., Wang K.;

RT Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.;
RL Gene 257:119-130(2000).
RN [4]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Wallbrandt P., Egelrud T.;
RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
RT mice; a model for chronic itchy dermatitis.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6]

RP NUCLEOTIDE SEQUENCE [RNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
RP AND TISSUE SPECIFICITY.
RC "TISSUE-Ovarian carcinoma;
RX MEDLINE=22823266; PubMed=12738725;
RA Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.;
RT "Differential splicing of KIK5 and KLK7 in epithelial ovarian cancer
RT produces novel variants with potential as cancer biomarkers.";
RL Clin. Cancer Res. 9:1710-1720(2003).
RN [6]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]

RP CHARACTERIZATION.
RX MEDLINE=95314630; PubMed=7794273;
RA Skytt A., Stroemqvist M., Egelrud T.;
RT "Primary substrate specificity of recombinant human stratum corneum
RT chymotryptic enzyme.";
RL Biochem. Biophys. Res. Commun. 211:586-589(1995).

CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
CC structures in the cornified layer of the skin in the continuous
CC shedding of cells from the skin surface. Specific for amino acid
CC residues with aromatic side chains in the P1 position. SCCE
CC cleaves insulin B chain at 6-Leu|-Cys-7, 16-Tyr|-Leu-17, 25-
CC Phe|-Tyr-26, and 26-Tyr|-Thr-27. Could play a role in the
CC activation of precursors to inflammatory cytokines.
CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
CC also observed at the apical membrane and in cytoplasm at the
CC invasive front.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=P49862-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=P49862-2; Sequence=VSP_013581;

CC TISSUE SPECIFICITY: Abundantly expressed in the skin and is
CC expressed by keratinocytes in the epidermis. Also expressed in the
CC brain, mammary gland, cerebellum, spinal cord and kidney. Lower
CC levels in salivary glands, uterus, thymus, thyroid, placenta,
CC trachea and testis. Up-regulated in ovarian carcinoma, especially
CC late-stage serous carcinoma, compared with normal ovaries and
CC benign adenomas (at the protein level).

CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
CC cell line.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: L33404; AAC37551.1; -; mRNA.
DR EMBL: AF166330; AAD49718.1; -; Genomic DNA.
DR EMBL: AF243527; AAG33360.1; -; Genomic DNA.
DR EMBL: AF332589; AAK69624.1; -; Genomic DNA.
DR EMBL: AF411214; AAN03662.1; -; mRNA.
DR EMBL: AF411215; AAN03663.1; -; mRNA.
DR EMBL: BC032005; AAH32005.1; -; mRNA.
DR PIR: A53968; A53968.
DR HSSP: P00760; 1EZX.
DR MEROPS: S01.300; -.
DR Ensembl: ENSG00000169035; Homo sapiens.
DR HGNC: HGNC:6368; KLK7.
DR H-InvDB: HIX0015373; -.
DR MIM: 604438; -.
DR GO: GO:0008236; P:serine-type peptidase activity; TAS.
DR GO: GO:0008544; P:epidermis development; TAS.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYPSIN; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydrolase; Protease; Serine protease; Signal; Zymogen.
FT SIGNAL 1 22 Activation peptide.
FT PROPEP 23 29 Kallikrein 7.
FT CHAIN 30 253 Peptidase S1.
FT DOMAIN 30 250 Charge relay system (By similarity).
FT ACT_SITE 70 70 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 205 205 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 246 246 By similarity.
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 /FTID=VSP_013581.
FT CONFLICT 226 226 C -> W (in Ref. 6; AAH32005).
SQ SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A668 CRC64;

Alignment Scores:
Pred. No.: 1,24e-108 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 1 Gaps: 0

US-09-905-083A-30 (1-969) x KLK7_HUMAN (1-253)

QY 16 ATGGCAAGATCCCTCTCTCTGCCCCCTGCAGATCTTACTCTATCTTCTAGCCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAACCCAGGGTGACAGATATTATTGATGGGCCCCCATGTGCAAGAGCTCC 135

Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaAaGlySer 40
QY 136 CACCATGGAGGAGGCGCTCTCAGTGGCAATCAGCTCCAGTGGAGGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGTGGTCTCAGTGGCGCCCTCAGTGGCAATCAGTGGAGGCGCTCTGGTC 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
QY 256 GGCAGTGTATCGCTGGCGCAGCAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCGGCTACTCCACAGACCCATGTTAATGACCTCATGCTGTGTAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGCCAGGCTGTCATCCATGCTGAGAAAGTCAAGGCTGGCTGGCTGGCAACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACACCTGTACTCTCCGCTGGCGCACTACACAGAGCCAGATGTGACTTTCCTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCGCAGGAGCTCAGCAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuLysLeuLysLeuLysValThr 180
QY 556 AAGGACTTACTGAAATTCATGCTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGCATGTGTGACTCAGGGGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTCCGCGCCCAACCAATGACCCAGGAGTGTACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValThrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGTAATGACATCATCATCATCATCATCATCATCATCATCATCATCAT 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 2
ID_KLK7_MOUSE STANDARD; PRT; 249 AA.
AC Q91VE3; Q9R048;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (Thymopain).
DE Names:KLK7; Synonyms:Prss6, Scce;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=C57BL/6; TISSUE=Thymus;
CC Yamauchi N.;
RT "A novel cDNA cloning of mouse serine protease, thymopain.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=129/SvJ;
RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
RA Wallbrant P., Egelrud T.;
RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in

RT mice; a model for chronic itchy dermatitis.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikiaki I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gliss C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierzki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reid D.J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Huan Z., Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Waki J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Iotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 1-234, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Tail;
RX MEDLINE=99399282; PubMed=10469296;
DOI=10.1046/j.1523-1747.1999.00662.x;
RA Baekman A., Strandén P., Bratteand M., Hansson L., Egelrud T.;
RT "Molecular cloning and tissue expression of the murine analog to human
RT stratum corneum chymotryptic enzyme.";
RL J. Invest. Dermatol. 113:152-155 (1999).
CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
CC structures in the cornified layer of the skin in the continuous
CC shedding of cells from the skin surface. Specific for amino acid
CC residues with aromatic side chains in the P1 position. SCCE
CC cleaves insulin B chain at 6-Leu-I-Cys-7, 16-Tyr-I-Leu-17, 25-


```

Pred. No.: 1-23e-56 Length: 140
Score: 760.00 Matches: 138
Percent Similarity: 99.3% Conservative: 1
Best Local Similarity: 98.6% Mismatches: 1
Query Match: 42.7% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x QSR567_PONPY (1-140)

QY 355 ATGCTCGTGAAGTCAATACCCAGGCGAGCTGTCTATCCATGTGTGAAGAAAGTCAGCGTG 414
Db 1 MetLeuValLysLeuAenSerGlnAlaArgLeuSerMetValLysLysValArgLeu 20
QY 415 CCTCCCGCTGCAGACCCCTGCAGACCTGTACTGTCTCCGCTGGGCGATACCAAG 474
Db 21 ProSerArgCysGlyProProGlyThrThrCysThrValSerGlyTrpGlyThrThrThr 40
QY 475 AGCCAGATGTGACCTTTCCTCTGACCTCATGTGCGTGTGATGTCAAGCTCATCTCCCC 534
Db 41 SerProAspValThrPheProSerAspLeuMetCysValAspValLysLeuLysSerPro 60
QY 535 CAGGACTGCACGAAGTTTACAAGGACTTACTCGAAATTTCCATGCTGTGCGTGCATC 594
Db 61 GlnAspCysThrLysValTyrLysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIle 80
QY 595 CCGGACTCCAGAAAACGCTCGCATGTGACTCAGGGGACCGTGTGTGTCAGAGGT 654
Db 81 ProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyProLeuValCysArgGly 100
QY 655 ACCCTGCAGGCTGTGTCTCTCGGGAACCTTCCCTTGGCGGCAACCCCAATGACCCAGGA 714
Db 101 ThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGlnProAsnAspProGly 120
QY 715 GTCTACACTCAAGTGTGCAAGTTCACCAAGTGTGATAATGACACCATGATAAAAGCATCGC 774
Db 121 ValTyrThrGlnValCysLysPheThrLysTrpIleAsnAspThrIleLysLysHisArg 140

RESULT 4
NRPN MOUSE
ID NRPN MOUSE STANDARD; PRT; 260 AA.
AC O6195;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE Neuropein precursor (SC 3.4.21.-) (NP) (Kallikrein 8).
GN Names=Klk8; Synonyms=Nrpn; Prrs19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Hippocampus;
RX MEDLINE=95348817; PubMed=7623137;
RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
RA Ito J., Nishino H., Aikawa S., Kiyama H., Shiosaka S.;
RT "Expression and activity-dependent changes of a novel limbic-serine
RT protease gene in the hippocampus.";
RL J. Neurosci. 15:5088-5097(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
RT "Cloning and assignment of mouse neuropein gene, Prrs19 to chromosome
RT 7B4.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Czech II; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Capletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROTEIN SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS
RP SPECTROMETRY.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
RA Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
RT "Characterization of recombinant and brain neuropein, a plasticity-
RT related serine protease.";
RL J. Biol. Chem. 273:11189-11196(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
RC TISSUE=Hippocampus;
RX MEDLINE=99134351; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
RA Shiosaka S., Hakoshima T.;
RT "Crystal structure of neuropein, a hippocampal protease involved in
RT kindling epileptogenesis.";
RL J. Biol. Chem. 274:4220-4224(1999).
CC -I- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin.
CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -I- ENZYME REGULATION: Strongly inhibited by diisopropyl
CC fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
CC fluoride.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
CC mouse brain and is localized at highest concentration in pyramidal
CC neurons of the hippocampal CA1-3 subfields.
CC -I- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260;
CC NOTE=Ref.4.
CC -I- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
CC NOTE=Ref.4.
CC -I- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -I- SIMILARITY: Contains 1 peptidase S1 domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; D30785; BAA06451.1; -; mRNA.
CC EMBL; AB032202; BAA92435.1; -; Genomic_DNA.
CC EMBL; BC055895; AAH55895.1; -; mRNA.
CC PIR; I56559; I56559.
CC PDB; 1NPM; X-ray; A/B=33-257.
CC MEROPS; S01.244; -.
CC Ensembl; ENSMUSG00000064023; Mus musculus.
CC MGI; MGI:892018; Klk8.
CC InterPro; IPR001254; Peptidase_S1_S6.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC

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RL J. Biol. Chem. 274:30033-30040(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4".
RL Anticancer Res. 19:2843-2852(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepier B., Wang X.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Genes 257:119-130(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in desquamation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF168768; AAF03101.1; -; mRNA.
CC EMBL; AF135028; AAD26429.1; -; Genomic DNA.
CC EMBL; AF243527; AAG3358.1; -; Genomic DNA.
CC EMBL; AY359010; AAG89369.1; -; mRNA.

DR EMBL; BC008036; AAH08036.1; -; mRNA.
DR HSSP; P00760; 1EZX.
DR MEROPS; S01.017; -.
DR Ensembl; ENSG00000167754; Homo sapiens.
DR HGNC; HGNC:6366; KLK5.
DR MIM; 605643; -; C:extracellular space; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
DR GO; GO:0008544; P:epidermis development; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 293 Kallikrein 5.
FT DOMAIN 67 290 Peptidase S1.
FT ACT_SITE 108 108 Charge relay system (By similarity).
FT ACT_SITE 153 153 Charge relay system (By similarity).
FT ACT_SITE 245 245 Charge relay system (By similarity).
FT CARBOHYD 69 69 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 208 208 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 252 252 N-linked (GlcNAc...) (Potential).
FT DISULFID 73 206 By similarity.
FT DISULFID 93 109 By similarity.
FT DISULFID 178 279 By similarity.
FT DISULFID 185 251 By similarity.
FT DISULFID 217 231 By similarity.
FT DISULFID 241 266 By similarity.
FT CONFLICT 25 56 Missing (in Ref. 3).
SQ SEQUENCE 293 AA; 32020 MW; D92C2F5609E5946 CRC64;

Alignment Scores:
Pred. No.: 7,32e-44 Length: 293
Score: 612.50 Matches: 114
Percent Similarity: 66.0% Conservative: 43
Best Local Similarity: 47.9% Mismatches: 72
Query Match: 34.4% Indels: 9
DB: 1 Gaps: 4

US-09-905-083a-30 (1-969) x KLK5_HUMAN (1-293)

QY 76 GCAGGAGAGAGAGCCAGGCGTGC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAspAlaArgSerSerSerArgIleAsnGlySerAspCys 73
QY 124 GCAAGAGAGGTCCTCCACCCATGGCAGGTGGCC---CTGCTCAGTGGCAATCAGTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaLeuLeuLeuArgProAsnGlnLeuTyrCys 93
QY 181 GGAGGCGTCTCGTCAATGAGCGCTGGTCTCCTCCTCCGCGCCCATCTCAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysArgLysVal 113
QY 241 TACACCGTCACCTGGCGAGTATACGCTGGGC-----GACAGGAGAGCTCAGAGG 291
Db 114 PheArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnMet 133
QY 292 ATCAAGGCGCTCAAGTCATTCCCGCCACCCCGGCTACTCCACAGACCCCATGTTAATGAC 351
Db 134 PheGlnGlyValIysSerIleProHisProGlyTyrSerHisProGlyHisSerAsnAsp 153
QY 352 CTCATGCTCGTGAAGCTCAATAGCCAGCCAGGCGTCTCATCCATGCTGTAAGAAGTCAGG 411
Db 154 LeuMetLeuIleLeuLeuAsnArgAlaIleArgProThrLysAspValArgProIleAsn 173
QY 412 CTGCGCCCTCCGCTGGCGAACCCCTGGAACCACTGTACTGTCTCCGGCTGGGCGACTACC 471
Db 412 CTGCGCCCTCCGCTGGCGAACCCCTGGAACCACTGTACTGTCTCCGGCTGGGCGACTACC 471

RT, "Serine proteases in rodent hippocampus.";
 RL J. Biol. Chem. 273:23004-23011(1998).
 CC -I- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity. Has a strong proteolytic activity against
 CC fibronectin (By similarity).
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -I- TISSUE SPECIFICITY: Restricted to hippocampus.
 CC -I- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -I- SIMILARITY: Contains 1 peptidase S1 domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AJ005641; CRA06643.1; -; mRNA.
 DR HSSP: Q61955; INPM.
 DR SMR: O88780; 33-256.
 DR MEROPS: S01.244; -.
 DR Ensembl: ENSRNOG0000018580; Rattus norvegicus.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYPSIN_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Glycoprotein; Hydrolase; Protease; Serine protease; Signal; Zymogen.
 KW SIGNAL 1 28 Potential.
 FT PROPEP 29 32 By similarity.
 FT CHAIN 33 260 Neuropein.
 FT DOMAIN 33 257 Peptidase S1.
 FT ACT_SITE 73 73 Charge relay system (By similarity).
 FT ACT_SITE 120 120 Charge relay system (By similarity).
 FT ACT_SITE 212 212 Charge relay system (By similarity).
 FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
 FT DISULFID 39 173 By similarity.
 FT DISULFID 58 74 By similarity.
 FT DISULFID 145 246 By similarity.
 FT DISULFID 152 218 By similarity.
 FT DISULFID 184 198 By similarity.
 FT DISULFID 208 233 By similarity.
 SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;
 Alignment Scores:
 Pred. No.: 8.71e-44 Length: 260
 Score: 611.50 Matches: 114
 Percent Similarity: 62.3% Conservative: 40
 Best Local Similarity: 46.2% Mismatches: 86
 Query Match: 34.4% Indels: 7
 DB: 1 Gaps: 4
 US-09-905-083a-30 (1-969) x NRPN_RAT (1-260)
 QY 46 ATCTTACTGTATCTTCTAGCTTGGAACTGCAGGA---GAAGAAGCCAGGCTGACAG 102
 Db 13 IleLeuLeuPheLeuLeuMetGlyAlaTrpAlaGlyLeuThrArgAlaGlnGlySerLys 32
 QY 103 ATTATTGATGGCCCCCATGTGCAAGAGGCTCCACCCATGGCAGGTGGCCCTGCTCAGT 162
 Db 33 IleLeuGluGlnGluCysLysProHisSerGlnProTrpGlnThrAlaLeuPheGln 52
 QY 163 GGAATCACTCCACTCGGAGCGGCTCTGTCATAGCGTGGGTCTCACTGCGGCC 222
 Db 53 GlyGluArgLeuValCysGlyGlyValLeuValGlyAspArgTrpValLeuThrAlaAla 72
 QY 223 CACTGCAAGATGATGAGTACACCGCTGCACCTGGCAGTCATACGCTG-----GGCGAC 276
 Db 73 HisCysLeuLysAspLysTyrSerValArgLeuGlyAspHisSerLeuGlnLysArgAsp 92

QY 277 AGGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGCGCACCCCGGCTACTCCACA--- 333
 Db 93 GluProGluGlnGluIleGlnValAlaArgSerIleGlnHisProCysPheAsnSerSer 112
 QY 334 -----CAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGCCAGGCTG 387
 Db 113 AsnProGluAspHisSerHisAspIleMetLeuIleArgLeuGlnAsnSerAlaAsnLeu 132
 QY 388 TCATCCATGGTGAAGAAGTCAAGCTCCTCCCGCTCCCGCTGCGAACCCTCGAACCACCTGT 447
 Db 133 GlyAspLysValLysProIleGluLeuAlaAsnLeuCysProLysValGlyGlnLysCys 152
 QY 448 ACTGTCTCCGCTGGGCGACTACACGAGCCAGATGTGACCTTTCCTCTGACCTCATG 507
 Db 153 IleIleSerGlyTrpGlyThrValThrSerProGlnGluAsnPheProAsnThrLeuAsn 172
 QY 508 TGGCTGGATGTCAAGTCAATCTCCCGCCAGGACTGCGACGAGGTTTACAGGACTTACTG 567
 Db 173 CysAlaGluValLysIleTyrSerGlnAsnLysCysGluArgAlaTyrProGlyLysIle 192
 QY 568 GAAATTCATGCTGTGCGCTGCGCTCCCGACTCCAGAGAAACCGCTGCAATGGTGAC 627
 Db 193 ThrGluGlyMetValCysAlaGly---SerSerAsnGlyAlaAspThrCysGlnGlyAsp 211
 QY 628 TCAGGGGACCGTTGTTGTCGACAGGTACCTCCAGAGTGTGCTGCTGCTGGGAACCTTC 687
 Db 212 SerGlyGlyProLeuValCysAsnGlyValLeuGlnGlyIleThrTrpGlySerAsp 231
 QY 688 CTTTGGGCGCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGG 747
 Db 232 ProCysGlyLysProGluLysProGlyValTyrThrLysIleCysArgTyrThrAsnTrp 251
 QY 748 ATAAATGACACCATGAAAAAG 768
 Db 252 IleLysLysThrMetGlyLys 258
 RESULT 8
 Q8CGR6 MOUSE PRELIMINARY; PRT; 276 AA.
 AC Q8CGR6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Glandular kallikrein KLK13.
 GN Name=KLK13;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;
 RA Olsson A.Y., Lundwall A.;
 RT "Organization and evolution of the glandular kallikrein locus in Mus
 musculus.";
 RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Adams M., Murai R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY152432; AAN78420.1; -; Genomic_DNA.
 DR HSSP: P00760; 1EZX.
 DR MEROPS: S01.306; -.
 DR Ensembl: ENSMUSG00000054046; Mus musculus.
 DR MGI: MGI:95292; Klk13.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00089; Trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYPSIN_SPC; 1.

DR PROSITE; PS00240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30360 MW; 33E189C67492FDCA CRC64;

Alignment Scores:
Pred. No.: 1 31e-43 Length: 276
Score: 609.50 Matches: 120
Percent Similarity: 63.2% Conservative: 43
Best Local Similarity: 46.5% Mismatches: 76
Query Match: 34.2% Indels: 19
DB: 2 Gaps: 6

US-09-905-083A-30 (1-969) x Q8CGR6_MOUSE (1-276)

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QY 46 ATCTTACTGCTATCCCTTACCTTGGAACTGCAGGAGAGAACCCAGGGTGACAAAGATT 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 IleAlaCysLeuThrLeuAlaLeu---SerGluGlyIleSerArgAspTyrProLysIle 26
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 106 ATGTATGGCGCC-----CCATGTGCAGAGGC 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 27 LeuAsnGlyThrAsnGlyThrSerGlyPheLeuProGlyTyrThrCysLeuProHis 46
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 133 TCCACCCCATGCGAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACCTGCGAGGCGCTCTG 192
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 47 SerGlnProTrrpGlnAlaLeuLeuIleArgGlyArgLeuLeuCysGlyGlyValLeu 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 193 GTCATATGAGCGTGGTGTCTACTGCGCCCACTGCAAGATGAATGAGTACACCGTGCAC 252
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 67 ValHisProLysTrrpValLeuThrAlaHisCysArgLysAspGlyTyrThrValHis 86
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 253 CTGGGAGTGTATCGCTGGCC-----GACAGGAGAGCTCAGAGATCAAGSCCTCGAG 306
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 LeuGlyLysHisAlaLeuLeuArgValGluAsnGlyGluGlnAlaMetGluValValArg 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 307 TCATTCGCGCACCCCGCTACTCC---ACACAGACCCATGTTAAT-----GACCTC 354
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 107 SerIleProHisProGluTyrGlnValThrProThrHisLeuAsnHisAspHisAspIle 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 355 ATGCTCTGTAAGCTCAATAGCAGGCGCAGCTGTCTATCCATGGTGAAGAAATCAGGCTG 414
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 127 MetLeuLeuGluLeuLysSerProValGlnLeuSerSerHisValArgThrLeuLysLeu 146
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 415 CCTTCC--CGTGGCAACCCCTGCAACCACTGTACTGTCTCCGGCTGGGGCACTACC 471
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 SerAlaAspAspCysLeuProThrGlyThrCysCysArgValSerGlyTrrpGlyThrThr 166
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 472 ACAGGCCAGAGTGTGACCTTCCCTCTGACCTCATGTGGTGGATGTCAAGCTCATCTCC 531
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 167 ThrSerProGlnValAsnTyrProLysThrLeuGlnCysAlaAsnIleGluLeuArgSer 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 532 CCCCAGGACTGCAGAGGTTTACAAAGGACTTACTGGAAATTTCCATGTGTGCGCTGCG 591
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 AspGluGluCysArgGlnValTyrProGlyLysIleThrAlaAsnMetLeuCysAlaGly 206
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 592 ATCCCGCACTCCNAGAAAAACGCTCAATGTGACTCAGGGGACCGTGGTGTGTCAGA 651
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 207 ThrLysGluGlyLysAspSerCysGluGlyAspSerGlyGlyProLeuIleCysAsn 226
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 652 GTTACCTCCAAAGTCTGTGTCTGGGAACCTTTCCTTGGCGGCAACCCCAATGACCCA 711
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 227 GlyLysLeuTyrGlyIleSerTrrpGlyAspPheProCysGlyGlnProAsnArgPro 246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 712 GGAGTCTACCACTCAAGTGTGCAAGTTTACCACCAATGGATGAATGACACCACTGAAA 765
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 247 GlyValTyrThrArgValSerLysTyrLeuArgTrrpIleArgGluIleIleArg 264
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 9

Q53F68 HUMAN

ID Q53F68_HUMAN PRELIMINARY; PRT; 293 AA.

AC Q53F68;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

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DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Kallikrein 5 preproprotein variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Maruyama K., Sugano S.;
RT "Oligo-capping : a simple method to replace the cap structure of
RT eucaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174 (1994).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT "Construction and characterization of a full length-enriched and a 5'-
RT end-enriched cDNA library.";
RL Gene 200:149-156 (1997).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK223421; BAD97141.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 293 AA; 32034 MW; B24E30C4FDCA51DF CRC64;
```

Alignment Scores:
Pred. No.: 1 62e-43 Length: 293
Score: 608.50 Matches: 113
Percent Similarity: 65.8% Conservative: 43
Best Local Similarity: 47.7% Mismatches: 72
Query Match: 34.2% Indels: 9
DB: 2 Gaps: 4

US-09-905-083A-30 (1-969) x Q53F68_HUMAN (1-293)

```
QY 79 GGAGAGAAGCCCGGCTGAC-----AAGATTATTGATGGCGCCCATGTGCA 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 55 GlyGluAspAlaAspSerAspAspSerSerArgIleAsnGlySerAspCysAsp 74
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 127 AGAGGCTCCCACTGCGAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGCGGA 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 75 MetHisThrGlnProTrrpGlnAlaProLeuLeuAcgProAsnGlnLeuTyrCysGly 94
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 184 GCGCTCTGTCATAGAGCGGTGGTGTCTACTGCGGCCCATGCAAGATGAATGATGATAC 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 95 AlaValLeuValHisProGlnTrrpLeuLeuThrAlaHisCysArgLysLysValPhe 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 244 ACCGTGCACTGGGCGAGTATACGCTGGGC-----GACAGGAGAGCTCAGAGGATC 294
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 115 ArgValArgLeuGlyHisTyrSerLeuSerProValTyrGluSerGlyGlnMetPhe 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 295 AAGGCTCGAAGTCAATCCCGCCACTCTCCACAGACCCCATGTTAATGACCTTC 354
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 135 GlnGlyValLysSerIleProHisProGlyTyrSerHisProGlyHisSerAsnAspLeu 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 355 ATGCTCTGTAAGCTCAATAGCAGGCGCAGCTGTCTATCCATGGTGAAGAAATCAGGCTG 414
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 155 MetLeuIleLysLeuAsnArgIleArgProThrLysAspValArgProIleAsnVal 174
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 415 CCCTCCCGCTCGAACCCTGGAACCTGTACTGTCTCCGGTGGGGCACTACCAAG 474
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 SerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrrpGlyThrThrLys 194
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 475 AGCCCAAGATGTGACCTTTCCCTCTCACTCATGTGCTGGATGTCGAAGCTCATCTCCCC 534
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 195 SerProGlnValHisPheProLysValLeuGlnCysLeuAsnIleSerValLeuSerGln 214
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 535 CAGGACTGCAGCAAGGTTTACAAAGGACTTACTGGAATAATTCATGTCGCTGGCATC 594
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 215 LysArgCysGluAspAlaTyrProArgGlnIleAspAspThrMetPheCysAlaGly--- 233
```


QY	595	CCC	GACTCCCAAGAAAACCGCTGCCTGAATGGTGA	CTCAGGGGGAGCCGTTGGTGTGCAGAGCT	654
		:::			
Db	234	AspLySaLaGlyA	ArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsnGly		253
QY	655	ACCCTGCAAGGTCTGGTGTCTCTGGGGAACTTTCCCTTGGCGGCAACCCCAATGACCCAGGA			714
Db	254	SerLeuGlnGlyLeuValSerTrpGlyAspTrpCysAlaArgProAsnArgProGly			273
QY	715	GTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAA			765
Db	274	ValTyrThrAsnLeuCysLysPheThrIysTrpIleGlnGluThrIleGln			290
RESULT 10					
Q6P3Z0 MOUSE					
ID	Q6P3Z0	MOUSE PRELIMINARY;	PRT;	246	AA.
AC	Q6P3Z0;				
DT	05-JUL-2004	(TrEMBLrel. 27, Created)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)			
DE	Hypotheoretical protein.				
GN	Name=klk13;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;				
OC	Muridae; Murinae; Mus.				
NCBI_TaxID	10090;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Jaw and Limb.				
RX	MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,				
RA	Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RL	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Jaw and Limb.				
RC	Strausberg R.;				
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; BC063763; AAH63763.1; -, mRNA.				
DR	HSSP; P00761; 1AKS				
DR	MGI; MGI:195922; Klk13.				
DR	GO; GO:0005615; C:extracellular space; TAS.				
DR	InterPro; IPR001254; Peptidase S1 S6.				
DR	InterPro; IPR001314; Peptidase_S1A.				
DR	Pfam; PF00089; Trypsin; 1.				
DR	PRINTS; PR00722; CHYMOTRYPSIN.				
DR	SMART; SM00020; Tryp_Spc; 1.				
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.				
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.				
DR	PROSITE; PS00135; TRYPSIN_SER; 1.				
KW	Hydrolase; Hypothetical protein; Protease; Serine protease.				
SEQUENCE	246 AA;	27213 MW;	0BC1454D6CC8CDEC	CRG64;	

Alignment Scores:

Pred. No.:

3.45e-43

Length:

246

Score:	604.50	Matches:	112
Percent Similarity:	67.1%	Conservative:	39
Best Local Similarity:	49.8%	Mismatches:	67
Query Match:	34.0%	Indels:	7
DB:	2	Gaps:	4

US-09-905-083A-30 (1-969) x Q6P320_MOUSE (1-246)

Qy	112	GGCGCCCCATGTGCAAGAGGCTCCACCCCATGGCAGGTGGCCCTGCTCAGTGGCAATCAG	171
Db	10	GlyTyrThrCysLeuProHisSerGlnProTrpGlnAlaLeuLeuLeuArgGlyArg	29
Qy	172	CTCCACTGGCGAGGCGTCTGCTCAATGAGCGCTGGGTGCTCACTCCGCCCCCTGCAG	231
Db	30	LeuLeuCysGlyGlyValLeuValHisProLysTrpValLeuThrAlaAlaHisCysArg	49
Qy	232	ATGAATCAGTACACCGTGCACTGGCGAGTGATACGCTGGGC-----GACAGGAGAGCT	285
Db	50	LysAspGlyTyrThrValHisLeuGlyLysHisAlaLeuGlyArgValGluAsnGlyGlu	69
Qy	286	CAGAGGATCAAGGCTCGAAGTCAATCCGCCACCCCGCTACTCC---ACACAGACCCCAT	342
Db	70	GlnAlaMetGluValValArgSerIleProHisProGluTyrGlnValThrProThrHis	89
Qy	343	GTTAAT-----GACCTCATCTCGTGAAGCTCAATAGCAGGCCAGGCTGCATCC	393
Db	90	LeuAsnHisAspHisAspIleMetLeuLeuGluLeuLysSerProValGlnLeuSerSer	109
Qy	394	ATGGTGAAGAAAGTCAGGCTGCCCTCC---CGCTGCGAACCCTCGGAACCACTGTACT	450
Db	110	HisValArgThrLeuLysLeuSerAlaAspAspCysLeuProThrGlyThrCysCysArg	129
Qy	451	GTCTCCCGCTGGGCGACTACCAAGAGCCAGATGTGACTTTCCTCTGACCTCATGTGC	510
Db	130	ValSerGlyTrpGlyThrThrSerProGlnValAsnTyrProLysThrLeuGlnCys	149
Qy	511	GTGATGTCAAGCTCATCTCCCCCAGACATGACAGAGTTTACAGGACTTACTGGAA	570
Db	150	AlaAsnIleGluLeuArgSerAspGluGluCysArgGlnValTyrProGlyLysIleThr	169
Qy	571	AARTCCATGTGCGCTGGCATCCCGACTCCCAAGAAAACGCTGCAATGGTGACTCA	630
Db	170	AlaAsnMetLeuCysAlaGlyThrLysGluGlyGlyLysAspSerCysGluGlyAspSer	189
Qy	631	GGGCGACGTTGGTGTGCAGAGGTACCTGCAAGTCTGGTGTCTCGGGGAACCTTCCCT	690
Db	190	GlyGlyProLeuIleCysAsnGlyLysLeuTyrGlyIleIleSerTrpGlyAspPhePro	209
Qy	691	TGCGGCGCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTCCACCAAGTGGATA	750
Db	210	CysGlyGlnProAsnArgProGlyValTyrThrArgValSerLysTyrLeuArgTrpIle	229
Qy	751	AATGACACCATGAAA	765
Db	230	ArgGluIleIleArg	234

RESULT 11

Q8CGR5_MOUSE

ID Q8CGR5_MOUSE PRELIMINARY; PRT; 250 AA.

AC Q8CGR5;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Glandular kallikrein KLK14.

GN Name=KLK14;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NCBI_EOTIDE SEQUENCE.

RX MEDLINE=22325484; PubMed=12437987; DOI=10.1016/S0006-291X(02)02629-3;

Alignment Scores:
Pred. No.:

RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RL Genes Res. 10:1617-1630(2000)."
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shino K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genes Res. 10:1757-1771(2000)."
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK003996; BAB23113.1; -, mRNA.
 DR HSSP; P00760; 1EZX.
 DR MEROPS; S01.418; -.
 DR MGI; MGI:1915918; 1110030019rik.
 DR GO; GO:0003615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 293 AA; 31908 MW; ED1F45D08226FE911 CRC64;
 Alignment Scores:
 Pred. No.: 7,75e-42 Length: 293
 Score: 589.00 Matches: 108
 Percent Similarity: 63.6% Conservative: 44
 Best Local Similarity: 45.2% Mismatches: 79
 Query Match: 33.1% Indels: 8
 DB: 2 Gaps: 4
 US-09-905-083a-30 (1-969) x Q9D140_MOUSE (1-293)
 QY 76 GCAGGAGNAGAGCCAGGCTGAC-----AAGATTATTGATGGCCCATGTGCA 126
 Db 56 SerGlycluaSpThrArgSerAspSerSerArgIleValAsnGlySerAspCysGln 75
 QY 127 AGAGGCTCCACCCAGGAGGCTGCTCCTCAGTGGC---AATCAGCTCCACTGGGA 183
 Db 76 LysAspAlaGlnProTrpGlnGlyAlaLeuLeuGlyProAlnLysLeuTyfCysGly 95
 QY 184 GGCGTCTGTGTCATGAGCGCTGGGTCTCAGTCTGCGCCGCCCATGCAAGATGAGTAC 243

Db 96 AlaValLeuIleSerProGlnTrpLeuLeuThrAlaAlaHisCysArgLysProValPhe 115
 QY 244 ACCGTGCACCTGGGAGTAGTATCGCTGGGC-----GACAGGAGAGCTCAGAGGATC 294
 Db 116 ArgIleArgLeuGlyHisHisSerMetSerProValTyfGluSerGlyGlnGlnMetPhe 135
 QY 295 AAGGCTCGAAGTCAATCCGCCACCCCGCTGCTACTCCACAGACCCATGTTAATGACTC 354
 Db 136 GlnGlyIleLeuSerIleProHisProGlyTyfSerHisProGlyHisSerAsnAspLeu 155
 QY 355 ATGCTCGTGAAGCTCAATGACGAGGCGAGCTGCTATCCATGCTGAGAAAGTCAGGCTG 414
 Db 156 MetLeuIleLysMetAsnArgLysIleArgAspSerHisSerValLysProValGluIle 175
 QY 415 CCCTCCGCTGGCAACCCCTGGCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 474
 Db 176 AlaCysAspCysAlaThrGluGlyThrArgCysMetValSerGlyTrpGlyThrSer 195
 QY 475 AGCCAGATGTGACCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 534
 Db 196 SerSerHisAsnAsnPheProLysValLeuGlnCysLeuAsnIleThrValLeuSerGlu 215
 QY 535 CAGGACTGCACGAGGCTTACAGAGGACTTACGAAATTCATGCTGCTGCTGCTGCTGCTG 594
 Db 216 GluArgCysLysAsnSerTyfProGlyGlnIleAspLysThrMetPheCysAlaGly--- 234
 QY 595 CCGAGCTCCAAGAAACCGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 654
 Db 235 AspGluGluGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsnGly 254
 QY 655 ACCCTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 714
 Db 255 LysLeuGlnGlyLeuValSerTrpGlyAspPheProCysAlaGlnArgAsnArgProGly 274
 QY 715 GCTACACTCAAGTGTGCAAGTTCACCAAGTGTGTAATAATGACACCACTGAAAGCAT 771
 Db 275 ValTyfThrAsnLeuCysGluPheValLysTrpIleLysAspThrMetAsnSerAsn 293
 RESULT 13
 Q80VS4_MOUSE
 ID Q80VS4_MOUSE PRELIMINARY; PRT; 242 AA.
 AC Q80VS4; 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Kik14 protein (Fragment).
 GN Name=Kik14;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Director MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC074905; AAH74905.1; -; mRNA.
 DR EMBL; BC074904; AAH74904.1; -; mRNA.
 DR Ensembl; ENSG00000129437; Homo sapiens.
 DR GO; GO:004263; F:chymotrypsin activity; IEA.
 DR GO; GO:008233; F:peptidase activity; IEA.
 DR GO; GO:004295; F:trypsin activity; IEA.
 DR GO; GO:006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 251 AA; 27507 MW; C353A7D8B1960BD2 CRC64;

Alignment Scores:

Pred. No.:	2,47e-41	Length:	251
Score:	583.00	Matches:	110
Percent Similarity:	61.2%	Conservative:	43
Best Local Similarity:	44.0%	Mismatches:	89
Query Match:	32.8%	Indels:	8
DB:	2	Gaps:	4

US-09-905-083A-30 (1-969) x Q6B089_HUMAN (1-251)

QY	28	CTTCTCTGCCCTGCAGATCTTACTGTCTATCGCTTAGCCTTGGAACTCGCAGGAGAAGAA	87
Db	4	LeuLeuThrAlaLeuGlnValLeuAlaIleAlaMet-----ThrArgSerGlnGlu	20
QY	88	GCCCAGGGTGACAGATTATTGATGCGCCCATGTGCAAGAGGCTCCACCACATGGCGAG	147
Db	21	AspGlu---AsnIleIleGlyGlyThrCysThrArgSerSerGlnProTrpGln	39
QY	148	GTGGCCCTGCTCAGTGGC-----ATCAGTCCACTCGGAGGCTCCTGCTCAATGAG	201
Db	40	AlaAlaLeuLeuAlaGlyProArgArgPheLeuCysGlyGlyAlaLeuLeuSerGly	59
QY	202	CGTGGGTGCTCACTCCGCCCTCAGATGAATGAGTACACCGCTGCACCTGGGCGAGT	261
Db	60	GlnTrpValIleThrAlaAlaHisCysGlyArgProIleLeuGlnValAlaLeuGlyLys	79
QY	262	GATACGCTG-----GGCAGCAGGAGAGCTCAGAGATCAAGGCTCGAAGTCATTCGCG	315
Db	80	HisAsnLeuArgTrpGlnAlaThrGlnGlnValLeuArgValValArgGlnValThr	99
QY	316	CACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC	375
Db	100	HisProAsnTrpAsnSerArgThrHisAspAsnAppLeuMetLeuLeuGlnGln	119
QY	376	CAGGCGAGGCTGTCTCATCCATGGTGAAGAAGTCAGGCTCCCTCCGCTCGAACCCCTC	435

Search completed: March 11, 2006, 01:53:58
 Job time : 272.5 secs

Db	120	ProAlaArgIleGlyArgAlaValArgProIleGluValThrGlnAlaCysAlaSerPro	139
QY	436	GGAAACCACTGTACTGTCTCCGGCTGGGCACACTACCAGAGCCAGATGTGACCTTTCC	495
Db	140	GlyThrSerCysArgValSerGlyTrpGlyThrIleSerSerProIleAlaArgTyrPro	159
QY	496	TCTGACCTCATGTGGTGGATGTCAAGTCTATCTCCCCCAGGACTCGCACGAGGTTTAC	555
Db	160	AlaSerLeuGlnCysValAsnIleAsnIleSerProAspGluValCysGlnLysAlaTyr	179
QY	556	AAGGACTTACTGGAAAATTCCATGTGTGGCTGCATCCCGACTCCCAAGAAAACGCC	615
Db	180	ProArgThrIleThrProGlyMetValCysAlaGlyValProGlnGlyGlyLysAspSer	199
QY	616	TGCAATGGTGAATCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAGGCTGTGGTGCC	675
Db	200	CysGlnGlyAspSerGlyGlyProLeuValCysArgGlyGlnLeuGlnGlyLeuValSer	219
QY	676	TGGGGAACCTTTCCCTTGGGGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG	735
Db	220	TrpGlyMetGluArgCysAlaLeuProGlyTyrProGlyValTyrThrAsnLeuCysLys	239
QY	736	TTCCACCAAGTGATTAATGACACCATGAAA	765
Db	240	TyrArgSerTrpIleGluGluThrMetArg	249

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 11, 2006, 01:54:13 ; Search time 8.5 Seconds
(without alignments)
1885.005 Million cell updates/sec

Title: US-09-905-083A-30

Perfect score: 1780

Sequence: 1 ggaattccgggtccatggc.....aagaaacacaaacccctcag 969

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/abes/ABSSWEB-spool/US0905083/runat_10032006_152457_29754/app_query.fasta_1
-DB=Issued Patents AA -QFWT=faetan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs02p -USER=US0905083 @CGN 1 1 71 @runat_10032006_152457_29754
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pcp:*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pcp:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pcp:*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pcp:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1371	77.0	265	2	US-09-949-016-7716 Sequence 7716, Ap
2	1364	76.6	253	1	US-08-557-146-2 Sequence 2, Appli
3	1364	76.6	253	1	US-08-824-874-3 Sequence 3, Appli
4	1364	76.6	253	1	US-09-154-344-2 Sequence 2, Appli
5	1364	76.6	253	2	US-08-930-188-2 Sequence 2, Appli
6	1364	76.6	253	2	US-09-210-084-3 Sequence 3, Appli
7	1364	76.6	253	2	US-09-764-762-3 Sequence 3, Appli
8	1364	76.6	253	4	PCT-US96-04294-2 Sequence 4, Appli
9	1235	69.4	225	1	US-09-027-337-4 Sequence 4, Appli
10	1235	69.4	225	2	US-09-644-600-4 Sequence 4, Appli
11	1235	69.4	225	2	US-09-654-600A-4 Sequence 4, Appli
12	1230	69.1	224	2	US-08-944-483-33 Sequence 33, Appli

13	1215.5	68.3	225	1	US-08-557-146-12 Sequence 12, Appli
14	1215.5	68.3	225	1	US-09-154-344-12 Sequence 12, Appli
15	829	46.6	154	2	US-09-261-416-7 Sequence 7, Appli
16	773	43.4	144	2	US-09-618-259-4 Sequence 4, Appli
17	614	34.5	260	2	US-09-025-059-3 Sequence 3, Appli
18	614	34.5	260	2	US-09-618-259-8 Sequence 8, Appli
19	612.5	34.4	270	2	US-09-949-016-7712 Sequence 7712, Ap
20	612.5	34.4	293	2	US-09-509-908-2 Sequence 2, Appli
21	612.5	34.4	293	2	US-09-991-181-309 Sequence 309, App
22	612.5	34.4	293	2	US-09-990-444-309 Sequence 309, App
23	612.5	34.4	293	2	US-09-997-333-309 Sequence 309, App
24	612.5	34.4	293	2	US-09-992-598-309 Sequence 309, App
25	582.5	32.7	260	2	US-09-070-526-2 Sequence 2, Appli
26	582.5	32.7	260	2	US-09-618-259-7 Sequence 7, Appli
27	582.5	32.7	260	2	US-09-999-833A-395 Sequence 395, App
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30	580.5	32.6	260	2	US-09-008-271A-7 Sequence 7, Appli
31	580.5	32.6	260	2	US-09-968-415-7 Sequence 7, Appli
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33	573.5	32.2	282	2	US-09-856-320A-2 Sequence 2, Appli
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35	571.5	32.1	250	2	US-10-004-860-427 Sequence 427, App
36	571.5	32.1	250	2	US-10-012-231A-170 Sequence 170, App
37	571.5	32.1	250	2	US-10-015-389A-170 Sequence 170, App
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40	571.5	32.1	250	2	US-10-015-393A-170 Sequence 170, App
41	571.5	32.1	250	2	US-10-011-833A-170 Sequence 170, App
42	571.5	32.1	250	2	US-10-006-041A-170 Sequence 170, App
43	571.5	32.1	250	2	US-10-012-064A-170 Sequence 170, App
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45	567.5	31.9	254	2	US-09-439-313-525 Sequence 525, App

ALIGNMENTS

RESULT 1

US-09-949-016-7716
; Sequence 7716, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7716
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7716

Alignment Scores:
Pred. No.: 2,33e-131 Length: 265
Score: 1371.00 Matches: 254
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 0
Query Match: 77.0% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-949-016-7716 (1-265)

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130 GGTCTCCACCCATGAGGAGTGGCCCTGCTCAGTGGCAATCAGCTCCACATGCGGAGCGTC 189
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91 HisLeuGlySerAspThrLeuGlyAepArgAlaGlnArgIleLysAlaSerLysSer 110
310 TTCGGCCACCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTC 369
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131 AsnSerGlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGlu 150
430 CCCCCTGGAAACCACTGTACTGTCTCGGCTGGGGCACTACACAGAGCCAGATGTGACC 489
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171 PheProSerAspLeuMetCysValAepValLysLeuIleSerProGlnAspCysThrLys 190
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191 ValTyrLysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLys 210
610 AAGCCTTGCAATGGTGACTCAGGGGACCGTTGGTGTGACAGAGTACCTCGAAGTCTG 669
211 AsnAlaCysAenGlyAepSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeu 230
670 GTGCTCTGGGAATTTCCCTTGGCGCAACCAATGACCCAGGAGCTTACACTCAAGTG 729
231 ValSerTrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnVal 250
730 TGCAAGTTCCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
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RESULT 2

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US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-557-146-2

Alignment Scores:
Pred. No.: 1,19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 1 Gaps: 0
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US-09-905-083A-30 (1-969) x US-08-557-146-2 (1-253)

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QY 76 GCAGAGAAGAAGCCAGGCTGACAGATATTATGATGGCGCCCATCTGTCCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAepGlyAlaProCysAlaAArgGlySer 40
QY 136 CACCCATGCGAGCTGGCCCTGCTCAGTGGCAATCAGTCCACTGCGAGGCGCTCTGGTGC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGGTGCTCCTGCGCCCACTGCAAGATGAATCAGTACACCGTGCACTCG 255
Db 61 AsnGluAArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GCAGTGATACCTCGGCGACAGAGCTCAGAGATCAAGGCTCGAAGCTCAGATTCATCCGC 315
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QY 616 TGCATGTGTGACTCAGGGGACCGTTGTTGTCAGAGGTACCTCGCAAGGCTCTGGTGTCC 675
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QY 676 TGGGAACTTCCCTTGGCGCCACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
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RESULT 3
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; US-08-824-874-3

Alignment Scores:
Pred. No.: 1.19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 1 Gaps: 0

US-09-905-083A-30 (1-969) x US-08-824-874-3 (1-253)

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Db 21 AlaGlyGluIleAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGGTGGCCCTTGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCTGGTC 195

Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGGTGCTCACTGCGCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCCTCCG 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCGCGCTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTCCATCGTGTGAAGAAAGTCAAGGCTGCCCTCCCGCTCGAAGACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCCGCTGGGGGACTTACACAGAGCCAGATGTGACCTTTCC 495
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QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774
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RESULT 4
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egeirud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Alignment Scores:
Pred. No.: 1,19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 1 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-154-344-2 (1-253)

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QY 76 GCAGGAGAAGAGCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGCGCTCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGGTGCTCACTCGCGCCCACTGCAGATGAATGAGTACACCGTGACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCACAGGAGCTCAGAGGATCAAGGCTCGAAGTCATTCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGTACTCCACAGACCCATGTTATGACCTCATGCTGTGAAGCTCAATAGC 375
DB 101 HisProGlyTyxSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTCAATCGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACCTGTACTGTCTCCGCTGGGCACTTACCACGAGCCAGATGTGACCTTTCC 495
DB 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGATGCAAGTCATCTCTCCCGCCAGACTGACGACGAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTy 180
QY 556 AAGGACTTACTGGAAATTCATGCTGCTGGCATCCCGACTCCCAAGAAAACGCC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAla 200
QY 616 TGCATGTGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTCGTGGTCC 675
DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACTTTCCTTGGCGCCAAACCCAAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyxThrGlnValCysLys 240

QY 736 TTCACAAAGTGATTAATGACACCACTGAAAGACATCGC 774
DB 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 5
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2
Alignment Scores:
Pred. No.: 1,19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0
US-09-905-083A-30 (1-969) x US-08-930-188-2 (1-253)
QY 16 ATGGCAAGATCCCTCTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACGCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGCGCTCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGGTGCTCACTCGCGCCCACTGCAGATGAATGAGTACACCGTGACCTG 255

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Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
QY 256 GGCAAGTATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACTGCTTGGAAACT 75
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CAGGAGAAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 101 HisProGlyTyTrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGAGAAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACTGCTTGGAAACT 75
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGATGTCAGAGTCAAGTCAATCCAGTCAATCCAGTCAATCCAGT 255
Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuLysLeuLysLeuLysLeuLys 80
QY 556 AGGAGTCTACTGGAATAATTCATGCTGCGCTGGCATCCCGCTCCGCTCCGCTCCGCTCC 435
Db 181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATATGGTGACTCAGGGGACCGTTGGTGTGAGAGTCAAGTCAATCCAGTCAATCCAGT 255
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAACTTTCCTTCCGCGCCCAACCAATGACCCAGAGTCTTACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240
QY 736 TTCACCAAGTGGTAATGACACCATGAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 6

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US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
```

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; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-09-210-084-3
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Alignment Scores: 1.19e-130 Length: 253
Pred. No.: 1364.00 Matches: 253
Score: 1364.00 Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 76.6% Gaps: 0
DB: 2
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US-09-905-083A-30 (1-969) x US-09-210-084-3 (1-253)

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QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACTGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaAaGlySer 40
QY 136 CAGGAGAAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGCTGGGTGCTCACTGCGCCCTGCAGATCTTACTGCTGCAATCAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGGACAGAGAGCTCAGAGGATCAAGGCTCCGCTCCGCTCCGCTCC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CAGGAGAAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 101 HisProGlyTyTrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGAGAAAGAGCCAGGGTGACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACTGCTTGGAAACT 75
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGATGTCAGAGTCAAGTCAATCCAGTCAATCCAGTCAATCCAGT 255
Db 161 SerAspLeuMetCysValAspValLysLeuLysLeuLysLeuLysLeuLysLeuLys 80
QY 556 AGGAGTCTACTGGAATAATTCATGCTGCGCTGGCATCCCGCTCCGCTCCGCTCCGCTCC 435
Db 181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATATGGTGACTCAGGGGACCGTTGGTGTGAGAGTCAAGTCAATCCAGTCAATCCAGT 255
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAACTTTCCTTCCGCGCCCAACCAATGACCCAGAGTCTTACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240
QY 736 TTCACCAAGTGGTAATGACACCATGAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 7
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Alignment Scores:
Pred. No.: 1.19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-764-762-3 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCGAGATCTTACTGCTATCTCTTACGCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGNAGAGAGCCAGAGTGCACAGATTATGATGGCGCCCATGTCAGAGAGCTCC 135
Db 21 AlaGlyGluAlaGlnGlyAspIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCATGCGAGTGGCCCTGCTGCTAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 ATGAGCGCTGGGTGCTACTGCGCGCCCACTGCAAGATGAATGAGTACACCGTGACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
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QY 256 GGCAGTGATACGCTGGCGACAGAGAGCTCAGAGATCAAGGCTTCGAAGTCAATTCGCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLeuAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATACCTCATGCTGCTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGCTGTTCATCCATGCTGAAGAAGTCAGGCTGCCCTCCGCTGCCGACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACACTGTACTGTCTCCGCTGGGCACTTACCACAGAGCCAGATGTGACCTTTCCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCTGGATGTCAAGTCTATCTCCCCCAGGACTGACAGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAAAATTCATGCTGTGCGCTGGCATCCCGACTCCCAAGAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATATGGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTTGCAAGTCTGGTGTCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGAACCTTTCCTTGGCGCAACCCAAATGACACCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAGAGCATCCG 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 8
PCT-US96-04294-2
; Sequence 2, Application PC/TUS9604294
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; APPLICANT: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04294
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861
```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-04294-2

Alignment Scores:
Pred. No.: 1.19e-130 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x PCT-US96-04294-2 (1-253)

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QY 16 ATGCGAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGTATCCTTAGCCTTGGAAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAACAGCCAGGCTGCAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluGlnAlaGlnGlyAspLysIleLeuLeuLeuProCysAlaArgGlySer 40
QY 136 CACCCATGGCAGGTGGCCCTGCTCAGTGCGCAATCAGCTCCACTGCGGAGGCGTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGCTGGTGTCTACTCGGCCCTGCAAGATGATGATGATGATGATGATGATGATG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCAGCAGAGATCAAGGATCAAGGCTCGAAGTCAATCCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGCTACTCCACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGCGCAGCTGTCTATCCATGTTGAAGAAAGTCAAGGCTGCCCTCCCGCTCGAAGCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTGTCTCCGCTGGGCACTTACCAGAGCCAGATGTGACCTTTCCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGCAAGCTCATCTCCCCCAGGACTGCACGAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValThr 180
QY 556 AAGGACTTACTGAAATTCATGCTGTGCTGGCATCCCGCTCCAGTCCCAAGAAACGCC 615
Db 181 LysAspLeuLeuGlnAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGCATGTGTCACTCAGGGGACCTGTGTGTGTCAGAGGTACCTGCAAGGTCTGTGTC 675
Db 201 CysAsnGlyAspSerGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTCGCGGCCAACCCCAATGACCCAGAGGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValThrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 9

US-09-027-337-4

; Sequence 4, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15; An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
; OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Alignment Scores:
Pred. No.: 1.69e-117 Length: 225
Score: 1235.00 Matches: 225
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 69.4% Indels: 0
DB: 1 Gaps: 0

US-09-905-083A-30 (1-969) x US-09-027-337-4 (1-225)

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QY 100 AAGATTATTGATGGCGCCCATGTCGCAAGGGTCCACCACCATGGCAGGTGGCCCTGCTC 159
Db 1 LysIleIleAspGlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuLeu 20
QY 160 AGTGGCAATCAGCTCCACTCGCGAGGCGTCTCGTCAATGAGCGCTGGGTGCTCAGTCC 219
Db 21 SerGlyAsnGlnLeuHisCysGlyValLeuValAsnGluArgTrpValLeuThrAla 40
QY 220 GCCACTGCAAGATGAATGAGTACACCGTCACCTGGCGAGTGAATACGCTGGCGCAGCAG 279
Db 41 AlaHisCysLysMetAsnGluTrpValHisLeuGlySerAspThrLeuGlyAspArg 60
QY 280 AGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGGCCACCCCGCTACTCCACAGACCC 339
Db 61 ArgAlaGlnArgIleLysAlaSerLysSerPheArgHisProGlyTrpSerThrGlnThr 80
QY 340 CATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGGCCAGGCTGTCTCATCGTGTG 399
Db 81 HisValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeuSerMetVal 100
QY 400 AGAAAGTCAGGCTGCCCTCCCGCTCGAAACCCCTCGAAACCCCTGTACTGTCTCCGGC 459
Db 101 LysLysValArgLeuProSerArgCysGluProProGlyThrThrCysThrValSerGly 120
QY 460 TGGGGCACTACACAGAGCCCGAGATGACCTTCCCTCTGACCTCATGTCGCTGGATGTC 519
Db 121 TrpGlyThrThrThrSerProAspValThrPheProSerAspLeuMetCysValAspVal 140
QY 520 AAGCTCATCTCCCCCAGGACTGCACGAAGGTTTACAAGGACTTACTTGGAAATTTCCATG 579
Db 141 LysLeuIleSerProGlnAspCysThrLysValTrpLysAspLeuLeuGlnAsnSerMet 160
QY 580 CTGTGCGCTGGCATCCCGCACTCCAAAGAAAAACCCCTGCAATGGTGAATCAGGCGGACCG 639
Db 161 LeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyPro 180
QY 640 TTGGTGTGAGAGGTACCTGCAAGGTCTGCTGCTCTGGGAACTTCCCTTCGCGGCCAA 699
Db 181 LeuValCysArgGlyThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGln 200
QY 700 CCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATGAATGACACC 759
Db 201 ProAsnAspProGlyValThrThrGlnValCysLysPheThrLysTrpIleAsnAspThr 220
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QY 460 TGGGGCACTACACGAGCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTC 519
Db 121 TrpGlyThrThrSerProAspValThrPheProSerAspLeuMetCysValAspVal 140
QY 520 AAGCTCATCTCCCCCAGGACTGCACGAAAGTTTACAAGGACTTACTGGAAATTCATG 579
Db 141 LysLeuIleSerProGlnAspCysThrLysValThrLysAspLeuLeuGluAsnSerMet 160
QY 580 CTGTGCGCTGGCACTCCCGACTCCAAAGAAAGCGCTGCAATGGTGACTCAGGGGACCG 639
Db 161 LeuCysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyPro 180
QY 640 TTGCTGTGCAGAGTACCTGCAAGTCTGGTGTCTCTGGGAACTTTCCCTTGGCGCCAA 699
Db 181 LeuValCysArgGlyThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGln 200
QY 700 CCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATTAATGACAC 759
Db 201 ProAsnAspProGlyValTyrThrGlnValCysLysPheThrLysTrpIleAsnAspThr 220
QY 760 ATGAAAAGCATCGC 774
Db 221 MetLysLysHisArg 225

RESULT 12
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-33
Alignment Scores:
Pred. No.: 5,48e-117 Length: 224
Score: 1230.00 Matches: 224
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 69.1% Indels: 0
DB: 2 Gaps: 0

US-09-905-083A-30 (1-969) x US-08-944-483-33 (1-224)
QY 103 ATTATTGATGGGGCCCCCATGTGCAAGAGGCTCCACCACCTGGCAGGTGGCCCTGCTCAGT 162
Db 1 IleIleAspGlyAlaProCysAlaArgGlySerHisProTrpGlnValAlaLeuSer 20
QY 163 GGCATTCAGCTCCACTGCGAGGCGTCTGGTCAATGAGCGCTGGGTGCTCCTGCTGCTGCTG 222
Db 21 GlyAsnGlnLeuHisCysGlyValLeuValAsnGluArgTrpValLeuThrAlaAla 40
QY 223 CACTGCAAGATGAATGAGTACACCGTGCACCTGGGCGAGTGATACGCTGGGCGACAGAGA 282
Db 41 HisCysLysMetAsnGluTyrThrValHisLeuGlySerAspThrLeuGlyAspArg 60
QY 283 GCTCAGAGGATCAAGGCTCGAAGTCATTCGCGCACCCCGGCTACTCCACACAGACCCAT 342
Db 61 AlaGlnArgIleLysAlaSerLysSerPheArgHisProGlyTyrSerThrGlnThrHis 80
QY 343 GTTAATGACCTCATGCTCTGTAAGTCAATAGCAGCGCAGGCTGCTCATCTCATGTGTAAG 402
Db 81 ValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLys 100
QY 403 AAGTCAGGCTGCCCTCCGCTCGGAAACCCCTGGAAACCCACTGACTGCTCCTCGGCTGG 462
Db 101 LysValArgLeuProSerArgCysGluProProGlyThrThrCysThrValSerGlyTrp 120
QY 463 GGCACCTACCACAGCCCGAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAG 522
Db 121 GlyThrThrSerProAspValThrPheProSerAspLeuMetCysValAspValLys 140
QY 523 CTCATCTCCCCCAGGACTGCACGAAAGTTTACAAGACTTACTGAAATTCATGCTGCTG 582
Db 141 LeuIleSerProGlnAspCysThrLysValTyrLysAspLeuLeuGluAsnSerMetLeu 160
QY 583 TGGCTGGCATCCCCGACTCCAGAAAGAAACGCTGCAATGCTGCTGCTGCTGCTGCTGCTG 642
Db 161 CysAlaGlyIleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeu 180
QY 643 GTGTGCAGAGGTACCTCGAAGTCTGGTGTCTGGGGAACCTTCCCTTGGCGGCCAACCC 702
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Db 221 LysLysHisArg 224

RESULT 13
US-08-557-146-12
; Sequence 12, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
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/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case, Patent Department
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2787
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sterner, Richard J.
/ REGISTRATION/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
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/ US-08-557-146-12
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/ Alignment Scores:
/ Pred. No.: 1.66e-115 Length: 225
/ Score: 1215.50 Matches: 223
/ Percent Similarity: 99.6% Conservative: 1
/ Best Local Similarity: 99.1% Mismatches: 0
/ Query Match: 68.3% Indels: 1
/ DB: 1 Gaps: 1
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/ QY 163 GCAATCAGCTC---CACTGCGAGGCGCTCTGGTCAATGAGCGCTGGGTCTCACTGCC 219
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/ QY 220 GCCCACTGCAAGTGAATGATACACCGTGACCTGGCGAGTGATACCGTGGCGGACAGG 279
/ Db 41 AlaHisCysLeuMetAsnGluTrpThrValHisLeuGlySerAspThrLeuGlyAspArg 60
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/ QY 280 AGAGCTCAGAGATCAAGCGCTCGAAGTCATTCCCGCACCCCGGCTACTCCACACAGACC 339
/ Db 61 ArgAlaGlnArgLlelyslaserlySerPheArgHisProGlyTySerThrGlnThr 80
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/ QY 340 CATGTTAATGACTCATGCTCGTGAAGCTCAATAGCCAGCGCTGTCATCCATGGTG 399
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/ QY 400 AGAAAGTCAGCTGCCCTCCGCTCGGACCCCTGGACCCCTGTAACCTGCTCTCCGCG 459
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/ QY 460 TCGGGCAGCTACACAGAGCCAGATGTGACTTTCCCTCTGACTCATGTCGCTGGATGTC 519
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/ QY 700 CCCAATGACCCAGGAGTCTTACACTCAAGTGTGCAAGTTCCACCAAGTGGTAATAATGACACC 759
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/ QY 760 ATGAAAAAGCATCGC 774
/ Db 221 MetLysLysHisArg 225
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/ RESULT 14
/ US-09-154-344-12
/ Sequence 12, Application US/09154344
/ Patent No 5981256
/ GENERAL INFORMATION:
/ APPLICANT: Egelrud, Torbjorn
/ APPLICANT: Hansson, Lennart
/ TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
/ TITLE OF INVENTION: Enzyme (SCCE)
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case, Patent Department
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/154,344
/ FILING DATE: 16-SEP-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sterner, Richard J.
/ REGISTRATION/DOCKET NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
/
/ US-09-154-344-12
/
/ Alignment Scores:
/ Pred. No.: 1.66e-115 Length: 225
/ Score: 1215.50 Matches: 223
/ Percent Similarity: 99.6% Conservative: 1
/ Best Local Similarity: 99.1% Mismatches: 0
/ Query Match: 68.3% Indels: 1
/ DB: 1 Gaps: 1
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/ US-09-905-083A-30 (1-969) x US-09-154-344-12 (1-225)
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; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: Chymotryptic enzyme (Scce) homologous to similar
; OTHER INFORMATION: domain in TADG-12
US-09-261-416-7
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Alignment Scores: 4.24e-76 Length: 154
Pred. No.:

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Job time : 48.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: March 11, 2006, 02:13:49 ; Search time 35.4 Seconds
(without alignments)
2287.439 Million cell updates/sec

Title: US-09-905-083A-30

Perfect score: 1780

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
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Database : Published Applications AA Main.*

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- 6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1364	76.6	253	3	US-09-764-762-3
3	1364	76.6	253	4	US-10-071-214-2
4	1364	76.6	253	4	US-10-071-214-48
5	1364	76.6	253	4	US-10-264-283-90
6	1364	76.6	253	4	US-10-295-027-498
7	1364	76.6	253	4	US-10-173-999-48
8	1364	76.6	253	4	US-10-408-765A-639
9	1364	76.6	253	5	US-10-643-795A-95
10	1364	76.6	253	5	US-10-948-518-95
11	1364	76.6	253	5	US-10-868-490A-1

12	1350	75.8	250	4	US-10-262-511-92	Sequence 92, Appl
13	1337	75.1	257	4	US-10-344-394-38	Sequence 38, Appl
14	1252	70.3	247	4	US-10-262-511-102	Sequence 102, App
15	1252	70.3	252	4	US-10-262-511-94	Sequence 94, Appl
16	1235	69.4	225	4	US-10-600-187-4	Sequence 4, Appli
17	1230	69.1	224	3	US-09-789-210-33	Sequence 33, Appl
18	1119	62.9	224	4	US-10-262-511-104	Sequence 104, App
19	1085.5	61.0	249	4	US-10-071-214-47	Sequence 47, Appl
20	1035.5	58.2	198	4	US-10-262-511-96	Sequence 96, Appl
21	1011.5	56.8	249	4	US-10-071-214-50	Sequence 50, Appl
22	996.5	56.0	243	4	US-10-071-214-46	Sequence 46, Appl
23	940.5	52.8	226	4	US-10-071-214-49	Sequence 49, Appl
24	937.5	52.7	181	4	US-10-262-511-98	Sequence 98, Appl
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26	773	43.4	144	4	US-10-461-787-4	Sequence 4, Appli
27	641.5	36.0	136	5	US-10-450-763-53737	Sequence 53737, A
28	614	34.5	260	3	US-09-796-294-8	Sequence 8, Appli
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31	612.5	34.4	293	3	US-09-739-907-82	Sequence 82, Appl
32	612.5	34.4	293	3	US-09-739-907-97	Sequence 97, Appl
33	612.5	34.4	293	3	US-09-989-722-309	Sequence 309, App
34	612.5	34.4	293	3	US-09-989-723-309	Sequence 309, App
35	612.5	34.4	293	3	US-09-989-279-309	Sequence 309, App
36	612.5	34.4	293	3	US-09-989-727-309	Sequence 309, App
37	612.5	34.4	293	3	US-09-989-731-309	Sequence 309, App
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45	612.5	34.4	293	3	US-09-992-598-309	Sequence 309, App

ALIGNMENTS

RESULT 1
US-09-888-615-98
; Sequence 98, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARVDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

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DB:	3	Gaps:	0

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; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

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Score: 1364.00 Matches: 253
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; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Alignment Scores:
Pred. No.: 1.26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-071-214-48 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCCTTAGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAGATTATTGATGGGCCCCCCTGTCGAGAGCTCC 135
Db 21 AlaGlyGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCCGGTACTCCACAGACCCCATGTTAATGACTCATGCTCGTGAAGTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCCGAAACCCCT 195
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Db	41	His	Pro	T	Trp	Gln	Val	Ala	Leu	Leu	Ser	Gly	Asn	Gln	Leu	His	Cys	Gly	Gly	Val	Leu	Val	60
Qy	196	AAT	GAC	GCT	GCT	GCT	CAC	TCC	CGC	CCC	ACT	GC	CAAG	TAC	GAAT	GAT	GAT	CAC	CGT	GAC	CTG	355	
Db	61	Asn	Glu	A	G	T	Trp	Val	Leu	Thr	Ala	His	Cys	Leu	Met	Asn	Glu	Tyr	Thr	Val	His	Leu	80
Qy	256	GGC	AGT	GAT	TAC	GCT	GGG	CGA	CAG	GAG	AGT	CAG	AGG	ATC	AA	GCG	CTC	GAA	GCT	CAT	TTC	CGC	315
Db	81	Gly	Ser	Asp	Thr	Leu	Gly	Asp	Arg	Ala	Gln	Arg	Ile	Leu	Ala	Ser	Leu	Ser	Phe	Asn	Arg	100	
Qy	316	CAC	CCCG	GCT	ACT	CC	CAC	CAG	ACC	ATG	TAA	TG	ACCT	CAT	GCT	CGT	GAAG	GCT	CAAT	ATC	375		
Db	101	His	Pro	Gly	Tyr	Ser	Thr	Gln	Thr	His	Val	Asn	Asp	Leu	Met	Leu	Val	Leu	Asn	Ser	120		
Qy	376	CAG	CC	CAG	GCT	GCT	CA	TG	TG	TGA	AGA	AA	GTC	CAG	GCT	CC	CGT	CC	CGT	CGC	AA	CC	435
Db	121	Gln	Ala	Arg	Leu	Ser	Ser	Met	Val	Val	Val	Val	Arg	Leu	Pro	Ser	Arg	Cys	Glu	Pro	140		
Qy	436	GGA	ACC	ACT	G	T	ACT	G	T	CTC	CGG	CT	GGG	CA	CT	TAC	CAG	AGC	CAG	ATG	TTC	495	
Db	141	Gly	Thr	Thr	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Thr	Thr	Ser	Pro	Asp	Val	Thr	Phe	Pro	160	
Qy	496	TCT	GAC	CT	CAT	G	T	G	T	G	G	T	G	T	C	CAAG	CT	CAT	C	CC	CC	CC	555
Db	161	Ser	Asp	Leu	Met	Cys	Val	Asp	Val	Leu	Leu	Ile	Ser	Pro	Gln	Asp	Cys	Thr	Leu	Val	Tyr	180	
Qy	556	AAG	GA	CTT	ACT	TG	GA	AA	ATT	CC	AT	G	T	G	T	G	CGT	CGC	TG	CA	TCC	CGC	615
Db	181	Lys	Asp	Leu	Leu	Gln	U	Asn	Ser	Met	Leu	Cys	Ala	Gly	Ile	Pro	Asp	Ser	Leu	Val	Asn	Ala	200
Qy	616	TGC	AA	TG	T	G	ACT	CAG	GGG	AC	CGT	TG	TG	TG	TC	CAG	AGT	TAC	CT	GCA	AGG	CT	675
Db	201	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg	Gly	Thr	Leu	Gln	Gly	Leu	Val	Ser	220	
Qy	676	TGG	GA	ACT	T	T	CC	T	T	CGG	CC	AA	C	CA	TG	AC	CC	AG	G	AGT	CT	CA	735
Db	221	Trp	Gly	Thr	Phe	Pro	Cys	Gly	Gln	Pro	Asn	Asp	Pro	Gly	Val	Tyr	Thr	Gln	Val	Cys	Lys	240	
Qy	736	TTC	CA	CA	AGT	TG	GA	TAA	TG	AC	CA	CC	AT	G	AC	AAAA	AG	CA	T	CCG	774		
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RESULT 5

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; SEQUENCE 90, Application US/10264283
; Publication No. US2003014494A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-283-90

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US-09-905-083A-30 (1-969) x US-10-264-283-90 (1-253)

16 ATGGCAAGATCCCTTCTCCTGCCCTGCAGATCTTACTGCTATCCTTAGCCTTGGAACCT 75

;; PRIOR APPLICATION NUMBER: US 60/350,666
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 60/335,394
;; PRIOR FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: US 60/332,464
;; PRIOR FILING DATE: 2001-11-21
;; PRIOR APPLICATION NUMBER: US 60/334,393
;; PRIOR FILING DATE: 2001-11-29
;; PRIOR APPLICATION NUMBER: US 60/340,376
;; PRIOR FILING DATE: 2001-12-14
;; PRIOR APPLICATION NUMBER: US 60/347,211
;; PRIOR FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 60/347,349
;; PRIOR FILING DATE: 2002-01-10
;; PRIOR APPLICATION NUMBER: US 60/355,250
;; PRIOR FILING DATE: 2002-02-08
;; PRIOR APPLICATION NUMBER: US 60/356,714
;; PRIOR FILING DATE: 2002-02-13
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 1386
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 498
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-295-027-498
Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0
US-09-905-083A-30 (1-969) x US-10-295-027-498 (1-253)
QY 16 ATGGCAAGATCCCTTCTGCGCCCTGCAGATCTTACTGCTATCCTTAGCTTGAACCT 75
Db 1 MetAlaArgSerLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGCCAGCGGTGACAGATTATTGATGGCGCCCACTGTCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCCCTGCTCAGTGGCAATCAGCTCAGCTGCGAGCGCTGCTGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGACGCTGGTGTCTACTGCGCCCACTGCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluThrValHisLeu 80
QY 256 GCGAGTGATACCTGGCGACAGGAGCTCAGAGGATCAAGCCCTCGAAGTATTCGCG 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTTAATGACTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTTCATCCATGGTGAAGAAAGTCAAGCTGCCCTCCCGCTCCGACCCCT 435
Db 121 GlnAlaArgLeuSerSerMetValLysValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGNACCACTGTACTGCTCCGCTGGGCACTACACAGGCCCACTGACCTTTCC 495
Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCGCCAGGACTGACAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValThr 180

QY 556 AAGGACTTACTGGAAAATTCCATGCTGTGGCTGGCATCCCCGACTCCCAAGAAAAGCCG 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCAATGGTGACTCAGCGGACCGTTGGTGTGCAGAGGTACCCCTGCAAGGTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTTACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTrpThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCACTGAAAAAGCATGCG 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 7
US-10-173-999-48
;; Sequence 48, Application US/10173999
;; Publication No. US2004000563A1
;; GENERAL INFORMATION:
;; APPLICANT: Mack, David H.
;; APPLICANT: Gish, Kurt C.
;; APPLICANT: Ros Biotechnology, Inc.
;; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
;; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
;; TITLE OF INVENTION: Cancer
;; FILE REFERENCE: 018501-002420US
;; CURRENT APPLICATION NUMBER: US/10/173,999
;; CURRENT FILING DATE: 2002-06-17
;; PRIOR APPLICATION NUMBER: US 60/299,234
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: US 60/315,287
;; PRIOR FILING DATE: 2001-08-27
;; PRIOR APPLICATION NUMBER: US 60/350,666
;; PRIOR FILING DATE: 2001-11-13
;; PRIOR APPLICATION NUMBER: US 60/372,246
;; PRIOR FILING DATE: 2001-04-12
;; NUMBER OF SEQ ID NOS: 163
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 48
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-173-999-48
Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0
US-09-905-083A-30 (1-969) x US-10-173-999-48 (1-253)
QY 16 ATGGCAAGATCCCTTCTGCGCCCTGCAGATCTTACTGCTATCCTTAGCTTGAACCT 75
Db 1 MetAlaArgSerLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGCCAGCGGTGACAGATTATTGATGGCGCCCACTGTCAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGGCCCTGCTCAGTGGCAATCAGCTCAGCTGCGAGCGCTGCTGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGACGCTGGTGTCTACTGCGCCCACTGCAAGATGAATGAGTACACCGTGCACTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluThrThrValHisLeu 80
QY 256 GCGAGTGATACCTGGCGACAGGAGCTCAGAGGATCAAGCCCTCGAAGTATTCGCG 315

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Db      81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
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QY      316 CACCCGGCTACTCCACAGACCCATGTTAATGACTCATGCTCTGTAAGCTCAATAGC 375
      |||
Db      101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
      |||
QY      376 CAGGCCAGGCTGTCATCCATGGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT 435
      |||
Db      121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
      |||
QY      436 GGAACACACCTGTACTCTCCGGCTGGGCACTTACCACAGAGCCAGCTGTGACCTTTCC 495
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Db      141 GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro 160
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QY      496 TCTGACTCATGTGCTGATGATCAAGCTCATCTCCCCCAGGACTGCGACGAAGGTTTAC 555
      |||
Db      161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
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QY      556 AAGGACTTACTGGAAATTCATGCTGTGGCTGGCATCCCGACTCCCAAGAAACGCC 615
      |||
Db      181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
      |||
QY      616 TGCATGTGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTCGCAAGGCTCTGGTGTC 675
      |||
Db      201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
      |||
QY      676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
      |||
Db      221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
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QY      736 TTCACCAAGTGGTAATGACACCATGAAAGACATCGC 774
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Db      241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 8

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US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639
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Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 4 Gaps: 0
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US-09-905-083A-30 (1-969) x US-10-408-765A-639 (1-253)

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QY      16 ATGGCAAGATCCCTCTCTCGCCCTGCGAGATCTTACTGCTATCTCTGAGAACT 75
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Db      1 MetAlaArgSerLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
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QY      76 GCAGGAAGAAGCCAGGGTCACAAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
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Db      21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
      |||
QY      136 CACCCATGCGAGGTGGCCCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTGC 195
      |||
Db      41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
      |||
QY      196 AATGAGCGTGGGTGCTCTACTCCGCCCTCTCCCAAGATGAATGAGTACACCGTGCACCTG 255
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Db      61 AsnGluArgTyrValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
      |||
QY      256 GGCAGTGTATACCTCGCGGACAGAGAGCTCAGAGGATCAAGGCTTCGAAGTCATTCGCCG 315
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Db      81 GlySerAspThrLeuGlyAspArgArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
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QY      316 CACCCCGGCTACTCCACACAGACCCCATGTTAATGACCTCATCTCGTGAAGTCAATAGC 375
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Db      101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
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QY      376 CAGGCCAGGCTGTATCATGTTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCT 435
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Db      121 GlnAlaArgLeuSerSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
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QY      436 GGAACACACCTGTACTGTCTCGGCTGGGCACTTACCACAGGACCCAGATGTGACCTTTCC 495
      |||
Db      141 GlyThrThrCysThrValSerGlyTyrGlyThrThrThrSerProAspValThrPhePro 160
      |||
QY      496 TCTGACCTCATGTGCTGGATGTCAAGCTCATCTCCCCCAGGACTGCGACGAAGGTTTAC 555
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Db      161 SerAspLeuMetCysValAspValLysLeuIleSerProGlnAspCysThrLysValTyr 180
      |||
QY      556 AAGGACTTACTGGAAAAATTCATGCTGTGCTGGCTGGGCACTTACCAGAGGTACCTCGCAAGAAAAACGCC 615
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Db      181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
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QY      616 TGCATGTGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTCGCAAGGCTCTGGTGTC 675
      |||
Db      201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
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QY      676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
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Db      221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
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QY      736 TTCACCAAGTGGTAATGACACCATGAAAGACATCGC 774
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Db      241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
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RESULT 9

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US-10-643-795A-95
; Sequence 95, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN PRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
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; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 95
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-643-795A-95

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-643-795A-95 (1-253)
QY 16 ATGCGAAGATCCCTTCTCCCTGCGCCCTGCAGATCTTACTGCTATCTTATGCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAACCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGlnAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGCGCCCTGCTCAGTGCGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGTGGTGCTCACTGCGCCCTGCAGATGAATGAATGATGACCTGACCTGACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCACGAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
DB 101 HisProGlyTrpSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGCTGATCCATCGGTGAGAGAAAGTCAAGGCTGCGCTCCCGCTCGAAGCCCT 435
DB 121 GlnAlaArgLeuSerSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACACACCTGTACTGTCCTCGGCTGGGCGACTACACAGAGCCAGCATGTGACCTTCCC 495
DB 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCGCCAGGACTGCGACGAAGGTTTAC 555
DB 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValThr 180
QY 556 AAGGACTTACTGGAAATTCATGCTGTGGCTGGGATCCCGCTCCAGTCCCAAGAAACGCC 615
DB 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGCTGCTACCTCAGGGGACCGTGGTGTGAGAGGTACCTGCAAGGCTGCTGGTCC 675
DB 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTGGCGGCCAACCCCAATGACCCAGGAGCTTACACTCAAGTGTGCAAG 735
DB 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValThrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAAAGCATCGC 774
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Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 10
US-10-948-518-95
; Sequence 95, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 95
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-948-518-95

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-948-518-95 (1-253)
QY 16 ATGCGAAGATCCCTTCTCCCTGCGCCCTGCAGATCTTACTGCTATCTTATGCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAACCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGlnAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGTGCGCCCTGCTCAGTGCGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
QY 196 AATGAGCGTGGTGCTCACTGCGCCCTGCAGATGAATGAATGATGACCTGACCTGACCTG 255
DB 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GGCAGTGATACGCTGGCGCACGAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
DB 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
```

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QY 316 CACCCGGCTACTCCACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTATCCATGTTGTAAGAAGTACAGGCTGCCCTCCCGCTGCCAACCCTT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTCTCCGGCTGGGCACCTACCACGAGCCAGATGTGACCTTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATAATTCCATGTGTGCGTGGCATCCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGCMAATGTTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTCTCAAGTCTGGTGCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTTCGGGCCAACCCCAATGACCCAGAGGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253

RESULT 11
US-10-868-490A-1
; Sequence 1, Application US/10868490A
; Publication No. US20050106586A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios
; TITLE OF INVENTION: Detection of Neurodegenerative Diseases
; FILE REFERENCE: 11757.96USU1
; CURRENT APPLICATION NUMBER: US/10/868,490A
; PRIOR FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,486
; PRIOR FILING DATE: 2003-06-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-490A-1

Alignment Scores:
Pred. No.: 1,26e-118 Length: 253
Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 5 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-868-490A-1 (1-253)

QY 16 ATGGGAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTCTATCTCTAGCTTGGAACTC 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAAGCCAGAGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCC 135
Db 21 AlaGlyGluGluAlaGlnGlyAspLysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGCCCTCTGTCTAGTGGCAATACAGCTCCACTGCGGAGCGGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuVal 60
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QY 196 AATGAGCGCTGGGTGCTCACTGCCCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeu 80
QY 256 GGCAGTGTATAGCTCGGCGACAGAGAGCTCAGAGGATCAAGGCTCGAAGTCATTTCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCCAGGCTGTATCCATGTTGTAAGAAGTACAGGCTGCCCTCCCGCTGCCAACCCTT 435
Db 121 GlnAlaArgLeuSerMetValLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTCTCCGGCTGGGCACCTACCACGAGCCAGATGTGACCTTTTCC 495
Db 141 GlyThrThrCysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGCATGTCAGCTCATCTCCCGCCAGACTGCACGAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTyr 180
QY 556 AAGGACTTACTGGAATAATTCCATGTGTGCGTGGCATCCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyLeuProAspSerLysLysAsnAla 200
QY 616 TGCMAATGTTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTCTCAAGTCTGGTGCC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAATTTTCCCTTTCGGGCCAACCCCAATGACACCATGAAAAAGCATCGC 774
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
```

RESULT 12

```
US-10-262-511-92
; Sequence 92, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
```

```
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 92
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-92

Alignment Scores:
Pred. No.: 2,56e-117 Length: 250
Score: 1350.00 Matches: 250
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 75.8% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-262-511-92 (1-250)

QY 25 TCCCTTCTCTCCCTCCAGATCTTACTGCTATCTTACGCTTCTAGCCTTGAAACTGCAGAGAA 84
DB 1 SerLeuLeuLeuProLeuGlnLeuLeuLeuLeuLeuLeuSerLeuAlaLeuGluThrAlaGlyGlu 20
QY 85 GAAGCCAGGGTGACAAGATTATTGATGCGCCCATGTGCAAGAGGCTCCCAACCCATGG 144
DB 21 GluAlaGlnGlyAspIysIleIleAspGlyAlaProCysAlaArgGlySerHisProTrp 40
QY 145 CAGGTGGCCCTCTCAGTGGCAATCAGCTCCACTGCGGAGGGCTCTGCTCAATGAGCC 204
DB 41 GlnValAlaLeuSerGlyAsnGlnLeuHisCysGlyValLeuValAsnGluArg 60
QY 205 TGGGTGCTCACTGCGCCCTCCAGATGAATGAGTACACCGTGCACCTGGCGCAGTGAT 264
DB 61 TrpValLeuThrAlaAlaHisCysIysMetAsnGluTyrThrValHisLeuGlySerAsp 80
QY 265 ACGCTGGCGCAGGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGCCCAACCCCGC 324
DB 81 ThrLeuGlyAspArgArgAlaGlnArgIleIysAlaSerLysSerPheArgHisProGly 100
QY 325 TACTCCACAGACCCCATTTAATGACCTCAGCTCGTGAAGCTCATAGCCAGCCAGC 384
DB 101 TyrSerThrGlnThrHisValAsnAspLeuMetLeuValIysLeuAsnSerGlnAlaArg 120
QY 385 CTGTCACTCAGTGAAGAAGTCAGGCTGCCCTCCCGCTGCGAACCCCTCGAACCCACC 444
DB 121 LeuSerSerMetValIysValArgLeuProSerArgCysGluProProGlyThrThr 140
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QY 445 TGTACTGTCTCCGGCTGGGGCACTACCAGAGCCAGATGTGACCTTCCCTCTGACCTC 504
DB 141 CysThrValSerGlyTrpGlyThrThrThrSerProAspValThrPheProSerAspLeu 160
QY 505 ATGTGCGTGGATGTCAAGCTCATCTCCCGCCAGGACTGCACGAAGGTTTACAAAGACTTA 564
DB 161 MetCysValAspValIysLeuIleSerProGlnAspCysThrIysValTyrIysAspLeu 180
QY 565 CTGGAAATTCATGCTGTGCGCTGGCATCCCGGATCCCAAGAAAAACCGCTCGCAATGGT 624
DB 181 LeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysIysAsnAlaCysAsnGly 200
QY 625 GACTCAGGGGACCGTTGGTGTGCAGAGCTACCTCGCAAGGCTGTCTCTGGGNACT 684
DB 201 AspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSerTrpGlyThr 220
QY 685 TTCCCTTTGGCGCAACCCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCCACCAAG 744
DB 221 PheProCysGlyGlnProAsnAspProGlyValTyrThrGlnValCysIysPheThrLys 240
QY 745 TCGATAAATGACACCATGAAAGCATCGC 774
DB 241 TrpIleAsnAspThrMetLysLysHisArg 250

RESULT 13
US-10-344-394-38
; Sequence 38, Application US/10344394
; Publication No. US20040058342A1
; GENERAL INFORMATION:
; APPLICANT: Yousef, George M.
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: NOVEL KALLIKREIN GENE
; FILE REFERENCE: 11757-51USWO
; CURRENT APPLICATION NUMBER: US/10/344,394
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/CA01/01141
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,853
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-344-394-38

Alignment Scores:
Pred. No.: 4,26e-116 Length: 257
Score: 1337.00 Matches: 252
Percent Similarity: 97.7% Conservative: 0
Best Local Similarity: 97.7% Mismatches: 0
Query Match: 75.1% Indels: 6
DB: 4 Gaps: 2

US-09-905-083A-30 (1-969) x US-10-344-394-38 (1-257)

QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACCTTGGAACT 75
DB 1 MetAlaArgSerLeuLeuLeuProLeuGlnIleLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAAGAGCCAGGGTGACAAGATTATTGATGCGCCCATGTGCAAGAGGCTCC 135
DB 21 AlaGlyGluGluAlaGlnGlyAspIysIleIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGGCCCTGCTCAGTGCATCAGCTCCACTGC----- 180
DB 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysHisSerCysGlu 60
QY 181 GGAGGCGCTCTGGTCAATGAGCGCTGGGTGCTCACTGCCGCCCACTGCAAGATGATGAG 240
DB 61 GlyGlyValLeuValAsnGluArgTrpValLeuThrAlaAlaHisCysIysMetAsnGlu 80
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QY 241 TACACGTCACCTGGCGCAGTGATACGCTGGCGCAGCAGGAGCTCAGAGGATCAAGGCC 300
Db |||||
81 TyrThrValHisLeuGlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAla 100
QY 301 TCGAAGTCAATCGGCACCCCGCTACTCCACACAGACCCATGTTAATGACCTCATGCTC 360
Db |||||
101 SerLysSerPheArgHisProGlyTyrSerThrGlnThrHisValAsnAspLeuMetLeu 120
QY 361 GTGAAGCTCAATAGCCAGGCGAGGCTGTCATCCATGGTGAAGAAAGTCAGGTCGCCCTCC 420
Db |||||
121 ValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLysLysValArgLeuProSer 140
QY 421 CGCTCGGAACCCCTGGAAACCACTGTACTGCTCCGGCTGGCGCACTACCAAGGCCCA 480
Db |||||
141 ArgCysGluProProGlyThrThrCysThrValSerGlyTyrGlyThrThrSerPro 160
QY 481 GATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCAGGAC 540
Db |||||
161 AspValThrPhePro---AspLeuMetCysValAspValLysLeuIleSerProGlnAsp 179
QY 541 TGCACGAAGTTTACNAGCACTTACTGGGAAATTCATGCTGTGGCTGGCATCCCGNC 600
Db |||||
180 CysThrLysValTyrLysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAsp 199
QY 601 TCCAGAAACCGCTCGCAATGGTGACTCAGGGGACCGTGTGTGTCAGAGGTACCCCTG 660
Db |||||
200 SerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeu 219
QY 661 CAAGTCTCGTCTCTGGGAACTTTTCCCTTCCGGCCAAACCAATGACCCAGAGGTCTAC 720
Db |||||
220 GlnGlyLeuValSerTrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyr 239
QY 721 ACTCAAGTGTCAAGTTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
Db |||||
240 ThrGlnValCysLysPheThrLysTrpIleAsnAspThrMetLysLysHisArg 257
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RESULT 14

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US-10-262-511-102
; Sequence 102, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
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; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 102
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-102

Alignment Scores:
Pred. No.: 3,84e-108 Length: 247
Score: 1252.00 Matches: 228
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 0
Query Match: 70.3% Indels: 0
DB: 4 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-262-511-102 (1-247)
QY 88 GCCCAGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCCTGGCGAG 147
Db |||||
11 AlaArgGlyAspLysIleAspGlyAlaProCysAlaArgGlySerHisProTrpGln 30
QY 148 GTGGCCCTGCTCAGTGGCAATCAGCTCCACCTCGCGAGGCTCTGTCATCAATCAGCGCTGG 207
Db |||||
31 ValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyGlyValLeuValAsnGluArgTrp 50
QY 208 GTGCTCACTGCGCCGCTGCAAGATGAATGAGTACACCGTGCACCTGGCGCAGTGATACG 267
Db |||||
51 ValLeuThrAlaAlaHisCysLysMetAsnGluTyrThrValHisLeuGlySerAspThr 70
QY 268 TTGGCGCAGCAGAGAGCTCAGAGGATCAAGGCTCGAAGTCAATTCGCCGCCACCCCGCTAC 327
Db |||||
71 LeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArgHisProGlyTyr 90
QY 328 TCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGTCAATAGCCAGGCCAGGCTG 387
Db |||||
91 SerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSerGlnAlaArgLeu 110
QY 388 TCATCCATGTTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCTGGAAACCACTGT 447
Db |||||
111 SerSerMetValLysValArgLeuProSerArgCysGluProProGlyThrThrCys 130
QY 448 ACTGTCTCCGCTGGGCGACTACACAGAGCCCGATGTGACCTTCCCTCTGACCTCATG 507
Db |||||
131 ThrValSerGlyTrpGlyThrThrThrSerProAspValThrPheProSerAspLeuMet 150
QY 508 TCGGTGGATGTCAAGCTCATCTCCCCCGCAGGACTCCACGAGGTTTACAGGACTTACTG 567
Db |||||
151 CysValAspValLysLeuIleSerProGlnAspCysThrLysValTyrLysAspLeuLeu 170
QY 568 GAAATTCATGCTGTGCGCTGGCATCCCGCATCCAGAAACCAACCCCTGCAATGCTGAC 627
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Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGAGAGAGAGAGATATTGATGGCGCCCACTGTGCAAGAGCTCC 135
Db 21 AlaGlyGluAlaGlnGlyAspYsIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGGCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGGTGCTACTGCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GCGAGTGATACCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCAGAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGTGTCATCCATGTGTGAAGAAGTCAAGCTCCGCTCCGCTGCGAACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGNACCACTGTACTGCTCCGGCTGGGCACTTACCAGGCGCCAGATGTGACCTTTCC 495
Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGTGATGCAAGCTCATCTCCCGCCAGGACTGCAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTy 180
QY 556 AAGGACTTACTGGAATAATTCATGTGTGCTGGTGGCATCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGGTGACTCAGGGGACCGTGGTGTGCGAGAGTACCTGCAAGTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240

RESULT 2

US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Alignment Scores: 7.13e-116 Length: 253
Pred. No.:

Score: 1364.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.6% Indels: 0
DB: 6 Gaps: 0
US-09-905-083A-30 (1-969) x US-10-412-748-14 (1-253)
QY 16 ATGGCAAGATCCCTTCTCTGCGCCCTGCAGATCTTACTGCTATCTTACGCTTGGAACT 75
Db 1 MetAlaArgSerLeuLeuLeuProLeuGlnLeuLeuSerLeuAlaLeuGluThr 20
QY 76 GCAGGAGAGAGAGAGAGAGATATTGATGGCGCCCACTGTGCAAGAGCTCC 135
Db 21 AlaGlyGluAlaGlnGlyAspYsIleAspGlyAlaProCysAlaArgGlySer 40
QY 136 CACCCATGCGAGGTGGCTGCTCAGTGGCAATCAGCTCCACTGCGGAGCGCTCTGGTC 195
Db 41 HisProTrpGlnValAlaLeuLeuSerGlyAsnGlnLeuHisCysGlyValLeuVal 60
QY 196 AATGAGCGTGGGTGCTCAGTGGCGCCCACTGCAAGATGAATGAGTACACCGTGCACCTG 255
Db 61 AsnGluArgTrpValLeuThrAlaAlaHisCysLysMetAsnGluTrpThrValHisLeu 80
QY 256 GCGAGTGATACCTGGCGGACAGGAGCTCAGAGGATCAAGGCTCAGAGTCAATCCGC 315
Db 81 GlySerAspThrLeuGlyAspArgAlaGlnArgIleLysAlaSerLysSerPheArg 100
QY 316 CACCCCGGCTACTCCACACAGACCCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGC 375
Db 101 HisProGlyTySerThrGlnThrHisValAsnAspLeuMetLeuValLysLeuAsnSer 120
QY 376 CAGGCGAGGTGTCATCCATGTGTGAAGAAGTCAAGCTCCGCTCCGCTGCGAACCCCT 435
Db 121 GlnAlaArgLeuSerMetValLysLysValArgLeuProSerArgCysGluProPro 140
QY 436 GGAACCACTGTACTGCTCTCCGGCTGGGCACTTACCAGGCGCCAGATGTGACCTTTCC 495
Db 141 GlyThrCysThrValSerGlyTrpGlyThrThrSerProAspValThrPhePro 160
QY 496 TCTGACCTCATGTGCGTGTGATGCAAGCTCATCTCCCGCCAGGACTGCAAGGTTTAC 555
Db 161 SerAspLeuMetCysValAspValLysLeuLeuSerProGlnAspCysThrLysValTy 180
QY 556 AAGGACTTACTGGAATAATTCATGTGTGCTGGTGGCATCCCGACTCCCAAGAAAAACGCC 615
Db 181 LysAspLeuLeuGluAsnSerMetLeuCysAlaGlyIleProAspSerLysLysAsnAla 200
QY 616 TGCATGGTGACTCAGGGGACCGTGGTGTGCGAGAGTACCTGCAAGTCTGGTGTC 675
Db 201 CysAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAAATGACACCATGAAAGAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHisArg 253
RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14


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QY 616 TGCAATGGTGACTCAGGGGACGTTGGTGTGCAGAGGTACCTCGCAAGGTCTGGTGTC 675
Db 201 CyAsnGlyAspSerGlyGlyProLeuValCysArgGlyThrLeuGlnGlyLeuValSer 220
QY 676 TGGGGAACCTTTCCCTTTCGGGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 221 TrpGlyThrPheProCysGlyGlnProAsnAspProGlyValTyThrGlnValCysLys 240
QY 736 TTCACCAAGTGGATAATGACACCATGAAAAAGCATCGC 774
Db 241 PheThrLysTrpIleAsnAspThrMetLysLysHieArg 253

RESULT 5
US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19

Alignment Scores:
Pred. No.: 7,72e-82 Length: 181
Score: 988.00 Matches: 181
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 55.5% Indels: 0
DB: 6 Gaps: 0

US-09-905-083A-30 (1-969) x US-10-412-748-19 (1-181)
QY 232 ATCAATGATGTACACCTGTGCACCTGGSCAGTGTACCTGGGCACAGGAGCTCAGAG 291
Db 1 MetAsnGluTyThrValHisLeuGlySerAspThrLeuGlyAspArgAlaGlnArg 20
QY 292 ATCAAGGCCTCGAAGTCATTCCGCCACCCCGCTACTCCACACAGACCCCATGTTAATGAC 351
Db 21 IleLysAlaSerLysSerPheArgHisProGlyTyThrSerThrGlnThrHisValAsnAsp 40
QY 352 CTCATGCTCGTGAAGTCAATAGCCAGGCCAGGCTGTCTATCCATGTGTGAAGAAAGTCAGG 411
Db 41 LeuMetLeuValLysLeuAsnSerGlnAlaArgLeuSerSerMetValLysLysValArg 60
QY 412 CTGCCCTCCCGTCGCCAACCCCTCGAACCACTGTACTGTCTCCGGCTGGGGCACTACC 471
Db 61 LeuProSerArgCysGluProProGlyThrThrCysThrValSerGlyTrpGlyThrThr 80
QY 472 ACAGAGCCAGATGTGACCTTTCCTCTGACCTCATGTGGGTGGATGTCAAGTCTCATCTCC 531
Db 81 ThrSerProAspValThrPheProSerAspLeuMetCysValAspValLysLeuIleSer 100
QY 532 CCCAGAGTGCACGAAGTTTACAGGACTTACTCGAAATTTCCATGTGTGCGGTGCG 591
Db 101 ProGlnAspCysThrLysValTyLysAspLeuLeuGluAsnSerMetLeuCysAlaGly 120
QY 592 ATCCCGACTCCNAGAAAAACGCTGCATGTGACTCAGGGGACCGTTGGTGTGCAGA 651
Db 121 IleProAspSerLysLysAsnAlaCysAsnGlyAspSerGlyGlyProLeuValCysArg 140
QY 652 GGTACCTCGAAGGTCTGTGTCTCTGGGAACTTTCCCTTGGCGGCCAACCAATGACCCA 711
```

```
Db 141 GlyThrLeuGlnGlyLeuValSerTrpGlyThrPheProCysGlyGlnProAsnAspPro 160
QY 712 GGAGTCTACACTCAAGTGTGCAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCAT 771
Db 161 GlyValTyThrGlnValCysLysPheThrLysTrpIleAsnAspThrMetLysLysHis 180
QY 772 CGC 774
Db 181 Arg 181

RESULT 6
US-10-131-826A-456
; Sequence 456, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 456
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-456

Alignment Scores:
Pred. No.: 8.12e-48 Length: 293
Score: 612.50 Matches: 114
Percent Similarity: 65.0% Conservative: 43
Best Local Similarity: 47.9% Mismatches: 72
Query Match: 34.4% Indels: 34
DB: 6 Gaps: 4
```


; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-7

Alignment Scores:
Pred. No.: 293
Score: 612.50 Length: 8,12e-48
Matches: 114
Percent Similarity: 66.0% Conservative: 43
Best Local Similarity: 47.9% Mismatches: 72
Query Match: 34.4% Indels: 9
DB: 6 Gaps: 4

US-09-905-083A-30 (1-969) x US-10-412-748-7 (1-293)

```
QY 76 GCAGGAGAGAGAGCCAGGGTGAC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAaspAlaAargSerAaspSerSerArgIleAaengGlySerAaspCys 73
QY 124 GCAAGAGGCTCCACCCATGGCAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaLeuLeuLeuAargProAasnGlnLeuTrCys 93
QY 181 GGAGGCGTCTGTGTCATAGAGCGCTGGTGCTCACTGCCGCCACTGCAAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysAargLysLysVal 113
QY 241 TACACCGTGCACCTGGCGAGTATACGCTGGGC-----GACAGGAGAGCTCAGAGG 291
Db 114 PheArgValAargLeuGlyHisTySerLeuSerProValTyGluSerGlyGlnGlnMet 133
QY 292 ATCAAGCGCTCGAAGTCATTCCGCCACCCGGCTACTCCACACAGACCCATGTTAATGAC 351
Db 134 PheGlnGlyValLysSerIleProHisProGlyTySerHisProGlyHisSerAasnA 153
QY 352 CTCATGCTCGTGAAGTCAATAGCCAGCGAGCGCTGTCTATCCATGTGTGAAGAAAGTCAGG 411
Db 154 LeuMetLeuIleLysLeuAasnArgAlleAArgProThrLysAaspValAargProIleA 173
QY 412 CTGCGCTCCGTCGGAACCCCTCGGAACACCTGTACTGTCTCCGGCTGGGGCCTACCTCC 471
Db 174 ValSerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThr 193
QY 472 ACGAGCCAGATGTGACCTTCCTCTGACCTCATGTGCTGATGTCAAGTCTCATCTCC 531
Db 194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAasnIleSerValLeuSer 213
QY 532 CCCCAGGACTGCAGGAAGCTTTACAGGACTTACTGGAAATTTCCATGCTGTGCGCTGCG 591
Db 214 GlnLysAArgCysGluAaspAlaTyProAArgGlnIleAaspAaspThrMetPheCysAlaGly 233
QY 592 ATCCCGGACTCCAGAAAACCGCTGCATGTGACTCAGGGGACCGTGGTGTGCAGA 651
Db 234 ---AaspLysAlaGlyAargAaspSerCysGlnGlyAaspSerGlyGlyProValValCysA 252
QY 652 GTTACCTCCAGGCTGTGTGCTGGGAACTTTCCTTTGGGCAACCCCAATGACCCA 711
Db 253 GlySerLeuGlnGlyLeuValSerTrpGlyAaspTyProCysAlaAargProAasnArgPro 272
QY 712 GGAGTCTACACTCAAGTGTGCAAGTTTCACCAAGTGGATAAATGACACCATGAAA 765
Db 273 GlyValTyThrAasnLeuCysLysPheThrLysTrpIleGlnGluThrIleGln 290
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RESULT 9

US-10-973-115B-456
; Sequence 456, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Quiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 456
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-456

Alignment Scores:
Pred. No.: 293
Score: 612.50 Length: 8,12e-48
Matches: 114
Percent Similarity: 66.0% Conservative: 43
Best Local Similarity: 47.9% Mismatches: 72
Query Match: 34.4% Indels: 9
DB: 6 Gaps: 4

US-09-905-083A-30 (1-969) x US-10-973-115B-456 (1-293)

```
QY 76 GCAGGAGAGAGAGCCAGGGTGAC-----AAGATTATTGATGGCGCCCATGT 123
Db 54 AlaGlyGluAaspAlaAargSerAaspSerSerArgIleAaengGlySerAaspCys 73
QY 124 GCAAGAGGCTCCACCCATGGCAGGTGGCC---CTGCTCAGTGGCAATCAGCTCCACTGC 180
Db 74 AspMetHisThrGlnProTrpGlnAlaLeuLeuLeuAargProAasnGlnLeuTrCys 93
QY 181 GGAGGCGTCTGTGTCATAGAGCGCTGGTGCTCACTGCCGCCACTGCAAGATGAATGAG 240
Db 94 GlyAlaValLeuValHisProGlnTrpLeuLeuThrAlaAlaHisCysAargLysLysVal 113
QY 241 TACACCGTGCACCTGGCGAGTATACGCTGGGC-----GACAGGAGAGCTCAGAGG 291
Db 114 PheArgValAargLeuGlyHisTySerLeuSerProValTyGluSerGlyGlnGlnMet 133
QY 292 ATCAAGCGCTCGAAGTCAATAGCCAGCGAGCGCTGTCTATCCATGTGTGAAGAAAGTCAGG 351
Db 134 PheGlnGlyValLysSerIleProHisProGlyTySerHisProGlyHisSerAasnA 153
QY 352 CTCATGCTCGTGAAGTCAATAGCCAGCGAGCGCTGTCTATCCATGTGTGAAGAAAGTCAGG 411
Db 154 LeuMetLeuIleLysLeuAasnArgAlleAArgProThrLysAaspValAargProIleA 173
QY 412 CTGCGCTCCGTCGGAAGCTTTACAGGACTTACTGGAAATTTCCATGCTGTGCGCTGCG 471
```

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Db 174 ValSerSerHisCysProSerAlaGlyThrLysCysLeuValSerGlyTrpGlyThrThr 193
Qy 472 ACAGCCAGCATGATGACCTTTCCTCTGACCTCATGCTGCGTGGATGTCAGGTCATCTCC 531
Db 194 LysSerProGlnValHisPheProLysValLeuGlnCysLeuAanLysSerValLeuSer 213
Qy 532 CCCAGGACTGCAGGAGTTTACAGGACTTACTGGAATTCATGCTGCTGGCTGGC 591
Db 214 GlnLysArgCysGluAspAlaTrpProArgGlnIleAspAspThrMetPheCysAlaGly 233
Qy 592 ATCCCCGACTCCAAAGAAACCGCTGCAATGGTGACTCAGGGGACCGTTGGTGTCAGA 651
Db 234 ---AspLysAlaGlyArgAspSerCysGlnGlyAspSerGlyGlyProValValCysAsn 252
Qy 652 GTACCTGCAAGTCTGGTGTCTGCGGAACTTCCCTTGGCGCCCAACCAATGACCCA 711
Db 253 GlySerLeuGlnGlyLeuValSerTrpGlyAspTrpProCysAlaArgProAsnArgPro 272
Qy 712 GGAGTCTACACTCAAGTGTCAAGTTCCACCAAGTGGATAATGACACCATGAAA 765
Db 273 GlyValTrpThrAsnLeuCysLysPheThrLysTrpIleGlnGlnThrIleGln 290

RESULT 10
US-10-995-561-552
; Sequence 552, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-552

Alignment Scores:
Pred. No.: 3,78e-45 Length: 267
Score: 583.00 Matches: 110
Percent Similarity: 61.2% Conservative: 43
Best Local Similarity: 44.0% Mismatches: 89
Query Match: 32.8% Indels: 8
DB: 6 Gaps: 4

US-09-905-083A-30 (1-969) x US-10-995-561-552 (1-267)
Qy 28 CTCTCTCTGCGCTGACAGATCTTACTGCTATCTCTAGCTTGGAACTGCAGGAGAA 87
Db 20 LeuLeuThrAlaLeuGlnValLeuAlaIleAlaMet-----ThrGlnSerGlnGlu 36
Qy 88 GCCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGCTCCCAACCCATGGCAG 147
Db 37 AspGlu---AsnLysIleIleGlyGlyHisThrCysThrArgSerSerGlnProTrpGln 55
Qy 148 GTGGCCCTGCTCAGTGGC-----ATCAGCTCCACTGCGGAGCGCTCTGGTCAATGAG 201
Db 96 HisAsnLeuArgArgTrpGluAlaThrGlnGlnValLeuArgValValArgGlnValThr 115
```

```
Qy 316 CACCCGGCTACTCCACACAGACCCATGTTAATGACTCTCATGCTCGTGAAGCTCAATAGC 375
Db 116 HisProAsnTrpAsnSerArgThrHisAspAspLeuMetLeuLeuGlnGlnGln 135
Qy 376 CAGGCAGGCTGTGTCATCGTGAAGAAAGTCAGGCTGCGCTCCCGCTCGGAACCCCT 435
Db 136 ProAlaArgIleGlyArgAlaValArgProIleGluValThrGlnAlaCysAlaSerPro 155
Qy 436 GGAACCACTGTACTGCTCCGCTGGGCACTACCAAGAGCCAGATGACCTTTCC 495
Db 156 GlyThrSerCysArgValSerGlyTrpGlyThrIleSerSerProIleAlaArgTrpPro 175
Qy 496 TCTGACTCATGTCGCTGGATGTCAGCTCATCTCCCGCCAGGACTGCACAGAGTTTAC 555
Db 176 AlaSerLeuGlnCysValAsnIleAsnIleSerProAspGluValCysGlnLysAlaTrp 195
Qy 556 AAGGACTTACTGGAATAATTCATGCTGTGCGTGGCATCCCGACTCCCAAGAAACGCC 615
Db 196 ProArgThrIleThrProGlyMetValCysAlaGlyValProGlnGlyGlyLysAspSer 215
Qy 616 TGAATGGTGACTCAGGGGACCGTTGGTGTGAGAGGTACCCCTGCAAGGTCTGGTGTCC 675
Db 216 CysGlnGlyAspSerGlyGlyProLeuValCysArgGlyGlnLeuGlnGlyLeuValSer 235
Qy 676 TGGGGAACTTCCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTGCAAG 735
Db 236 TrpGlyMetGluArgCysAlaLeuProGlyTrpProGlyValTrpThrAsnLeuCysLys 255
Qy 736 TTCACCAAGTGGATAAATGACACCATGAAA 765
Db 256 TyrArgSerTrpIleGluThrMetArg 265

RESULT 11
US-10-995-561-553
; Sequence 553, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-553

Alignment Scores:
Pred. No.: 3,78e-45 Length: 267
Score: 583.00 Matches: 110
Percent Similarity: 61.2% Conservative: 43
Best Local Similarity: 44.0% Mismatches: 89
Query Match: 32.8% Indels: 8
DB: 6 Gaps: 4

US-09-905-083A-30 (1-969) x US-10-995-561-553 (1-267)
Qy 28 CTCTCTCTGCGCTGACAGATCTTACTGCTATCTCTAGCTTGGAACTGCAGGAGAA 87
Db 20 LeuLeuThrAlaLeuGlnValLeuAlaIleAlaMet-----ThrGlnSerGlnGlu 36
Qy 88 GCCCAGGGTGACAGATTATTGATGGCGCCCATGTGCAAGAGCTCCCAACCCATGGCAG 147
Db 37 AspGlu---AsnLysIleIleGlyGlyHisThrCysThrArgSerSerGlnProTrpGln 55
Qy 148 GTGGCCCTGCTCAGTGGC-----ATCAGCTCCACTGCGGAGCGCTCTGGTCAATGAG 201
Db 56 AlaAlaLeuLeuAlaGlyProArgArgPheLeuCysGlyGlyAlaLeuLeuSerGly 75
Qy 202 CGTGGGTGCTCACTGCGCCCACTGCAAGATGATGAGTACACCGTGACCTGGCGCAGT 261
Db 76 GlnTrpValIleThrAlaAlaHisCysGlyArgProIleLeuGlnValAlaLeuGlyLys 95
Qy 262 GATACGCTG-----GGCGACGAGGAGCTCAGAGGATCAAGGCTCGAAGTCAATCCGC 315
Db 96 HisAsnLeuArgArgTrpGluAlaThrGlnGlnValLeuArgValValArgGlnValThr 115
```

```
QY 202 CGCTGGGTGCTCACTGCGGCCACTGCAAGATGAATGAGTACACCGTGACCTGGGCAGT 261
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
76 GlnTrpValIleThrAlaAlaHisCysGlyArgProIleLeuGlnValAlaLeuGlyLys 95
QY 262 GATACGCTG-----GGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGC 315
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
96 HisAsnLeuArgArgTrpGluAlaThrGlnValLeuArgValValArgGlnValThr 115
QY 316 CACCCCGGTACTCCACAGACCCCATGTTAATGACCTCATGCTGTGAAGCTCAATAGC 375
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
116 HisProAsnTyraenSerArgThrHisAspAsnAspLeuMetLeuLeuGlnGln 135
QY 376 CAGGCAGGCTGCATCCATGTTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCT 435
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
136 ProAlaArgIleGlyArgAlaValArgProIleGluValThrGlnAlaCysAlaSerPro 155
QY 436 GGAACACCTGTACTCTCCGCTGGGCACCTACACGAGGCCAGATGTGACCTTTCCC 495
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
156 GlyThrSerCysArgValSerGlyTTPGlyThrIleSerSerProIleAlaArgTyrPro 175
QY 496 TCTGACCTCATGTGCTGGATGTCAGCTCATCTCCCCCAGGACTGCAGAGGTTTAC 555
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
176 AlaSerLeuGlnCysValAsnIleAsnIleSerProAspGluValCysGlnLysAlaTyr 195
QY 556 AAGGACTTACTGAAATTCATGCTGTGCTGGCATCCCGACTCCCAAGAAAAAGCC 615
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
196 ProArgThrIleThrProGlyMetValCysAlaGlyValProGlnGlyGlyLysAspSer 215
QY 616 TGCATGTGTGACTCAGGGGACCGTTGGTGTGAGAGGTACCTGCAAGGTCTGGTGTC 675
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
216 CysGlnGlyAspSerGlyGlyProLeuValCysArgGlyGlnLeuGlnGlyLeuValSer 235
QY 676 TGGGGAACCTTCCCTTGGGCCCAACCCATGACCCAGGAGTCTACACTCAAGTGTCCAG 735
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
236 TrpGlyMetGluArgCysAlaLeuProGlyTyrProGlyValTyrThrAsnLeuCysLys 255
QY 736 TTCACCAAGTGGATAAATGACACCATGAAA 765
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
256 TyrArgSerTrpIleGluThrMetArg 265
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RESULT 12

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US-10-131-826A-396
; Sequence 396, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 396
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-396

Alignment Scores:
Pred. No.:      4,18e-45      Length:      260
Score:          582.50      Matches:    118
Percent Similarity: 59.3%      Conservative: 26
Best Local Similarity: 48.6%      Mismatches:  88
Query Match:    32.7%      Indels:     11
DB:              6          Gaps:         5

US-09-905-083A-30 (1-969) x US-10-131-826A-396 (1-260)
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QY 46 ATCTTACTGCTATCTTAGCTTGGAAACTGAGCA---GAAGAAGCCAGGGTGACAG 102
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
13 MetPheLeuLeuLeuLeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGlnAspLys 32
QY 103 ATTATTGATGGCGCCCATGTGCAAGAGGCTCCACCATGCGAGGTGGCTGCTGCTCAGT 162
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
33 ValLeuGlyGlyHisGluCysGlnProHisSerGlnProTrpGlnAlaAlaLeuPheGln 52
QY 163 GCGAATCAGCTCCACTGCGGAGCGCTCTGTGTCATAGCGCTGGGTGCTCACTGCGGCC 222
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
53 GlyGlnGlnLeuLeuCysGlyGlyValLeuValGlyGlyAsnTrpValLeuThrAlaAla 72
QY 223 CACTGCAAGATGAATGAGTACACCGTGCACCTGGCGCAGTGATACGCTG-----GSCGAC 276
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
73 HisCysLysLysProLysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAsp 92
QY 277 AGGAGAGCTCAGAGGATCAAGGCCTCGAAGTCATTCCGCCACCCCGGCTACTCCACA--- 333
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
93 GlyProGluGlnGluIleProValValGlnSerIleProHisProCysTyrAsnSerSer 112
QY 334 -----CAGACCCATGTTAATGACTCATGTCTGTGAAGCTCAATAGCCAGGCCAGGCTG 387
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
113 AspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeu 132
QY 388 TCATCCATGTTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCTCGAACCACCTGT 447
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
133 GlySerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCys 152
QY 448 ACTGTCTCGGCTGGGCACTTACCAGAGCCAGATGTGACCTTTCCCTCTGACCTCATG 507
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
153 ThrValSerGlyTyrGlyThrValThrSerProArgGluAsnPheProAspThrLeuAsn 172
QY 508 TCGTGGATGTCAAGCTCATCTCCCCCAGGACTGCACGAAAGTTTACAGGACTTACTG 567
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
173 CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle 192
QY 568 GAAATTCATGCTGCTGGCTGGCATCCCGACTCCAGAAAAACGCC-----TGCAT 621
Db   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
193 ThrAspGlyMetValCysAlaGly-----SerSerLysGlyAlaAspThrCysGln 209
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QY 622 GGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTCTGTGGTCTCTGGGA 681
Db 210 GlyAspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGly 229
QY 682 ACTTTCCTTCGCGCCCAACCAATGATCCAGGAGTCTTACACTCAAGTGTGCAAGTTCAC 741
Db 230 SerAspProCysGlyArgSerAspLysProGlyValThrAsnIleCysArgTyrLeu 249
QY 742 AAGTGCATA 750
Db 250 AspTrpIle 252

RESULT 13
US-10-510-321-2
; Sequence 2, Application US/10510321
; Publication No. US20050287528A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios P.
; APPLICANT: Kishi, Tadaaki
; TITLE OF INVENTION: Methods for Detecting Ovarian Cancer
; FILE REFERENCE: 11757.104USWO
; CURRENT APPLICATION NUMBER: US/10/510,321
; PRIOR FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/CA03/00495
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,559
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-321-2

Alignment Scores:
Pred. No.: 4.18e-45 Length: 260
Score: 582.50 Matches: 118
Percent Similarity: 59.3% Conservative: 26
Best Local Similarity: 48.6% Mismatches: 88
Query Match: 32.7% Indels: 11
DB: 6 Gaps: 5

US-09-905-083A-30 (1-969) x US-10-510-321-2 (1-260)
QY 46 ATCTTACTGTATCCCTTAGCTTGGAACTGCAGGA---GAAGAAGCCAGCGGTGACAAG 102
Db 13 MetPheLeuLeuLeuGlyGlyAlaTrpAlaGlyHisSerArgAlaGlnGluAspLys 32
QY 103 ATTATTGATGGCCGCCCATGTGCAAGAGGCTCCACCCATGGCAGGTGGCCCTGCTCAGT 162
Db 33 ValLeuGlyGlyHisGluCysGlnProHisSerGlnProTrpGlnAlaAlaLeuPheGln 52
QY 163 GCAATCAGCTCCACTGCGGAGCGCTCGGTCAATGAGCGCTGCTCACTGCGGCC 222
Db 53 GlyGlnGlnLeuLeuGlyGlyValLeuValGlyAsnTrpValLeuThrAlaAla 72
QY 223 CACTGCAAGATGAATGATACACCGCTGCACCTGGCAGTGATACGCTG-----GGCGAC 276
Db 73 HisCysGlyBlyProLysTyrThrValArgLeuGlyAspHisSerLeuGlnAsnLysAsp 92
QY 277 AGGAGAGCTCAGAGGATCAGGCTCGAAGTCAATCCGCCACCCCGGCTACTCCACA--- 333
Db 93 GlyProGluGlnGluIleProValValGlnSerIleProHisProCysTyrAsnSerSer 112
QY 334 -----CAGACCCATGTTAATGACCTCATGCTGTAAGTCAATAGCCAGCGGCTG 387
Db 113 AspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeu 132
QY 388 TCATCATGTGTGAAGAAAGTCAGGCTGCGCTCCCGTGGCAACCCCGCTGGAACCACTGT 447
Db 133 GlySerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCys 152
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QY 448 ACTGTCTCCGGCTGGGGCACTACCAAGAGCCAGATGTGACCTTCCCTCTGACCTCATG 507
Db 153 ThrValSerGlyTrpGlyThrValThrSerProArgGluAsnPheProAspThrLeuAsn 172
QY 508 TGGTGGATGTCAAGTCTCATCTCCCCCAGGACTGCACGAAGGTTTACAAGGACTTACTG 567
Db 173 CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle 192
QY 568 GAAATTCATGTGTGCGCTGCATCCCGACTCCCAAGAAACCGCC-----TGCAT 621
Db 193 ThrAspGlyMetValCysAlaGly-----SerSerLysGlyAlaAspThrCysGln 209
QY 622 GGTGACTCAGGGGACCGTTGGTGTGCAGAGGTACCTGCAAGGTCTGGTGTCTCTGGGA 681
Db 210 GlyAspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGly 229
QY 682 ACTTTCCTTCGCGCCCAACCAATGATCCAGGAGTCTTACACTCAAGTGTGCAAGTTCAC 741
Db 230 SerAspProCysGlyArgSerAspLysProGlyValThrAsnIleCysArgTyrLeu 249
QY 742 AAGTGCATA 750
Db 250 AspTrpIle 252

RESULT 14
US-10-973-115B-396
; Sequence 396, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Quiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
; FILE REFERENCE: 39870-333ORIC300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; PRIOR FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 396
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-396
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Alignment Scores:


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Db      113 AspValGluAspHisAsnHisAspLeuMetLeuLeuGlnLeuArgAspGlnAlaSerLeu 132
QY      388 TCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCTCGAACCCACCTGT 447
Db      133 GlySerLysValLysProIleSerLeuAlaAspHisCysThrGlnProGlyGlnLysCys 152
QY      448 ACTGTCTCCCGCTGGGGCACTACACGAGCCGAGATGTGACCTTCCCTCTGACCTCATG 507
Db      153 ThrValSerGlyTrpGlyThrValThrSerProArgGluAsnPheProAspThrLeuAsn 172
QY      508 TGGGTGGATGTCAGGCTCATCTCCCCCGCAGACTGCACGAAAGGTTTACAAGGACTTACTG 567
Db      173 CysAlaGluValLysIlePheProGlnLysLysCysGluAspAlaTyrProGlyGlnIle 192
QY      568 GAAATTCATGTGTGCGTGGCATCCCGCATCCCGACTCCCAAGAAACGCGCC-----TGCAAT 621
Db      193 ThrAspGlyMetValCysAlaGly-----SerSerLysGlyAlaAspThrCysGln 209
QY      622 GGTGACTCAGGGGACCGTTGGTGTGCGAGAGGTACCTGCAAGGTCTGGTGTCTCTGGGA 681
Db      210 GlyAspSerGlyGlyProLeuValCysAspGlyAlaLeuGlnGlyIleThrSerTrpGly 229
QY      682 ACTTTCCTTGGCGCCCAACCAATGACCCAGGAGTCTACACTCAAGTGTCAAGTTCCACC 741
Db      230 SerAspProCysGlyArgSerAspLysProGlyValTyrThrAsnIleCysArgTyrLeu 249
QY      742 AAGTGGATA 750
Db      250 AspTrpIle 252
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Search completed: March 11, 2006, 02:21:42
Job time : 22.5 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	4 AAE08294	Aae08294 Human str
2	49	100.0	9	4 AAE08236	Aae08236 Human str
3	49	100.0	9	8 ADR68850	Adr68850 Human str
4	49	100.0	9	8 ADR68792	Adr68792 Human str
5	49	100.0	9	8 ADR68870	Adr68870 Human str
6	49	100.0	97	6 ADA05740	Ada05740 Human NOV
7	49	100.0	97	8 ADNG2904	Adng2904 Human NOV
8	49	100.0	136	4 ABG23378	Abg23378 Novel hum
9	49	100.0	144	8 ADI39727	Adi39727 Stratum c
10	49	100.0	144	8 ADI37151	Adi37151 Stratum c
11	49	100.0	181	6 ADA05738	Ada05738 Human NOV
12	49	100.0	181	8 ADNG2902	Adng2902 Human NOV
13	49	100.0	198	6 ADA05736	Ada05736 Human NOV
14	49	100.0	198	8 ADNG2900	Adng2900 Human NOV
15	49	100.0	224	6 ADA05744	Ada05744 Human NOV
16	49	100.0	224	8 ADNG2908	Adng2908 Human NOV
17	49	100.0	224	9 ADV21100	Adv21100 Human str
18	49	100.0	225	4 AAB98502	Aab98502 Human str
19	49	100.0	247	6 ADA05742	Ada05742 Human NOV
20	49	100.0	247	8 ADNG2906	Adng2906 Human NOV
21	49	100.0	250	6 ADA05732	Ada05732 Human NOV
22	49	100.0	250	8 ADNG2896	Adng2896 Human NOV
23	49	100.0	252	6 ADA05734	Ada05734 Human NOV
24	49	100.0	252	8 ADNG2898	Adng2898 Human NOV

25	49	100.0	253	2 AAR67888	Aar67888 Human str
26	49	100.0	253	2 AAW05383	Aaw05383 Human amy
27	49	100.0	253	5 ABB84421	Abb84421 Human SCC
28	49	100.0	253	5 ABB84406	Abb84406 Human SCC
29	49	100.0	253	5 AAU82740	Aau82740 Amino aci
30	49	100.0	253	6 ABU07440	Abu07440 Protein d
31	49	100.0	253	6 ABU07471	Abu07471 Protein d
32	49	100.0	253	6 ABR58471	Abr58471 Human str
33	49	100.0	253	7 ADR80484	Adr80484 Ovarian c
34	49	100.0	253	7 ADJ68833	Adj68833 Human hea
35	49	100.0	253	7 ADN39180	Adn39180 Cancer/an
36	49	100.0	253	8 ADL06515	Adl06515 Human tum
37	49	100.0	253	8 ADN04182	Adn04182 Antipsori
38	49	100.0	253	8 ADR72880	Adr72880 Human ova
39	49	100.0	253	9 ADY67588	Ady67588 Human kal
40	49	100.0	253	9 AEC00353	Aec00353 Human kal
41	49	100.0	257	3 AAB21326	Aab21326 Human HSC
42	40	81.6	226	5 ABB84422	Abb84422 Rat SCCE
43	39	79.6	9	4 AAE08326	Aae08326 Human str
44	39	79.6	9	8 ADR68883	Adr68883 Human str
45	37	75.5	9	4 AAE08298	Aae08298 Human str

ALIGNMENTS

RESULT 1
AAE08294
ID AAE08294 standard; peptide; 9 AA.
AC AAE08294;
XX XX

DT 01-NOV-2001 (first entry)

XX Human stratum corneum chymotrypsin enzyme peptide #59 (residues 72-80).

XX Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
antisease therapy; malignant hyperplasia.

OS Homo sapiens.

XX WO200159158-A1.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US003977.

XX 11-FEB-2000; 2000US-00502600.

XX (UYAR-) UNIV ARKANSAS.

XX O'brien TJ;

XX WPI; 2001-514676/56.

XX Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

XX Disclosure; Page 115; 127pp; English.

XX The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

XX Sequence 9 AA;

SQ

```

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 2
AAE08236
ID AAE08236 standard; peptide; 9 AA.
XX
AC AAE08236;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #1 (residues 72-80).
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
PN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ;
XX
DR WPI; 2001-514676/56.
XX
PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin
PT enzyme.
XX
PS Claim 25; Page 102; 127pp; English.
XX
CC The invention relates to diagnosing cancer especially ovarian cancer, by
CC screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are
CC considered to be an integral part of tumour growth and metastasis, and
CC therefore, markers indicative of their presence or absence are useful for
CC the diagnosis of cancer. The method is useful for diagnosing cancer,
CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used
CC to treat a cancer selected from ovarian, breast, lung, colon, prostate
CC and other cancers in which SCCE is overexpressed. The present sequence is
CC human SCCE peptide
XX
Sequence 9 AA;

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 3
ADR68850
ID ADR68850 standard; peptide; 9 AA.
XX
AC ADR68850;
XX
DT 02-DEC-2004 (first entry)
XX

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```

DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:89.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
XX pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/53.
XX
PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
PS Disclosure; SEQ ID NO 89; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
Sequence 9 AA;

Query Match      100.0%; Score 49; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 4
ADR68792
ID ADR68792 standard; peptide; 9 AA.
XX
AC ADR68792;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:31.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.

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XX 20-FEB-2004; 2004WO-US005134.
 XX 21-FEB-2003; 2003US-00372521.
 XX (UYAR-) UNIV ARKANSAS.
 XX O'Brien TJ, Cannon MJ, Santin A;
 XX WPI; 2004-653294/63.
 XX Use of stratum corneum chymotryptic enzyme (SCCE) peptides, for
 PT vaccinating an individual against SCCE, and in monitoring and developing
 PT immunotherapies for ovarian and other malignancies.
 XX Claim 5; SEQ ID NO 31; 117pp; English.
 XX The invention relates to a novel method for vaccinating an individual
 CC against stratum corneum chymotryptic enzyme (SCCE), comprising inoculating
 CC an individual with a SCCE peptide, which elicits an immune response in
 CC the individual. A peptide of the invention acts as a stratum corneum
 CC chymotryptic enzyme inhibitor. The SCCE peptide is useful for vaccinating
 CC an individual against SCCE, particularly an individual having, suspected
 CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
 CC cancer. The oligonucleotide is useful for treating a neoplastic state in
 CC an individual, such as ovarian, breast, lung, colon, prostate, or
 CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
 CC peptides are also useful in the monitoring and development of
 CC immunotherapies for ovarian and other malignancies. The present sequence
 CC represents a peptide fragment of serine protease SCCE (stratum corneum
 CC chymotryptic enzyme).
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KMNEYTVHL 9
 Db |||||
 1 KMNEYTVHL 9
 RESULT 6
 ADA05740
 ID ADA05740 standard; protein; 97 AA.
 XX AC ADA05740;
 XX 06-NOV-2003 (first entry)
 DT Human NOV18e protein SEQ ID NO:100.
 DE human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX OS Homo sapiens.
 XX PN WO2003029424-A2.
 XX 10-APR-2003.
 PD 02-OCT-2002; 2002WO-US031373.
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.

XX 20-FEB-2004; 2004WO-US005134.
 XX 21-FEB-2003; 2003US-00372521.
 XX (UYAR-) UNIV ARKANSAS.
 XX O'Brien TJ, Cannon MJ, Santin A;
 XX WPI; 2004-653294/63.
 XX Use of stratum corneum chymotryptic enzyme (SCCE) peptides, for
 PT vaccinating an individual against SCCE, and in monitoring and developing
 PT immunotherapies for ovarian and other malignancies.
 XX Claim 5; SEQ ID NO 31; 117pp; English.
 XX The invention relates to a novel method for vaccinating an individual
 CC against stratum corneum chymotryptic enzyme (SCCE), comprising inoculating
 CC an individual with a SCCE peptide, which elicits an immune response in
 CC the individual. A peptide of the invention acts as a stratum corneum
 CC chymotryptic enzyme inhibitor. The SCCE peptide is useful for vaccinating
 CC an individual against SCCE, particularly an individual having, suspected
 CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
 CC cancer. The oligonucleotide is useful for treating a neoplastic state in
 CC an individual, such as ovarian, breast, lung, colon, prostate, or
 CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
 CC peptides are also useful in the monitoring and development of
 CC immunotherapies for ovarian and other malignancies. The present sequence
 CC represents a peptide fragment of serine protease SCCE (stratum corneum
 CC chymotryptic enzyme).
 XX SQ Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KMNEYTVHL 9
 Db |||||
 1 KMNEYTVHL 9
 RESULT 5
 ADR68870
 ID ADR68870 standard; peptide; 9 AA.
 XX AC ADR68870;
 XX 02-DEC-2004 (first entry)
 DT Human stratum corneum chymotryptic enzyme peptide fragment SEQ ID NO:109.
 DE serine protease; stratum corneum chymotryptic enzyme; SCCE;
 KW immune response; ovarian cancer; lung cancer; prostate cancer;
 KW pancreatic cancer; colon cancer.
 XX OS Homo sapiens.
 XX PN WO2004075723-A2.
 XX 10-SEP-2004.
 XX 20-FEB-2004; 2004WO-US005134.
 PR 21-FEB-2003; 2003US-00372521.
 XX (UYAR-) UNIV ARKANSAS.
 XX O'Brien TJ, Cannon MJ, Santin A;
 XX WPI; 2004-653294/63.

PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWV/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet J, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
WPI; 2004-213931/20.
DR N-PSDB; ADN62903.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 100; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 97 AA;
Query Match 100.0%; Score 49; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXNEYTVHL 9
|||||

QY 1 KXNEYTVHL 9
Db 53 KXNEYTVHL 61
|||||

RESULT 8
ABG23378
ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS87565.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 136 AA;
Query Match 100.0%; Score 49; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXNEYTVHL 9
|||||

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Db      78 KMNEYTVHL 86

RESULT 9
ADI39727
ID ADI39727 standard; protein; 144 AA.
XX
AC ADI39727;
XX
DT 15-APR-2004 (first entry)
XX
XX Stratum corneum chymotryptic enzyme (acce) catalytic domain.
DE
XX
XX Immune T cell; dendritic cell; extracellular serine protease;
KW tumour antigen derived gene-14; TAGD-14; carcinoma;
KW stratum corneum chymotryptic enzyme; scce.
XX
XX Unidentified.
OS
XX
XX US6642013-B1.
PN
XX
XX 04-NOV-2003.
PD
XX
XX 18-JUL-2000; 2000US-00618259.
PF
XX
XX 21-AUG-1997; 97US-00915659.
PR
XX 21-AUG-1998; 98US-00137944.
PR
XX (UYAR-) UNIV ARKANSAS MEDICAL SCI.
PA
XX O'brien TJ, Underwood LJ;
PI
XX WPI; 2004-118109/12.
DR
XX
XX Production of activated immune cells or dendritic cells by exposing
PT immune cells to tumor antigen derived gene protein fragment consisting of
PT amino acid sequences.
XX
XX Example 1; SEQ ID NO 4; 44pp; English.
PS
XX
XX The present invention relates to novel activated immune T cells or
CC dendritic cells directed toward extracellular serine protease termed
CC tumour antigen derived gene-14 (TAGD-14). The method of the invention
CC involves exposing the immune cells to a TAGD-14 protein fragment, where
CC exposure to the TAGD-14 protein fragment activates the immune cells. The
CC invention is used for the production of activated immune T cells or
CC dendritic cells. The invention allows screening to identify proteases
CC overexpressed in carcinoma. The present sequence is stratum corneum
CC chymotryptic enzyme (acce) catalytic domain. This sequence is used in the
CC invention.
XX
XX Sequence 144 AA;

Query Match 100.0%; Score 49; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
DB 9 KMNEYTVHL 17

RESULT 10
ADI37151
ID ADI37151 standard; protein; 144 AA.
XX
XX ADI37151;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Stratum corneum chymotryptic enzyme (acce) catalytic domain.
DE
XX
XX Serine protease; tumour antigen derived gene-14; TAGD-14;
KW

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KW neoplastic state; cancer; ovary; breast; lung; colon; prostate;
KW chymotryptic enzyme; scce; enzyme.
XX
XX Homo sapiens.
OS
XX
XX US2003199010-A1.
PN
XX
XX 23-OCT-2003.
PD
XX
XX 13-JUN-2003; 2003US-00461787.
PF
XX
XX 21-AUG-1997; 97US-00915659.
PR
XX 21-AUG-1998; 98US-00137944.
PR
XX 18-JUL-2000; 2000US-00618259.
XX
XX (UYAR-) UNIV ARKANSAS.
PA
XX
XX O'brien TJ, Underwood LJ;
PI
XX
XX WPI; 2004-141550/14.
DR
XX
XX Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful
PT for treating neoplastic state (such as ovarian cancer, breast cancer,
PT lung cancer, colon cancer, prostate cancer) in an individual.
XX
XX Example 1; SEQ ID NO 4; 46pp; English.
PS
XX
XX The invention relates to extracellular serine protease termed tumour
CC antigen derived gene-14 (TAGD-14) and its nucleic acid. Composition
CC comprising TAGD-14 peptide is useful for treating a neoplastic state in
CC an individual. The neoplastic state is chosen from ovarian cancer, breast
CC cancer, lung cancer, colon cancer, prostate cancer in which TAGD-14 is
CC overexpressed. The present sequence is Stratum corneum chymotryptic
CC enzyme (scce) catalytic domain. This sequence is used in the
CC exemplification of the invention.
XX
XX Sequence 144 AA;

Query Match 100.0%; Score 49; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
DB 9 KMNEYTVHL 17

RESULT 11
ADA05738
ID ADA05738 standard; protein; 181 AA.
XX
XX ADA05738;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
XX Human NOVI8d protein SEQ ID NO:98.
DE
XX
XX human; NOVI; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
XX Homo sapiens.
OS
XX
XX WO2003029424-A2.
PN
XX
XX 10-APR-2003.
PD
XX
XX 02-OCT-2002; 2002WO-US031373.
PF
XX
XX 02-OCT-2001; 2001US-0326483P.
PR

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PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 01-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ott T, Gorman L, Zehusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05737.
XX
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
PS Claim 1; Page 171; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The

CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 181 AA;

Query Match 100.0%; Score 49; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9
Db 53 KMNEYTVHL 61
|||||||

RESULT 12
ADN62902
ID ADN62902 standard; protein; 181 AA.
XX
AC ADN62902;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18d.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
XX US2004038223-A1.
PN
XX
PD 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0341058P.
PR 22-OCT-2001; 2001US-0343629P.
PR 24-OCT-2001; 2001US-0349575P.
PR 29-OCT-2001; 2001US-0346357P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 01-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
XX

PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYK/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALX/) MALYANKAR U M.
PA (ORTI/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
XX Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62901.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 98; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,

CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 181 AA;

Query Match 100.0%; Score 49; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVVHL 9
DB 53 KNEYTVVHL 61
|||||||

RESULT 13
ADAO5736
ID ADA05736 standard; protein; 198 AA.

XX
AC ADA05736;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18c protein SEQ ID NO:96.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 05-OCT-2001; 2001US-0327449P.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

XX 09-OCT-2001; 2001US-0328044P.

XX 09-OCT-2001; 2001US-0328056P.

XX 12-OCT-2001; 2001US-0328849P.

XX 15-OCT-2001; 2001US-0329414P.

XX 17-OCT-2001; 2001US-0330142P.

XX 18-OCT-2001; 2001US-0330309P.

XX 22-OCT-2001; 2001US-0341058P.

XX 24-OCT-2001; 2001US-0335266P.

XX 29-OCT-2001; 2001US-0343629P.

XX 01-NOV-2001; 2001US-0349575P.

XX 17-APR-2002; 2002US-0346357P.

XX 19-APR-2002; 2002US-0373260P.

XX 19-APR-2002; 2002US-0373815P.

XX 19-APR-2002; 2002US-0373826P.

XX 19-APR-2002; 2002US-0373884P.

XX 22-APR-2002; 2002US-0374977P.

XX 16-MAY-2002; 2002US-0381037P.

XX 16-MAY-2002; 2002US-0381039P.

XX 17-MAY-2002; 2002US-0381042P.

XX 28-MAY-2002; 2002US-0383656P.

XX 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytke KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zehusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 XX WPI; 2003-381626/36.
 DR N-PSDB; ADA05735.
 XX
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 XX Claim 1; Page 170; 586pp; English.
 PS
 XX The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
 CC and antilipidemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 XX Sequence 198 AA;
 XX
 XX Query Match 100.0%; Score 49; DB 6; Length 198;
 XX Best Local Similarity 100.0%; Pred. No. 0.27;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KNEYTVHL 9
 Db |||||
 72 KNEYTVHL 80
 RESULT 14
 ADN62900
 ID ADN62900 standard; protein; 198 AA.
 XX
 XX ADN62900;
 AC

XX 01-JUL-2004 (first entry)
 DT XX
 XX DE Human NOV18c.
 XX
 XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 XX Homo sapiens.
 OS
 XX US2004038223-A1.
 XX
 XX 26-FEB-2004.
 PD
 XX 01-OCT-2002; 2002US-00262511.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALI/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENNA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.

CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipase activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders, such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.

XX Sequence 224 AA;
SQ

Query Match 100.0%; Score 49; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKNYYTVHL 9
Db 58 KKNYYTVHL 66
|||||||

Search completed: March 11, 2006, 00:24:09
Job time : 89.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	253	2 A53968	serine proteinase
2	39	79.6	218	1 YVBPK3	lysis protein t -
3	39	79.6	218	1 YVBPT4	lysis protein t -
4	37	75.5	334	2 B98019	conserved hypotet
5	37	75.5	393	2 D75207	hypothetical prote
6	36	73.5	627	2 T25395	hypothetical prote
7	36	73.5	1829	2 T34239	hypothetical prote
8	35	71.4	159	2 A11406	spermidine/spermin
9	35	71.4	159	2 A11782	spermidine/spermin
10	35	71.4	505	2 H75431	conserved hypotet
11	35	71.4	555	2 AD1794	acylase and dieste
12	35	71.4	667	2 T09013	RING finger protei
13	35	71.4	667	2 T09482	ring finger protei
14	34	69.4	270	2 A43711	replication protei
15	34	69.4	270	2 S28582	replication protei
16	34	69.4	285	2 F70348	hypothetical prote
17	34	69.4	421	2 AH1120	B. subtilis YwBN p
18	34	69.4	421	2 AC1481	conserved hypotet
19	33	67.3	204	2 E95345	FixJ Transcription
20	33	67.3	204	2 B31227	nitrogen fixation
21	33	67.3	218	2 S53354	calflagin Tb-24 -
22	33	67.3	218	2 B83724	hypothetical prote
23	33	67.3	227	2 D83796	two-component resp
24	33	67.3	229	2 S53355	calflagin Tb-1.7 -
25	33	67.3	233	1 AOUT17	flagellar calcium
26	33	67.3	407	2 S53353	calflagin Tb-44A -
27	33	67.3	422	2 T11714	hypothetical prote
28	33	67.3	429	2 H70307	preprotein translo
29	33	67.3	525	2 B84028	oligopeptide ABC t

30	33	67.3	664	2 C72379	hypothetical prote
31	33	67.3	677	2 A87470	TonB-dependent rec
32	33	67.3	1042	2 S23738	pyr1-3 protein - s
33	33	67.3	1308	2 E71622	probable membrane
34	33	67.3	1481	1 QZDOP3	pyrimidine synthes
35	32	65.3	49	2 H89908	50S ribosomal prot
36	32	65.3	84	2 AE2172	hypothetical prote
37	32	65.3	116	2 S24989	ribosomal protein
38	32	65.3	130	2 E97262	hypothetical prote
39	32	65.3	144	2 F71215	hypothetical prote
40	32	65.3	192	2 G81301	MdaB protein homol
41	32	65.3	228	2 C90033	hypothetical prote
42	32	65.3	304	2 H75378	hypothetical prote
43	32	65.3	339	2 F97121	probable membrane
44	32	65.3	371	2 A89800	conserved hypotet
45	32	65.3	448	2 F82280	citrate/sodium sym

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:g521214; PIDN:
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRI>

RESULT 2

YVBPK3
lysis protein t - phage K3
C;Species: phage K3
A;Note: host Escherichia coli
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A27083
R;Riede, I.
J. Bacteriol. 169, 2956-2961, 1987
A;Title: Lysis gene t of T-even bacteriophages: evidence that colicins and bacteriophage
A;Reference number: A27083; MUID:87250254; PMID:3597316
A;Accession: A27083
A;Molecule type: DNA
A;Residues: 1-218 <RIE>
A;Cross-references: UNIPROT:PI0393; UNIPARC:UPI0000138941; GB:M16812; NID:g215503; PIDN:
A;Note: the author translated the codon CAA for residue 85 as Ile and CAG for residue 20;
C;Genetics:
A;Gene: t
C;Superfamily: phage T4 lysis protein t
C;Keywords: host cell lysis

Query Match 79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
|:|||||
Db 139 MDEYTVHL 146

RESULT 3

YVBPT4
Lysis protein t - phage T4
C:Species: phage T4
A:Note: host Escherichia coli
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JF0028; S07395
R:Montag, D.; Degen, M.; Henning, U.
Nucleic Acids Res. 15, 6736, 1987
A:Title: Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.
A:Reference number: S07395; MUID:8716934; PMID:3628006
A:Accession: JF0028
A:Molecule type: DNA
A:Residues: 1-218 <MON>
A:Cross-references: UNIPROT:P06808; UNIPARC:UPI000005CBE7; GB:Y00408; NID:g15368; PIDN:C

A:Note: the sequence is almost identical with that of the E.coli phage K3
C:Comment: At the end of the growth cycle, phage T4 expresses two genes with lysis function about the gene product of t, although it has been suggested that it acts as a phospholipase.
C:Genetics:
A:Gene: t

A:Map position: 157.985-158.639
C:Superfamily: phage T4 lysis protein t
C:Keywords: host cell lysis; transmembrane protein
F:35-49/Domain: transmembrane #status predicted <TM>

Query Match 79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
|:|||||
Db 139 MDEYTVHL 146

RESULT 4

B98019
conserved hypothetical protein spr1179 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98019
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Ee, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; et al.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: B98019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1334 <KUR>
A:Cross-references: UNIPROT:Q8DPC2; UNIPARC:UPI00000E35BF; GB:AE007317; PIDN:AAK99982.1;
C:Genetics:
A:Gene: spr1179

Query Match 75.5%; Score 37; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 9.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
|:|||||
Db 302 KMNEYITHI 310

RESULT 5

D75207
hypothetical protein PAB2235 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D75207
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: D75207
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <KAW>

A:Cross-references: UNIPROT:Q9V291; UNIPARC:UPI0000063251; GB:AJ248283; GB:AL096836; NID:
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2235
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0196

Query Match 75.5%; Score 37; DB 2; Length 393;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
|:|||||
Db 129 KLFYTHL 137

RESULT 6

T25395
hypothetical protein T28A8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25395
R:Illyod, C.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z20027
A:Accession: T25395
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-627 <WIL>
A:Cross-references: UNIPROT:Q9XU04; UNIPARC:UPI0000077722; EMBL:Z92813; PIDN:CAB07289.1;
A:Experimental source: clone T28A8
C:Genetics:
A:Gene: CESP:T28A8.6
A:Map position: 3

A:Introns: 51/2; 89/2; 183/2; 221/2; 296/2; 607/3
C:Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A.d

Query Match 73.5%; Score 36; DB 2; Length 627;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
|:|||||
Db 62 KMNEYSIEL 70

RESULT 7

T34239
hypothetical protein F26F12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34239
R:Wilson, R.; Bentley, D.; Gattung, S.

submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid F26F12.
A:Reference number: Z21493
A:Accession: T34239
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A;Residues: 1-1829 <WIL>
A;Cross-references: UNIPROT:Q19815; UNIPARC:UPI00000765C9; EMBL:U55373; PIDN:AAC25894.1;
A;Experimental source: strain Bristol N2; clone F26F12
C;Genetics:
A;Gene: CBSP:F26F12.7
A;Map position: 5
A;Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1

Query Match 73.5%; Score 36; DB 2; Length 1829;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 KMEYTVH 8
Db 765 KMEYTVH 771
:|||||

RESULT 8
A11406
spermidine/spermine N1-acetyl transferase homolog lmo2658 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11406
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <GLA>
A;Cross-references: UNIPROT:Q9Y419; UNIPARC:UPI000005520D; GB:NC_003210; PIDN:CAD00871.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2658

Query Match 71.4%; Score 35; DB 2; Length 159;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMEYTVH 8
Db 139 KMEYTVH 146
:|||||

RESULT 9
A11782
spermidine/spermine N1-acetyl transferase homolog lin2807 [imported] - Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: A11782
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11782
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <GLA>
A;Cross-references: UNIPROT:Q92711; UNIPARC:UPI00000CC9A2; GB:AL592022; PIDN:CAC98033.1;
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin2807

Query Match 71.4%; Score 35; DB 2; Length 159;

Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMEYTVH 8
Db 139 KMEYTVH 146
:|||||

RESULT 10
H75431
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: H75431
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Fsihi, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maok, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-505 <WHI>
A;Cross-references: UNIPROT:Q9RV79; UNIPARC:UPI00000C18AC; GB:AE001964; GB:AE000513; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1150
A;Map position: 1
C;Superfamily: conserved hypothetical protein b0835

Query Match 71.4%; Score 35; DB 2; Length 505;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVH 9
Db 57 QMNEYDTHL 65
:|||||

RESULT 11
AD1794
acylase and diesterase homolog lin2898 [imported] - Listeria innocua (strain Clp11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1794
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1794
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-555 <GLA>
A;Cross-references: UNIPROT:Q92621; UNIPARC:UPI00000CC9F2; GB:AL592022; PIDN:CAC98124.1;
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin2898

Query Match 71.4%; Score 35; DB 2; Length 555;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMEYTVH 9
Db 483 KINEYDTHL 491
:|||||

RESULT 12

T09013
RING finger protein FXY - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 04-Apr-2004
C:Accession: T09013
R:Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A.
Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
A:Title: A gene spans the pseudoautosomal boundary in mice.
A:Reference number: Z16531; MUID:98004518; PMID:9342357
A:Accession: T09013
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PAL>
A:Cross-references: UNIPARC:UPI000016C7E6; EMBL:AF026565; NID:g2589222; PIDN:AAB83986.1;
C:Genetics:
A:Gene: FXY
A:Map position: X; Y
C:Superfamily: rfp transforming protein
C:Keywords: zinc finger
P:6-65/Domain: RING finger homology <RRN>

Query Match 71.4%; Score 35; DB 2; Length 667;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNEYTVH 8
DB 444 KQNHVTVH 451

RESULT 13
T09482
ring finger protein FXY - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09482
R:Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
submitted to the EMBL Data Library, November 1997
A:Description: The human FXY maps to chromosome Xp22.3: Implications for evolution of th
A:Reference number: Z16687
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-667 <PER>
A:Cross-references: UNIPROT:Q15344; UNIPARC:UPI000012F0E6; EMBL:AF035360; NID:g2827993;
C:Genetics:
A:Gene: FXY
A:Map position: Xp22.3
C:Superfamily: rfp transforming protein
P:6-65/Domain: RING finger homology <RRN>

Query Match 71.4%; Score 35; DB 2; Length 667;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KNEYTVH 8
DB 444 KQNHVTVH 451

RESULT 14
A43711
replication protein repA 32K chain - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A43711
R:Erdile, L.F.; Wold, M.S.; Kelly, T.J.
J. Biol. Chem. 265, 3177-3182, 1990
A:Title: The primary structure of the 32-kDa subunit of human replication protein A.
A:Reference number: A43711; MUID:90153966; PMID:2406247
A:Accession: A43711
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-270 <ERD>
A:Cross-references: UNIPROT:P15927; UNIPARC:UPI000013379F; EMBL:J05249; NID:g337349; PIDN:
C:Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain

Query Match 69.4%; Score 34; DB 2; Length 270;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
DB 152 MNEFTTHI 159

RESULT 15
S28682
replication protein A 32K chain homolog - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S28682
R:Nakagawa, M.; Tsukada, S.; Soma, T.; Shimizu, Y.; Miyake, S.; Iwamatsu, A.; Sugiyama, T.
Nucleic Acids Res. 19, 4292, 1991
A:Title: cDNA cloning of the murine 30-kDa protein homologous to the 32-kDa subunit of h
A:Reference number: S28682; MUID:91334146; PMID:1908076
A:Accession: S28682
A:Molecule type: mRNA
A:Residues: 1-270 <NAG>
A:Cross-references: UNIPROT:Q62193; UNIPARC:UPI0000028990; EMBL:D00812; NID:g220583; PIDN:
C:Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain

Query Match 69.4%; Score 34; DB 2; Length 270;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
DB 152 MNEFTTHI 159

Search completed: March 11, 2006, 00:40:44
Job time : 16.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEEYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	253	1 KKK7_HUMAN	P49862 homo sapien
2	39	79.6	210	2 Q9G0B3_BPAR1	Q9G0B3 bacterioph
3	39	79.6	218	1 VLYS_BPK3	P10393 bacterioph
4	39	79.6	218	1 VLYS_BPT4	P06808 bacterioph
5	38	77.6	261	1 RFA4_HUMAN	Q13156 homo sapien
6	37	75.5	334	2 Q8DFG2_STRR6	Q8DFG2 streptococ
7	37	75.5	393	1 PRIL_PYRAB	Q9V291 pyrococcus
8	37	75.5	401	2 Q5LZS8_STRT1	Q5LZS8 streptococ
9	37	75.5	401	2 Q5M4D9_STRT2	Q5M4D9 streptococ
10	37	75.5	498	2 Q4UCK5_THEAN	Q4UCK5 theileria a
11	37	75.5	936	2 Q633P6_BACZ2	Q633P6 bacillus ce
12	36	73.5	445	2 Q67Z18_ARATH	Q67Z18 arabidopsis
13	36	73.5	446	2 Q5WPT2_LUTLO	Q5WPT2 lutomyia l
14	36	73.5	603	2 Q8L836_ARATH	Q8L836 arabidopsis
15	36	73.5	627	2 Q9XU04_CAEEL	Q9XU04 caenorhabdi
16	36	73.5	635	2 Q9LQW1_ARATH	Q9LQW1 arabidopsis
17	36	73.5	733	2 Q8VD00_STRMU	Q8VD00 streptococ
18	36	73.5	753	2 Q8E174_STRAS	Q8E174 streptococ
19	36	73.5	753	2 Q8EGM8_STRAS	Q8EGM8 streptococ
20	36	73.5	1829	2 Q19815_CAEEL	Q19815 caenorhabdi
21	36	73.5	1849	2 Q61KM2_CAEEL	Q61KM2 caenorhabdi
22	36	73.5	6481	2 Q4Q892_LEIMA	Q4Q892 leishmania
23	35	71.4	47	2 Q80274_MUSMA	Q80274 mus macedon
24	35	71.4	47	2 Q80277_MUSCE	Q80277 mus cervico
25	35	71.4	47	2 Q80280_9MURI	Q80280 mastomys hu
26	35	71.4	47	2 Q80283_ARVTE	Q80283 arvicola te
27	35	71.4	47	2 Q802B4_MUSPL	Q802B4 mus platyth
28	35	71.4	47	2 Q810Y2_MUSSI	Q810Y2 mus spicile
29	35	71.4	48	2 Q810X9_MUSSP	Q810X9 mus spratus
30	35	71.4	159	2 Q71WB4_LISMF	Q71WB4 listeria mo
31	35	71.4	159	2 Q8Y419_LISMO	Q8Y419 listeria mo

32 35 71.4 159 2 Q927I1_LISIN Q927I1 listeria in
33 35 71.4 197 2 Q7TSS2_GVCL Q7TSS2 cryptophleb
34 35 71.4 232 2 Q4RA68_TETNG Q4RA68 tetraodon n
35 35 71.4 258 2 Q4X8E6_PLACH Q4X8E6 plasmodium
36 35 71.4 294 2 Q4KC81_PSRF5 Q4KC81 pseudomonas
37 35 71.4 324 2 Q4Q709_LEIMA Q4Q709 leishmania
38 35 71.4 394 2 Q5SSA4_CRYNE Q5SSA4 cryptococcus
39 35 71.4 394 2 Q5KGQ1_CRYNE Q5KGQ1 cryptococcus
40 35 71.4 400 2 Q6PD02_MOUSE Q6PD02 mus musculus
41 35 71.4 429 2 Q51YK5_MAGGR Q51YK5 magnaporthe
42 35 71.4 459 2 Q4HB24_9DEIO Q4HB24 deinococcus
43 35 71.4 505 2 Q9RV79_DEIRA Q9RV79 deinococcus
44 35 71.4 513 2 Q5RFL0_PONPY Q5RFL0 pongo pygma
45 35 71.4 555 2 Q926Z1_LISIN Q926Z1 listeria in

ALIGNMENTS

RESULT 1
ID KKK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stromqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
RA Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum
RT chymotryptic enzyme. A skin-specific human serine proteinase.";
J. Biol. Chem. 269:19420-19426(1994).
RL [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC TISSUE=Keratinocyte;
RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
RA Diamandis E.P.;
RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
RT enzyme is a new member of the human kallikrein gene family - genomic
RT characterization, mapping, tissue expression and hormonal
RT regulation.";
RL Gene 254:119-128(2000).
RN [3]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Pieper B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
RA Wallbrandt P., Egelrud T.;
RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
RT mice; a model for chronic itchy dermatitis.";
RN Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
AND TISSUE SPECIFICITY.
RC TISSUE=Ovarian carcinoma;

RX MEDLINE=22623266; PubMed=12738725;
RA Dong Y., Kaushal A., Brattensand M., Nicklin J., Clements J.A.;
RT "differential splicing of KLKS and KIK7 in epithelial ovarian cancer
produces novel variants with potential as cancer biomarkers.";
RL Clin. Cancer Res. 9:1710-1720(2003).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins L.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=95314630; PubMed=7794273;
RA Skjott A., Stroemqvist M., Egeirud T.;
RT "Primary substrate specificity of recombinant human stratum corneum
chymotryptic enzyme.";
RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
structures in the cornified layer of the skin in the continuous
shedding of cells from the skin surface. Specific for amino acid
residues with aromatic side chains in the PI position. SCCE
cleaves insulin B chain at 4-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-
Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the
activation of precursors to inflammatory cytokines.
CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
also observed at the apical membrane and in cytoplasm at the
invasive front.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=P49862-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=P49862-2; Sequence=VSP_013581;
CC -!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
expressed by keratinocytes in the epidermis. Also expressed in the
brain, mammary gland, cerebellum, spinal cord and kidney. Lower
levels in salivary glands, uterus, thymus, thyroid, placenta,
trachea and testis. Up-regulated in ovarian carcinoma, especially
late-stage serous carcinoma, compared with normal ovaries and
benign adenomas (at the protein level).
CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
cell line.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; L33404; AAC37551.1; -; mRNA.
DR EMBL; AF166330; AAD49718.1; -; Genomic_DNA.

DR EMBL; AF243527; AAG33360.1; -; Genomic DNA.
DR EMBL; AF332583; AAK69624.1; -; Genomic_DNA.
DR EMBL; AF411214; AAN03662.1; -; mRNA.
DR EMBL; AF411215; AAN03663.1; -; mRNA.
DR EMBL; BC032005; AAH32005.1; -; mRNA.
DR PIR; A53968; A53968.
DR HSSP; P00760; IEZX.
DR MEROPS; S01.300; -.
DR Ensemble; ENSG00000169035; Homo sapiens.
DR HGNC; HGNC:16368; KLIK7.
DR H-InvDB; HIX0015373; -.
DR MIM; 604438; -.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR GO; GO:0008544; P:epidermis development; TAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydrolase; Protease; Serine protease; Signal; Zymogen.
FT SIGNAL 1 22
FT PROPEP 23 29 Activation peptide.
FT CHAIN 30 253 Kallikrein 7.
FT DOMAIN 30 250 Peptidase S1.
FT ACT_SITE 70 70 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 205 205 Charge relay system (By similarity).
FT CARboxYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 /FTId=VSP_013581.
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A668 CRC64;
SQ
Query Match 100.0%; Score 49; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KNEYTVHL 9
Db 72 KNEYTVHL 80
RESULT 2
Q9G0B3 BPARI
ID Q9G0B3 BPARI PRELIMINARY; PRT; 210 AA.
AC Q9G0B3
DT 01-WAR-2001 (TRENBLrel. 16, Created)
DT 01-WAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE T protein (Fragment).
OS Bacteriophage AR1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=66711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20485545; PubMed=11029414;
RX DOI=10.1128/JB.182.21.5962-5968.2000;
RA Yu S.L., Ko K.L., Chen C.S., Chang Y.C., Syu W.J.;
RT "Characterization of the distal tail fiber locus and determination of
the receptor for phage AR1, which specifically infects Escherichia
coli O157:H7.";
RL J. Bacteriol. 182:5962-5968(2000).

```

DR EMBL: AF208841; AAC29756.1; -; Genomic_DNA.
FT NON_TER 210 210
SQ SEQUENCE 210 AA; 24348 MW; C6FF585F9F0DF68 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 210;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
Db 139 MDEYTVHL 146

RESULT 3
VLVS_BPK3 STANDARD; PRT; 218 AA.
AC P10393;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lysis protein.
GN Name=T;
OS Bacteriophage K3.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=10674;

[1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=87250254; PubMed=3597316;
RA Riede I.;
RT "Lysis gene t of T-even bacteriophages: evidence that colicins and bacteriophage genes have common ancestors.";
RL J. Bacteriol. 169:2956-2961(1987).

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DR EMBL: M16812; AAA88415.1; -; Genomic_DNA.
DR PIR: A27083; YVBPk3.
KW Phage lysis protein.
SQ SEQUENCE 218 AA; 25223 MW; 21B4DC02ACA0ECF6 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
Db 139 MDEYTVHL 146

RESULT 4
VLVS_BPT4 STANDARD; PRT; 218 AA.
AC P06808;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lysis protein (Holin) (Protein rv).
GN Name=T; Synonyms=rv;
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae; T4-like viruses.
OX NCBI_TaxID=10665;

[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87316934; PubMed=3628006;
RA Montag D., Degen M., Henning U.;
RT "Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.";
RL Nucleic Acids Res. 15:6736-6736(1987).

[2]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22514363; PubMed=12626685; DOI=10.1128/MMBR.67.1.86-156.2003;
RA Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
RT "Bacteriophage T4 genome.";
RL Microbiol. Mol. Biol. Rev. 67:86-156(2003).
[3]
RN NUCLEOTIDE SEQUENCE OF 1-34.
RX MEDLINE=88011316; PubMed=2958637;
RA Montag D., Riede I., Eschbach M.-L., Degen M., Henning U.;
RT "Receptor-recognizing proteins of T-even type bacteriophages. Constant and hypervariable regions and an unusual case of evolution.";
RL J. Mol. Biol. 196:165-174(1987).
[4]
RN NUCLEOTIDE SEQUENCE OF 202-218.
RC STRAIN=D;
RX MEDLINE=93106978; PubMed=8416914;
RA Orsini G., Ouhammouch M., Le Caer J.-P., Brody E.N.;
RT "The asfA gene of bacteriophage T4 codes for the anti-sigma 70 protein.";
RL J. Bacteriol. 175:85-93(1993).
CC -I- FUNCTION: At the end of the growth cycle, phage T4 expresses two genes with lysis function, e and t. Nothing is known about the gene product of t, although it has been suggested that it acts as a phospholipase.

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DR EMBL: Y00408; CAA68470.1; -; Genomic_DNA.
DR EMBL: AF158101; AAD42661.1; -; Genomic_DNA.
DR EMBL: X05677; CAA29164.1; -; Genomic_DNA.
DR EMBL: M99441; AAA32481.1; -; Genomic_DNA.
DR PIR: JF0028; YVBPt4.
KW Phage lysis protein; Transmembrane.
FT TRANSMEM 35 49 Potential.
SQ SEQUENCE 218 AA; 25176 MW; 9110BE111D772DF5 CRC64;

Query Match 79.6%; Score 39; DB 1; Length 218;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVHL 9
Db 139 MDEYTVHL 146

RESULT 5
RFA4_HUMAN STANDARD; PRT; 261 AA.
AC Q13156;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Replication protein A 30 kDa subunit (RP-A) (RP-A) (Replication factor-A protein 4).
GN Name=RPt4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95280910; PubMed=7760808;
RA Keshav K.F., Chen C., Dutta A.;
RT "Rpt4, a homolog of the 34-kilodalton subunit of the replication protein A complex.";
RL Mol. Cell. Biol. 15:3119-3128(1995).
[2]

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RA Keshav K.F.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT THR-33.
 RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RT "NIHGS-SNPs, environmental genome project, NIHES ES15478, Department
 of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15772651; DOI=10.1038/nature03440;
 RA Ross M.T., Graham D.V., Coffey A.J., Scherer S., McMay K., Muzny D.,
 RA Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
 RA Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
 RA Jones M.C., Hultes M.E., Andrews T.D., Scott C.E., Searle S.,
 RA Ramer J., Whitaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
 RA Cree A., Gunaratne P., Havlik P., Hodgson A., Metzker M.L.,
 RA Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
 RA Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Atadhyia S.,
 RA Ashwell R.I., Babbage A.K., Baguley C.L., Ballabio A., Banerjee R.,
 RA Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.W.,
 RA Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
 RA Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
 RA Bruford E.A., Buhaq C., Burch P., Burford D., Burgess J., Burrill W.,
 RA Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
 RA Chavez D., Chen G., Chen Y., Chen Z., Chinault C.,
 RA Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 RA Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
 RA Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
 RA Delgado O., Deshazo D., Dhami P., Ding Y., Dinh H., Dodsworth S.,
 RA Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
 RA Eades T., Ellwood M., Emery-Cohen A., Errington A.E., Evans K.L.,
 RA Faulkner L., Francis F., Frankland J., Fraser A.E., Gargoczy P.,
 RA Griffiths C., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
 RA Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
 RA Hawes A., Heath P.D., Heitmann K., Hennig S., Hernandez J.,
 RA Hinemann B., Ho S., Hoffa M., Howden P.J., Huckle E.J., Hume J.,
 RA Hunt P.J., Hunt A.R., Islerwood J., Jacob L., Johnson D., Jones S.,
 RA de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
 RA Kischis P., Klages S., Knights A.J., Koslura A., Kovar-Smith C.,
 RA Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
 RA Lloyd C., Lloyd D.M., Loulèsed H., Loveland J.E., Lovell J.D.,
 RA Lozadó R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
 RA McDowell J., McLaren S., McMurray A., Meidl P., Meitinger T.,
 RA Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
 RA Mullikin J.C., Nguyen N., Nordiek G., Nyakatura G., O'dell C.N.,
 RA Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
 RA Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
 RA Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
 RA Ridler K.A., Schlessinger D., Schueler M.G., Sehra H.K.,
 RA Shaw-Smith C., Shen H., Sheridan E.M., Showkeen R., Skuce C.D.,
 RA Smith M.L., Sotheran E.C., Steingrubber H.E., Steward C.A., Storey R.,
 RA Swann R.M., Swarbreck D., Taber P.E., Taudien S., Taylor T.,
 RA Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
 RA Treagus A.C., d'Urso M., Verduco D., Villaseña D., Waldron L.,
 RA Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
 RA Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
 RA Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
 RA Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
 RA Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
 RA Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
 RA Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
 RA Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,
 RA Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
 RT "The DNA sequence of the human x chromosome.";
 RL Nature 434:325-337(2005).
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bosa S.S., Loguallano N.A., Peters G.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Rask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC "- FUNCTION: Absolutely required for simian virus 40 DNA replication
 in vitro. It participates in a very early step in initiation. RP-A
 is a single-stranded DNA-binding protein (By similarity).
 CC "- SURUNIT: Heterotrimer of 70, 32/30, and 14 kDa chains. The DNA-
 binding activity may reside exclusively on the 70 kDa subunit.
 CC "- SUBCELLULAR LOCATION: Nuclear.
 CC "- TISSUE SPECIFICITY: Preferentially expressed in placental and
 colon mucosa.
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 DR EMBL; U24186; AAB08488.2; -; mRNA.
 DR EMBL; AF494047; AB089569.1; -; Genomic DNA.
 DR EMBL; Z86061; CA142556.1; -; Genomic DNA.
 DR EMBL; BC069791; AAH69791.1; -; mRNA.
 DR EMBL; BC069808; AAH69808.1; -; mRNA.
 DR EMBL; BC069824; AAH69824.1; -; mRNA.
 DR HSSP; P15927; 1QJ0.
 DR HGNC; HGNC:30305; RPA4.
 DR Reactome; Q13156; -.
 DR GO; GO:0005662; C:DNA replication factor A complex; TAS.
 DR GO; GO:0003697; F:single-stranded DNA binding; TAS.
 DR GO; GO:0006270; P:DNA replication initiation; TAS.
 DR InterPro; IPR012340; OB_NA_bd_sub.
 DR InterPro; IPR004365; OB_TRNA_NA_bd.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 DR Pfam; PF01336; tRNA_anti; 1.
 KW Alternative splicing; DNA replication; Nuclear protein; Polymorphism.
 FT VARIANT 33 33 A -> T.
 FT SEQUENCE 261 AA; 28868 MW; 6A925FAEDBE21718 CRC64;
 /FTID=VAR 019170.
 Query Match 77.6%; Score 38; DB 1; Length 261;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MNEYTVHL 9
 DB 151 MNEFTVHI 158
 RESULT 6
 QSDPG2_STRR6 PRELIMINARY; PRT; 334 AA.
 ID QSDPG2;
 AC QSDPG2;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Hypothetical protein sprl179.
 GN Ordered locus names=sprl179;
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

```
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC BAA-255 / R6;
RX MEDLINE=21429245; PubMed=11544234;
RY DOI=10.1128/JB.183.19.5709-5717.2001;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA DeHoff B.S., Batrem S.T., Fritz L., Fu D.-J., Fuller W., Gerlinger C.,
RA Gilmore R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AE008490; AAK99982.1; -; Genomic_DNA.
DR F1R; B98019; B98019.
DR InterPro; IPR006314; Dyp_peroxidase.
DR Pfam; PF04261; Dyp_perox; 1.
DR TIGRFAMs; TIGR01413; Dyp_perox fam; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 334 AA; 38137 MW; E207F1BC267334E5 CRC64;

Query Match 75.5%; Score 37; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
DB 302 KXNEYITHI 310

RESULT 7
PRIL_PYRAB STANDARD; PRT; 393 AA.
AC Q9V291;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE DNA primase large subunit (EC 2.7.7.-) (DNA primase 46 kDa subunit)
DE [p46].
GN Name=priB; OrderedLocNames=PYRAB01830; ORFNames=PAB2235;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=GE5 / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RY DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O.N., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Coost J., Weissbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
CC -1- FUNCTION: DNA primase is the polymerase that synthesizes small RNA
CC primers for the Okazaki fragments on both template strands at
CC replication forks during chromosomal DNA synthesis (By
CC similarity).
CC -1- SUBUNIT: Heterodimer of a small subunit and a large subunit. Both
CC participate in formation of the active center, but the ATP-binding
CC site is exclusively located on the small subunit (By similarity).
CC -1- SIMILARITY: Belongs to the eukaryotic-type primase large subunit
CC family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ248283; CAB49107.1; -; Genomic_DNA.
CC PIR; D75207; D75207.
CC HAMAP; MF 00701; -; 1.
CC InterPro; IPR007238; DNA_primase_lrg.
CC InterPro; IPR008918; HnH2.
CC Pfam; PF04104; DNA_primase_lrg; 1.
KW Complete proteome; DNA replication; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Primosome; Transference.
SQ SEQUENCE 393 AA; 45486 MW; 9448642FBB3FBF43 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 393;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
DB 129 KXNEYITHI 137

RESULT 8
Q5LZS8_STR11 PRELIMINARY; PRT; 401 AA.
AC Q5LZS8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=stri1023;
OS Streptococcus thermophilus (strain CNRZ 1066).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=299768;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=1543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goltzman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcours J.,
RA Goffeau A., Hols F.;
RT "Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000024; AAV62601.1; -; Genomic_DNA.
DR InterPro; IPR006314; Dyp_peroxidase.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR006313; Tat_enzyme.
DR Pfam; PF04261; Dyp_perox; 1.
DR TIGRFAMs; TIGR01413; Dyp_perox fam; 1.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.
DR TIGRFAMs; TIGR01412; tat_substr_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 401 AA; 44973 MW; 1998CF52CB40CBAC CRC64;

Query Match 75.5%; Score 37; DB 2; Length 401;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
DB 370 KXNEYITHI 378

RESULT 9
Q5M4D9_STR12 PRELIMINARY; PRT; 401 AA.
AC Q5M4D9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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DE Hypothetical protein.
GN OrderedLocusNames=stul023;
OS Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=264199;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinkis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goltsman E., Mazur M., Pusch G.D.,
RA Fongstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngai K., Masuy D., Hancy F., Burteau S., Boutry M., Delcours J.,
RA Goffeau A., Hols P.;
RT "Complete sequence and comparative genome analysis of the dairy
bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000023; AAV60681.1; -; Genomic_DNA.
DR InterPro; IPR006314; DYP_peroxidase.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR006313; Tat_enzyme.
DR Pfam; PF04261; DYP_perox; 1.
DR TIGRFAMs; TIGR01413; Dyp_perox_fam; 1.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.
DR TIGRFAMs; TIGR01412; tat_substr_1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 401 AA; 44973 MW; 1998CF52CB40CBAC CRC64;

Query Match 75.5%; Score 37; DB 2; Length 401;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
|||:|
DB 370 KMEYTHI 378

RESULT 10
Q4UCK5 THEAN PRELIMINARY; PRT; 498 AA.
AC Q4UCK5;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE RNA 3'-terminal phosphate cyclase like-protein, putative.
OS ORNames=TA03460;
GN Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 3 genome sequence of Theileria annulata.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940352; CAI75446.1; -; Genomic DNA.
SQ SEQUENCE 498 AA; 55564 MW; 9135F3620AC4758A CRC64;

Query Match 75.5%; Score 37; DB 2; Length 498;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
|||:|
DB 447 KLNRYSVHL 455

RESULT 11
Q633P6 BACCZ
ID Q633P6 BACCZ PRELIMINARY; PRT; 936 AA.
AC Q633P6;

DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORNames=BCE33L4292;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU15977.1; -; Genomic_DNA.
DR InterPro; IPR006635; NEA_transpt.
DR Pfam; PF05031; NEAT; 5.
DR SMART; SM00725; NEAT; 5.
DR PROSITE; PS50378; NEAT; 5.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 936 AA; 104539 MW; D05C843D8B02DF8A CRC64;

Query Match 75.5%; Score 37; DB 2; Length 936;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMEYTVHL 8
|||:|
DB 749 KMHDYTVH 756

RESULT 12
Q67Z18 ARATH PRELIMINARY; PRT; 445 AA.
AC Q67Z18;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE MRNA, partial cds, clone: RAFL23-25-J01 (MRNA, partial cds, clone:
RAFL23-09-L14) (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
RA Hayashizaki Y., Shinozaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK176300; BAD44063.1; -; mRNA.
DR EMBL; AK176215; BAD43978.1; -; mRNA.
DR InterPro; IPR007145; MAP65_ASE1.
DR Pfam; PF03999; MAP65_ASE1; 1.
DR NON_TER
FT NON TER 1
SQ SEQUENCE 445 AA; 51244 MW; 00BD7C51A0D6EA45 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 445;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMEYTVHL 9
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DB 11 KUNEYQTHL 19

RESULT 13


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Q5WPT2_LUTLO
ID Q5WPT2_LUTLO PRELIMINARY; PRT; 446 AA.
AC Q5WPT2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 49 kDa salivary protein.
OS Lutzomyia longipalpis (Sand fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Lutzomyia; Lutzomyia.
OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT Identification of the most abundant secreted proteins from the
RT salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT Leishmania chagasi.
RL J. Exp. Biol. 207:3717-3729(2004).
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; AY455913; XAS16913.1; -; mRNA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 446 AA; 50670 MW; 0D8F747D8A6F1E30 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 446;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVH 8
Db 151 KSDYTVH 158

RESULT 14
Q8L836_ARATH
ID Q8L836_ARATH PRELIMINARY; PRT; 603 AA.
AC Q8L836;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At1g14690.
GN Name=At1g14690;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sekano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Heuan V.W., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY120768; AAM53326.1; -; mRNA.
DR EMBL; BT008373; AAP37732.1; -; mRNA.

GO; GO:0005096; F:GTPase activator activity; IEA.
DR InterPro; IPR007145; MAP65_ASE1.
DR Pfam; PF03999; MAP65_ASE1; 1.
KW Hypothetical protein.
SQ SEQUENCE 603 AA; 69060 MW; 7C2B37A23CBB899D CRC64;

Query Match 73.5%; Score 36; DB 2; Length 603;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 169 KLINEYQTHL 177

RESULT 15
Q9XU04_CAEEL
ID Q9XU04_CAEEL PRELIMINARY; PRT; 627 AA.
AC Q9XU04;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein T28A8.6.
GN ORFNames=T28A8.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z52813; CAB07289.1; -; Genomic_DNA.
DR PIR; T25395; T25395.
DR Ensembl; T28A8.6; Caenorhabditis elegans.
DR WormBase; WBGene00012112; T28A8.6.
DR WormPep; T28A8.6; CE18977.
DR InterPro; IPR006570; SPK.
DR Pfam; PF04435; SPK; 2.
DR SMART; SM00583; SPK; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 627 AA; 71794 MW; 4A56E4D3658EC1CC CRC64;

Query Match 73.5%; Score 36; DB 2; Length 627;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db 62 KMNEYSIEL 70

Search completed: March 11, 2006, 00:38:33
Job time : 99.3333 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-31

Perfect score: 49

Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	2	US-09-502-600-31
2	49	100.0	9	2	US-09-502-600-89
3	49	100.0	9	2	US-09-502-600-109
4	49	100.0	9	2	US-09-918-243-31
5	49	100.0	9	2	US-09-918-243-89
6	49	100.0	9	2	US-09-918-243-109
7	49	100.0	144	2	US-09-618-259-4
8	49	100.0	154	2	US-09-261-416-7
9	49	100.0	224	2	US-08-944-483-33
10	49	100.0	225	1	US-08-557-146-12
11	49	100.0	225	1	US-09-027-337-4
12	49	100.0	225	1	US-09-154-344-12
13	49	100.0	225	2	US-09-644-600-4
14	49	100.0	225	2	US-09-654-600A-4
15	49	100.0	253	1	US-08-557-146-2
16	49	100.0	253	1	US-08-824-874-3
17	49	100.0	253	1	US-09-154-344-2
18	49	100.0	253	2	US-08-930-188-2
19	49	100.0	253	2	US-09-210-084-3
20	49	100.0	253	2	US-09-764-762-3
21	49	100.0	253	4	PCT-US96-04294-2
22	49	100.0	265	2	US-09-949-016-7716
23	39	79.6	9	2	US-09-502-600-122
24	39	79.6	9	2	US-09-918-243-122
25	37	75.5	9	2	US-09-502-600-93
26	37	75.5	9	2	US-09-918-243-93
27	37	75.5	463	2	US-09-540-236-2942

28 35 71.4 415 2 US-09-949-016-11065 Sequence 11065, A
29 33 67.3 204 2 US-09-323-872A-13 Sequence 13, Appl
30 33 67.3 204 2 US-09-072-433-22 Sequence 22, Appl
31 33 67.3 358 2 US-09-710-279-2136 Sequence 2136, Ap
32 33 67.3 365 2 US-09-710-279-470 Sequence 470, App
33 33 67.3 366 2 US-09-134-001C-5502 Sequence 5502, Ap
34 33 67.3 799 2 US-08-909-954-4 Sequence 4, Appli
35 33 67.3 804 2 US-08-909-954-2 Sequence 2, Appli
36 32 65.3 60 2 US-09-134-001C-5184 Sequence 5184, Ap
37 32 65.3 116 2 US-09-732-210-882 Sequence 882, App
38 32 65.3 121 2 US-09-091-725-49 Sequence 49, Appl
39 32 65.3 144 2 US-09-270-767-47539 Sequence 47539, A
40 32 65.3 255 2 US-09-902-540-12375 Sequence 12375, A
41 32 65.3 393 2 US-09-248-796A-28699 Sequence 28699, A
42 32 65.3 698 2 US-09-949-016-10644 Sequence 10644, A
43 32 65.3 752 2 US-09-583-110-2714 Sequence 2714, Ap
44 32 65.3 755 2 US-09-107-433-4628 Sequence 4628, Ap
45 32 65.3 792 2 US-09-134-000C-5895 Sequence 5895, Ap

ALIGNMENTS

RESULT 1
US-09-502-600-31
; Sequence 31, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-502-600-31

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
| | | | | | | | | |
Db 1 KNEYTVHL 9

RESULT 2
US-09-502-600-89
; Sequence 89, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-502-600-31

; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-502-600-89

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db |||||||||

RESULT 3

US-09-502-600-109
; Sequence 109, Application US/09502600A
; Patent No. 6294344

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP-C

; CURRENT FILING DATE: 2000-02-11

; CURRENT APPLICATION NUMBER: US/09/502,600A

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 109

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 72-80 of the SCCE protein

US-09-502-600-109

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db |||||||||

RESULT 4

US-09-918-243-31

; Sequence 31, Application US/09918243

; Patent No. 6627403

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 31

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 72-80 of the SCCE protein

US-09-918-243-31

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db |||||||||

Db 1 KMNEYTVHL 9

RESULT 5

US-09-918-243-89

; Sequence 89, Application US/09918243

; Patent No. 6627403

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 89

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 72-80 of the SCCE protein

US-09-918-243-89

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db |||||||||

RESULT 6

US-09-918-243-109

; Sequence 109, Application US/09918243

; Patent No. 6627403

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 109

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 72-80 of the SCCE protein

US-09-918-243-109

Query Match 100.0%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KMNEYTVHL 9
Db |||||||||

RESULT 7

US-09-618-259-4

; Sequence 4, Application US/09618259

; Patent No. 6642013

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2
CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 4
LENGTH: 144
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: DOMAIN
OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-618-259-4

Query Match 100.0%; Score 49; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 9 KNEYTVHL 17

RESULT 8
US-09-261-416-7
Sequence 7, Application US/09261416A
Patent No. 6291663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: TAGD-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
LENGTH: 154
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar
OTHER INFORMATION: domain in TAGD-12
US-09-261-416-7

Query Match 100.0%; Score 49; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 18 KNEYTVHL 26

RESULT 9
US-08-944-483-33
Sequence 33, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.

APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match 100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 43 KNEYTVHL 51

RESULT 10
US-08-557-146-12
Sequence 12, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sterner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 49; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52

RESULT 11
US-09-027-337-4
/ Sequence 4, Application US/09027337B
/ Patent No. 5972616
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ APPLICANT: Tanimoto, Hirokoshi
/ TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease Overexpressed in
/ TITLE OF INVENTION: TAGD-15: Breast and Ovarian Carcinomas
/ FILE REFERENCE: D6064
/ CURRENT APPLICATION NUMBER: US/09/027,337B
/ CURRENT FILING DATE: 1998-02-20
/ NUMBER OF SEQ ID NOS: 13
/ SEQ ID NO 4
/ LENGTH: 225
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
/ OTHER INFORMATION: similar domain in TAGD-15
US-09-027-337-4

Query Match 100.0%; Score 49; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52

RESULT 12
US-09-154-344-12
/ Sequence 12, Application US/09154344
/ Patent No. 5981256
/ GENERAL INFORMATION:
/ APPLICANT: Egelrud, Torbjorn
/ APPLICANT: Hansson, Lennart
/ TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
/ TITLE OF INVENTION: Enzyme (SCCE)
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case, Patent Department
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
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/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/154,344
/ FILING DATE: 16-SEP-1998
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sterner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: polypeptide
US-09-154-344-12

Query Match 100.0%; Score 49; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52

RESULT 13
US-09-644-600-4
/ Sequence 4, Application US/09644600
/ Patent No. 6451500
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ APPLICANT: Tanimoto, Hirokoshi
/ TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
/ TITLE OF INVENTION: Overexpressed in Carcinomas
/ FILE REFERENCE: D6064CIP/D
/ CURRENT APPLICATION NUMBER: US/09/644,600
/ CURRENT FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: 09/421,213
/ PRIOR FILING DATE: 1999-10-20
/ PRIOR APPLICATION NUMBER: 09/027,337
/ PRIOR FILING DATE: 1998-02-20
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 4
/ LENGTH: 225
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: SCCE
US-09-644-600-4

Query Match 100.0%; Score 49; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
DB 44 KNEYTVHL 52
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RESULT 14
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CJP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; 09/027,337
; PRIOR FILING DATE: 1999-10-20
; 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4

Query Match 100.0%; Score 49; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
DB 44 KXNEYTVHL 52

RESULT 15
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match 100.0%; Score 49; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
DB 72 KXNEYTVHL 80

Search completed: March 11, 2006, 01:24:23
Job time : 22.2222 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	49	100.0	9	3	US-09-918-243-89
3	49	100.0	9	3	US-09-918-243-109
4	49	100.0	9	3	US-09-905-083-31
5	49	100.0	9	3	US-09-905-083-89
6	49	100.0	9	3	US-09-905-083-109
7	49	100.0	9	4	US-10-372-521-31
8	49	100.0	9	4	US-10-372-521-89
9	49	100.0	9	4	US-10-372-521-109
10	49	100.0	9	5	US-10-831-075-31
11	49	100.0	9	5	US-10-831-075-89
12	49	100.0	9	5	US-10-831-075-109
13	49	100.0	97	4	US-10-262-511-100
14	49	100.0	136	5	US-10-450-763-53737
15	49	100.0	144	3	US-09-796-294-4
16	49	100.0	144	4	US-10-461-787-4
17	49	100.0	181	4	US-10-262-511-98
18	49	100.0	198	4	US-10-262-511-96
19	49	100.0	224	3	US-09-789-210-33
20	49	100.0	224	4	US-10-262-511-104
21	49	100.0	225	4	US-10-600-187-4
22	49	100.0	247	4	US-10-262-511-102
23	49	100.0	250	4	US-10-262-511-92
24	49	100.0	252	4	US-10-262-511-94
25	49	100.0	253	3	US-09-888-615-98
26	49	100.0	253	3	US-09-764-762-3
27	49	100.0	253	4	US-10-071-214-2

28 49 100.0 253 4 US-10-071-214-48 Sequence 48, Appl
29 49 100.0 253 4 US-10-264-283-90 Sequence 90, Appl
30 49 100.0 253 4 US-10-295-027-498 Sequence 498, App
31 49 100.0 253 4 US-10-173-999-48 Sequence 48, Appl
32 49 100.0 253 4 US-10-408-765A-639 Sequence 639, App
33 49 100.0 253 5 US-10-643-795A-95 Sequence 95, Appl
34 49 100.0 253 5 US-10-948-518-95 Sequence 95, Appl
35 49 100.0 253 5 US-10-868-490A-1 Sequence 1, Appl
36 49 100.0 257 4 US-10-344-394-38 Sequence 38, Appl
37 40 81.6 141 4 US-10-437-963-194726 Sequence 194726,
38 40 79.6 226 4 US-10-071-214-49 Sequence 49, Appl
39 39 79.6 9 3 US-09-918-243-122 Sequence 122, App
40 39 79.6 9 3 US-09-905-083-122 Sequence 122, App
41 39 79.6 9 4 US-10-372-521-122 Sequence 122, App
42 39 79.6 9 5 US-10-831-075-122 Sequence 122, App
43 39 79.6 81 4 US-10-424-599-175183 Sequence 175183,
44 38 77.6 261 5 US-10-756-149-5592 Sequence 5592, Ap
45 37 75.5 9 3 US-09-918-243-93 Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-09-918-243-31
; Sequence 31, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-31

Query Match 100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Fred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
| | | | | | | | |
Db 1 KNEYTVHL 9

RESULT 2
US-09-918-243-89
; Sequence 89, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-89

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 3
US-09-918-243-109
; Sequence 109, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-109

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 4
US-09-905-083-31
; Sequence 31, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-31

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 5
US-09-905-083-89
; Sequence 89, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-89

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 6
US-09-905-083-109
; Sequence 109, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-109

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9

RESULT 7
US-09-905-083-109
; Sequence 109, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-905-083-109

Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KMNEYTVHL 9
Db      1 KMNEYTVHL 9
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US-10-372-521-31
; Sequence 31, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-31

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9

RESULT 8
US-10-372-521-89
; Sequence 89, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-89

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9

RESULT 9
US-10-372-521-109
; Sequence 109, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
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; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-109

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9

RESULT 10
US-10-831-075-31
; Sequence 31, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-31

Query Match 100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
Db 1 KNEYTVHL 9

RESULT 11
US-10-831-075-89
; Sequence 89, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Santin, Alessandro
; APPLICANT: Cannon, Martin J.
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
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; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-89

Query Match 100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 12
US-10-831-075-109
; Sequence 109, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 109
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-831-075-109

Query Match 100.0%; Score 49; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9
Db 1 KMNEYTVHL 9

RESULT 13
US-10-262-511-100
; Sequence 100, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei

; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 100
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-100

Query Match 100.0%; Score 49; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KMNEYTVHL 9
Db 53 KMNEYTVHL 61

RESULT 14
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737

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; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

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Query Match 100.0%; Score 49; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
Db 78 KXNEYTVHL 86

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RESULT 15
US-09-796-294-4
; Sequence 4, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4

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Query Match 100.0%; Score 49; DB 3; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXNEYTVHL 9
Db 9 KXNEYTVHL 17

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Search completed: March 11, 2006, 01:37:21
Job time : 70.4444 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-31
Perfect score: 49
Sequence: 1 KNEYTVHL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
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4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	253	6	US-10-412-748-11
2	49	100.0	253	6	US-10-412-748-14
3	49	100.0	253	6	US-10-412-748-17
4	49	100.0	253	7	US-11-037-243-98
5	44	89.8	181	6	US-10-412-748-19
6	33	67.3	176	7	US-11-087-099-6304
7	33	67.3	358	6	US-10-793-626-2136
8	33	67.3	365	6	US-10-793-626-470
9	32	65.3	137	6	US-10-485-517-159
10	32	65.3	688	7	US-11-113-424-49
11	32	65.3	688	7	US-11-040-218-25
12	32	65.3	1027	6	US-10-330-773-265
13	32	65.3	1051	6	US-10-330-773-268
14	31	63.3	22	6	US-10-895-064-2480
15	31	63.3	22	7	US-11-129-741-2480
16	31	63.3	178	7	US-11-072-512-3741
17	31	63.3	306	6	US-10-467-657-4304
18	31	63.3	690	7	US-11-087-099-2239
19	30	61.2	245	7	US-11-096-568A-10287
20	30	61.2	258	7	US-11-096-568A-10286
21	30	61.2	357	7	US-11-096-568A-9630
22	30	61.2	378	7	US-11-096-568A-9629
23	30	61.2	336	7	US-11-096-568A-9628
24	30	61.2	456	6	US-10-966-483-34
25	30	61.2	456	7	US-11-021-441-18

26 30 61.2 479 6 US-10-966-483-36 Sequence 36, Appl
27 30 61.2 479 6 US-11-021-441-20 Sequence 20, Appl
28 30 61.2 490 6 US-10-966-483-42 Sequence 42, Appl
29 30 61.2 490 7 US-11-021-441-26 Sequence 26, Appl
30 30 61.2 496 7 US-11-022-490A-4 Sequence 4, Appl
31 30 61.2 497 6 US-10-966-483-38 Sequence 38, Appl
32 30 61.2 497 6 US-10-966-483-40 Sequence 40, Appl
33 30 61.2 497 7 US-11-021-441-22 Sequence 22, Appl
34 30 61.2 497 7 US-11-021-441-24 Sequence 24, Appl
35 30 61.2 976 6 US-10-966-483-2 Sequence 2, Appl
36 30 61.2 976 7 US-10-511-273-1 Sequence 1, Appl
37 30 61.2 976 7 US-11-233-796-2 Sequence 2, Appl
38 30 61.2 976 7 US-11-072-175-138 Sequence 138, App
39 30 61.2 976 7 US-11-203-251A-77 Sequence 77, Appl
40 30 61.2 1035 6 US-10-966-483-20 Sequence 20, Appl
41 30 61.2 1035 7 US-11-021-441-4 Sequence 4, Appl
42 30 61.2 1730 7 US-11-192-967-4 Sequence 4, Appl
43 30 61.2 1730 7 US-11-193-715-4 Sequence 4, Appl
44 29 59.2 25 6 US-10-986-501-283 Sequence 283, App
45 29 59.2 79 6 US-10-986-501-281 Sequence 281, App

ALIGNMENTS

RESULT 1
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

Query Match 100.0%; Score 49; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNEYTVHL 9
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Db 72 KNEYTVHL 80

RESULT 2
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT

; ORGANISM: Human									
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Query Match 100.0%; Score 49; DB 6; Length 253;									
Best Local Similarity 100.0%; Pred. No. 0.011; Length 253;									
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	72	KMNEYTVHL	80						
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US-10-412-748-17									
; Sequence 17, Application US/10412748									
; Publication No. US20060035219A1									
; GENERAL INFORMATION:									
; APPLICANT: Queensland University of Technology									
; APPLICANT: Clements, Judith A									
; TITLE OF INVENTION: Aberrant Kallikrein Expression									
; FILE REFERENCE: DAV1172.003AUS									
; CURRENT APPLICATION NUMBER: US/10/412,748									
; CURRENT FILING DATE: 2003-04-09									
; PRIOR APPLICATION NUMBER: AU PS1616/02									
; PRIOR FILING DATE: 2002-04-09									
; NUMBER OF SEQ ID NOS: 41									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 17									
; LENGTH: 253									
; TYPE: PRT									
; ORGANISM: Human									
US-10-412-748-17									
Query Match 100.0%; Score 49; DB 6; Length 253;									
Best Local Similarity 100.0%; Pred. No. 0.011; Length 253;									
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	72	KMNEYTVHL	80						
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US-11-037-243-98									
; Sequence 98, Application US/11037243									
; Publication No. US20050287546A1									
; GENERAL INFORMATION:									
; APPLICANT: PLOWMAN, GREGORY									
; APPLICANT: WHYTE, DAVID									
; APPLICANT: CAENEPEEL, SEAN									
; APPLICANT: CHARVDCZAK, GLEN									
; APPLICANT: MANNING, GERARD									
; APPLICANT: SUDARSANAM, SUCHA									
; TITLE OF INVENTION: NOVEL PROTEASES									
; FILE REFERENCE: 038602/1214									
; CURRENT APPLICATION NUMBER: US/11/037,243									
; CURRENT FILING DATE: 2005-05-26									
; PRIOR APPLICATION NUMBER: US/09/888,615									
; PRIOR FILING DATE: 2001-06-26									
; PRIOR APPLICATION NUMBER: 60/214,047									
; PRIOR FILING DATE: 2000-06-26									
; NUMBER OF SEQ ID NOS: 150									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 98									
; LENGTH: 253									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
; ORGANISM: Homo sapiens									
US-11-037-243-98									

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RESULT 11
US-11-040-218-25
; Sequence 25, Application US/11040218
; Publication No. US20060029983A1
; GENERAL INFORMATION: ROBERT H.
; APPLICANT: OAKLEY, ROBERT H.
; APPLICANT: HUDSON, CHRISTINE C.
; TITLE OF INVENTION: CONSTITUTIVELY TRANSLOCATING CELL LINE
; FILE REFERENCE: NRK.108
; CURRENT APPLICATION NUMBER: US/11/040.218
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US/10/788.197
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: PCT/US03/14581
; PRIOR FILING DATE: 2003-05-12

;
; PRIOR APPLICATION NUMBER: 60/379,986
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/401,698
; PRIOR FILING DATE: 2002-08-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 25
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-040-218-25

Query Match 65.3%; Score 32; DB 7; Length 688;
Best Local Similarity 71.4%; Pred. No. 95;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNEYTVH 8
Db 188 MNEFSVH 194

RESULT 12
US-10-330-773-265
; Sequence 265, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-330-773-265

Query Match 65.3%; Score 32; DB 6; Length 1027;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVH 8
Db 161 KLNHHTVH 168

RESULT 13
US-10-330-773-268
; Sequence 268, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 1051
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-773-268

Query Match 65.3%; Score 32; DB 6; Length 1051;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KMNEYTVH 8

Db 152 KLNHHTVH 159

RESULT 14
US-10-895-064-2480
; Sequence 2480, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2480
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-10-895-064-2480

Query Match 63.3%; Score 31; DB 6; Length 22;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVH 9
Db 6 MNDYWVHV 13

RESULT 15
US-11-129-741-2480
; Sequence 2480, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2480
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2480

Query Match 63.3%; Score 31; DB 7; Length 22;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNEYTVH 9
Db 6 MNDYWVHV 13

Search completed: March 11, 2006, 01:38:38
Job time : 9 secs

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Sequence 9 AA;

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Query Match      100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 1 RLSSMVKKV 9

RESULT 2
ADR68793
ID ADR68793 standard; peptide; 9 AA.
XX
AC ADR68793;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotryptic enzyme peptide fragment SEQ ID NO:32.
XX
KW serine protease; stratum corneum chymotryptic enzyme; SCCE;
KW Immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/63.
XX
PT Use of stratum corneum chymotryptic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
PS Claim 5; SEQ ID NO 32; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotryptic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotryptic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotryptic enzyme).
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 1 RLSSMVKKV 9

RESULT 3
ADI39727
ID ADI39727 standard; protein; 144 AA.
XX
AC ADI39727;
XX
DT 15-APR-2004 (first entry)
XX
DE Stratum corneum chymotryptic enzyme (scce) catalytic domain.
XX
KW Immune T cell; dendritic cell; extracellular serine protease;
KW tumour antigen derived gene-14; TADG-14; carcinoma;
KW stratum corneum chymotryptic enzyme; scce.
XX
OS Unidentified.
XX
PN US6642013-B1.
XX
PD 04-NOV-2003.
XX
PF 18-JUL-2000; 2000US-00618259.
XX
PR 21-AUG-1997; 97US-00915659.
PR 21-AUG-1998; 98US-00137944.
XX
PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.
XX
PI O'brien TJ, Underwood LJ;
XX
DR WPI; 2004-118109/12.
XX
PT Production of activated immune cells or dendritic cells by exposing
PT immune cells to tumor antigen derived gene protein fragment consisting of
PT amino acid sequences.
XX
PS Example 1; SEQ ID NO 4; 44pp; English.
XX
CC The present invention relates to novel activated immune T cells or
CC dendritic cells directed toward extracellular serine protease termed
CC tumour antigen derived gene-14 (TADG-14). The method of the invention
CC involves exposing the immune cells to a TADG-14 protein fragment, where
CC exposure to the TADG-14 protein fragment activates the immune cells. The
CC invention is used for the production of activated immune T cells or
CC dendritic cells. The invention allows screening to identify proteases
CC overexpressed in carcinoma. The present sequence is stratum corneum
CC chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
CC invention.
XX
SQ Sequence 144 AA;

Query Match      100.0%; Score 40; DB 8; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.9; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 60 RLSSMVKKV 68

RESULT 4
ADI37151
ID ADI37151 standard; protein; 144 AA.
XX
AC ADI37151;
XX
DT 06-MAY-2004 (first entry)
XX
DE Stratum corneum chymotryptic enzyme (scce) catalytic domain.
XX
KW Serine protease; tumour antigen derived gene-14; TADG-14;
KW neoplastic state; cancer; ovary; breast; lung; colon; prostate;
KW chymotryptic enzyme; scce; enzyme.
XX
OS Homo sapiens.
XX

```


CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 40; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 109 RUSSMVKKV 117
|||||||

RESULT 6
ADN62908
ID ADN62908 standard; protein; 224 AA.
XX
AC ADN62908;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18g.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX Homo sapiens.
OS
XX
XX US2004038223-A1.
PN
XX
XX 26-FEB-2004.
PD
XX
XX 01-OCT-2002; 2002US-00262511.
PF
XX
XX 02-OCT-2001; 2001US-0326483P.
PR
XX 05-OCT-2001; 2001US-0327435P.
PR
XX 09-OCT-2001; 2001US-0327449P.
PR
XX 09-OCT-2001; 2001US-0327917P.
PR
XX 09-OCT-2001; 2001US-0328029P.
PR
XX 09-OCT-2001; 2001US-0328044P.
PR
XX 09-OCT-2001; 2001US-0328056P.
PR
XX 12-OCT-2001; 2001US-0328849P.
PR
XX 15-OCT-2001; 2001US-0329414P.
PR
XX 17-OCT-2001; 2001US-0330142P.
PR
XX 18-OCT-2001; 2001US-0330309P.
PR
XX 22-OCT-2001; 2001US-0341058P.
PR
XX 24-OCT-2001; 2001US-0339266P.
PR
XX 24-OCT-2001; 2001US-0343629P.
PR
XX 29-OCT-2001; 2001US-0349575P.
PR
XX 01-NOV-2001; 2001US-0346357P.
PR
XX 17-APR-2002; 2002US-0373260P.
PR
XX 19-APR-2002; 2002US-0373815P.
PR
XX 19-APR-2002; 2002US-0373817P.
PR
XX 19-APR-2002; 2002US-0373826P.
PR
XX 19-APR-2002; 2002US-0373884P.
PR
XX 22-APR-2002; 2002US-0374977P.
PR
XX 16-MAY-2002; 2002US-0381037P.
PR
XX 16-MAY-2002; 2002US-0381038P.
PR
XX 16-MAY-2002; 2002US-0381042P.
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XX 17-MAY-2002; 2002US-0381642P.
PR
XX 28-MAY-2002; 2002US-0383656P.
PR
XX 29-MAY-2002; 2002US-0383831P.
XX
XX 25-JUN-2002; 2002US-0391335P.

(SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA

PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP1/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62907.
DR
XX
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
XX Claim 1; SEQ ID NO 104; 395pp; English.
PS
XX
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 40; DB 8; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 109 RLSSMVKKV 117

RESULT 7

ADV21100
ID ADV21100 standard; protein; 224 AA.

XX
AC ADV21100;

XX 24-FEB-2005 (first entry)

XX Human stratum corneum chymotrypsin protein.

XX Protein purification; PS133 protein; serine protease; prostate disease;
KW andrology; genitourinary disease; prostatic cancer; cytostatic;
KW protein therapy; chymotrypsin; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 26..42
/note = Catalytically functional motif
FT Domain 83..87
/note = Catalytically functional motif
FT Domain 174..179
/note = Catalytically functional motif

XX US2004241646-A1.

XX 02-DEC-2004.

XX 20-FEB-2001; 2001US-00789210.

XX 06-OCT-1997; 97US-00944483.

XX (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GRAN/) GRANADOS E.

PA (KLAS/) KLAS M R.

PA (RUSS/) RUSSELL J C.

PA (STEW/) STEWART K D.

PA (STRO/) STROUPE S D.

XX Cohen M, Colpitts TL, Friedman PN, Granados E, KLAS MR;

PI Russell JC, Stewart KD, Stroupe SD;

XX WPI; 2005-011614/01.

DR GENBANK; L33404.

XX New isolated polypeptides, useful for detecting, diagnosing, staging,
PT monitoring, prognosticating, preventing or treating, or determining
PT predisposition to diseases or conditions of the prostate such as prostate
PT cancer.

XX Example 1; SEQ ID NO 33; 96pp; English.

XX The invention relates to PS133 protein, a member of the human serine
CC protease family and its corresponding nucleic acid sequence. PS133
CC polypeptide is useful for detecting, diagnosing, staging, monitoring,
CC prognosticating, preventing or treating or determining predisposition to

CC diseases or conditions of the prostate such as prostatic cancer. The
CC present sequence is the human stratum corneum chymotrypsin protein. This
CC sequence is used to align with PS133 consensus protein.

XX
SQ Sequence 224 AA;

Query Match 100.0%; Score 40; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 94 RLSSMVKKV 102

RESULT 8

AAB98502
ID AAB98502 standard; protein; 225 AA.

XX
AC AAB98502;

XX 03-AUG-2001 (first entry)

XX Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.

XX Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
KW tumour antigen-derived gene 15; serine protease;
KW Stratum Corneum Chymotryptic Enzyme; SCCE.

XX Homo sapiens.

XX WO200129056-A1.

XX 26-APR-2001.

XX 20-OCT-2000; 2000WO-US029095.

XX 20-OCT-1999; 99US-00421213.

XX (UYAR-) UNIV ARKANSAS.

XX O'brien TJ, Tanimoto H;

XX WPI; 2001-381031/40.

XX Novel extracellular serine protease, termed tumor antigen-derived gene 15
PT protein overexpressed in carcinomas and DNA encoding it, for diagnosis,
PT treatment, prevention of cancer, particularly breast, ovarian cancer.

XX Example 10; Fig 1; 130pp; English.

XX The present invention relates to human tumour antigen-derived gene 15
CC (TADG-15) protein and coding sequence (see AAB23601 and AAB98500). TADG-
CC 15 is an extracellular serine protease. It was found that TADG-15 is over
CC -expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20
CC residues that lack TADG-15 protease activity are useful for vaccinating
CC an individual against TADG-15, having, suspected of having or at risk of
CC getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic
CC or therapeutic target in cancer. The present sequence was used in a
CC sequence homology alignment with the catalytic domain of TADG-15

XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 40; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||
Db 95 RLSSMVKKV 103

RESULT 9

ADA05742
ID ADA05742 standard; protein; 247 AA.
XX
AC ADA05742;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18f protein SEQ ID NO:102.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
XX
PR 05-OCT-2001; 2001US-0327435P.
XX
PR 05-OCT-2001; 2001US-0327449P.
XX
PR 09-OCT-2001; 2001US-0327917P.
XX
PR 09-OCT-2001; 2001US-0328029P.
XX
PR 09-OCT-2001; 2001US-0328044P.
XX
PR 09-OCT-2001; 2001US-0328056P.
XX
PR 12-OCT-2001; 2001US-0328849P.
XX
PR 15-OCT-2001; 2001US-0329414P.
XX
PR 17-OCT-2001; 2001US-0330142P.
XX
PR 18-OCT-2001; 2001US-0330309P.
XX
PR 22-OCT-2001; 2001US-0341058P.
XX
PR 24-OCT-2001; 2001US-0339266P.
XX
PR 24-OCT-2001; 2001US-0343629P.
XX
PR 29-OCT-2001; 2001US-0349575P.
XX
PR 01-NOV-2001; 2001US-0346357P.
XX
PR 17-APR-2002; 2002US-0373260P.
XX
PR 19-APR-2002; 2002US-0373815P.
XX
PR 19-APR-2002; 2002US-0373817P.
XX
PR 19-APR-2002; 2002US-0373826P.
XX
PR 19-APR-2002; 2002US-0373884P.
XX
PR 22-APR-2002; 2002US-0374977P.
XX
PR 16-MAY-2002; 2002US-0381037P.
XX
PR 16-MAY-2002; 2002US-0381038P.
XX
PR 16-MAY-2002; 2002US-0381042P.
XX
PR 17-MAY-2002; 2002US-0381642P.
XX
PR 28-MAY-2002; 2002US-0383566P.
XX
PR 29-MAY-2002; 2002US-0383831P.
XX
PR 25-JUN-2002; 2002US-0391335P.
XX
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patkuraian M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Raestelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AV, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05741.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 172; 586pp; English.

XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 247 AA;
XX

Query Match 100.0%; Score 40; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLSSNVKKV 9
Db 109 RLSSNVKKV 117
|||||||
RESULT 10
ADN62906
ID ADN62906 standard; protein; 247 AA.
XX
AC ADN62906;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18f.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
XX
PR 05-OCT-2001; 2001US-0327435P.

PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327517P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383556P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.

XX (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATI/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JINW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPIPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI; 2004-213931/20.
 DR N-PSDB; ADN62905.
 XX

PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX Claim 1; SEQ ID NO 102; 395pp; English.
 XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX SQ Sequence 247 AA;

Query Match 100.0%; Score 40; DB 8; Length 247;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLSSMVKKV 9
 Db 109 RLSSMVKKV 117
 |||||

RESULT 11
 ADA05732
 ID ADA05732 standard; protein; 250 AA.
 XX ADA05732;
 XX ADA05732;
 DT 06-NOV-2003 (first entry)
 XX Human NOV18a protein SEQ ID NO:92.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.
 XX WO2003029424-A2.
 XX 10-APR-2003.
 PD 02-OCT-2002; 2002WO-US031373.
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 19-APR-2002; 2002US-0373260P.
PR 17-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehruen BD, Anderson DW, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eissen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI: 2003-381626/36.
DR N-PSDS; ADA05731.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1: Page 169-170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nontropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic

CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.
XX
XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 40; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLSSMVKKV 9
Db 120 RLSSMVKKV 128
|||||||
RESULT 12
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX
AC ADN62896;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18a.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327445P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383831P.
XX 25-JUN-2002; 2002US-0391335P.
XX 01-OCT-2002; 2002US-00262511P.

XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JULJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (WALX/) MALYANKAR U M.
PA (ORTI/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATI/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62895.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX Claim 1; SEQ ID NO 92; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative

CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 250 AA;

Query Match 100.0%; Score 40; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 120 RLSSMVKKV 128
|||||||

RESULT 13

ADA05734
ID ADA05734 standard; protein; 252 AA.

XX

AC ADA05734;

XX

DT 06-NOV-2003 (first entry)

XX

DE Human NOV18b protein SEQ ID NO:94.

XX

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

KW immunomodulator; cytostatic; neurotropic; neuroprotective;

KW antiparkinsonian; antilipemic; gene therapy; human disease;

KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003029424-A2.

XX

PD 10-APR-2003.

XX

PF 02-OCT-2002; 2002WO-US031373.

XX

PR 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 09-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 18-OCT-2001; 2001US-0330309P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0339266P.

PR 24-OCT-2001; 2001US-0343629P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 17-APR-2002; 2002US-0373260P.

PR 19-APR-2002; 2002US-0373815P.

PR 19-APR-2002; 2002US-0373817P.

PR 19-APR-2002; 2002US-0373826P.

PR 19-APR-2002; 2002US-0373884P.

PR 22-APR-2002; 2002US-0374977P.

PR 16-MAY-2002; 2002US-0381037P.

PR 16-MAY-2002; 2002US-0381038P.

PR 16-MAY-2002; 2002US-0381042P.

PR 17-MAY-2002; 2002US-0381642P.

PR 28-MAY-2002; 2002US-0383656P.

PR 29-MAY-2002; 2002US-0383811P.

PR 25-JUN-2002; 2002US-0391335P.

PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05733.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 170; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX Sequence 252 AA;
SQ
Query Match 100.0%; Score 40; DB 6; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLSSVMVKV 9
Db 122 RLSSVMVKV 130
RESULT 14
ADN62898
ID ADN62898 standard; protein; 252 AA.
XX
AC ADN62898;
XX
DT 01-JUL-2004 (first entry)

XX DE Human NOV18b.
XX KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-032914P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
(SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHINKETS R A.
PA (ROTH/) ROTHENBERG M E.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-32
Perfect score: 40
Sequence: 1 RLSSMVKKV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	253	2 A53968	serine proteinase
2	33	82.5	282	2 T35294	probable endo alpha
3	33	82.5	372	2 S20056	para-hydroxybenzoa
4	33	82.5	560	2 S50401	hypothetical prote
5	32	80.0	350	1 C70009	ABC transporter (l
6	32	80.0	351	2 D90264	biotin synthase (b
7	32	80.0	358	2 T38914	para-hydroxybenzoa
8	32	80.0	589	2 A71277	arginine-tRNA liga
9	32	80.0	664	2 T50316	hypothetical Armad
10	31	77.5	912	2 H85470	hypothetical prote
11	31	77.5	925	2 T05012	hypothetical prote
12	30	75.0	239	2 T02473	hypothetical prote
13	30	75.0	240	2 T32363	hypothetical prote
14	30	75.0	318	2 I56519	taipoxin-associate
15	30	75.0	319	2 JC5402	vitamin D receptor
16	30	75.0	373	2 G75073	hypothetical prote
17	30	75.0	457	2 D85429	cytochrome P450 11
18	30	75.0	532	2 T01759	glycine hydroxymet
19	30	75.0	647	2 A49218	hemagglutinin homo
20	30	75.0	833	2 A47528	transcription fact
21	30	75.0	986	2 E90220	isoleucine-tRNA sy
22	30	75.0	1167	2 A82543	chromosome segrega
23	30	75.0	1846	2 T33079	hypothetical prote
24	29	72.5	253	2 JC5511	TATA-binding prote
25	29	72.5	285	2 A97255	S-adenosylmethioni
26	29	72.5	336	2 E69214	GTP-binding protei
27	29	72.5	337	2 AH2591	membrane lipoprote
28	29	72.5	337	2 B97374	Deinococcus radiod
29	29	72.5	345	2 F90194	threonine synthase

30	29	72.5	349	2 F84246	hypothetical prote
31	29	72.5	357	2 D96986	probable lipoprote
32	29	72.5	379	2 H75318	membrane lipoprote
33	29	72.5	553	2 A72228	hypothetical prote
34	29	72.5	571	2 S65060	phytoene desaturas
35	29	72.5	578	2 H82872	hypothetical prote
36	29	72.5	582	2 S29314	phytoene dehydroge
37	29	72.5	583	2 A45381	phytoene dehydroge
38	29	72.5	656	2 T23338	hypothetical prote
39	29	72.5	691	2 E70906	probable beta-gluc
40	29	72.5	839	2 S62963	hypothetical prote
41	29	72.5	1360	2 F96596	hypothetical prote
42	29	72.5	4077	2 T17484	hypothetical prote
43	29	72.5	4589	2 T14914	dynein beta heavy
44	28	70.0	41	2 G71376	hypothetical prote
45	28	70.0	63	2 AH2565	hypothetical prote

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:7
C;Genetics:
A;Gene: GDB:PRS86; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 123 RLSSMVKKV 131

RESULT 2

T35294
probable endo alpha-1,4 polygalactosaminidase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35294
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
A;Accession: T35294
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-282 <SEE>
A;Cross-references: UNIPROT:Q9S208; UNIPARC:UPI000000DB294; EMBL:AL096872; PIDN:CAB51262.1
C;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5F7.23c

Query Match 82.5%; Score 33; DB 2; Length 282;
Best Local Similarity 87.5%; Pred. No. 13;

RESULT 7

T38914
para-hydroxybenzoate-polyphenyltransferase (EC 2.5.1.1-) precursor, mitochondrial - fission
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38914
R:Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z21817
A:Accession: T38914
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-358 <PEA>
A:Cross-references: UNIPROT:Q10252; UNIPARC:UPI0000127EF6; EMBL:Z69728; PIDN:CAA93575.1
A:Experimental source: strain 972h-; cosmid c56F8
C:Genetics:
A:Gene: SPDB:SPAC56F8.04c
A:Map position: 1
A:Genome: nuclear
C:Keywords: mitochondrion; transferase

Query Match 80.0%; Score 32; DB 2; Length 358;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 311 RLSSMIYKV 319

RESULT 8

A71277
arginine-tRNA ligase (EC 6.1.1.19) (args) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: A71277
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: A71277
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-589 <COL>
A:Cross-references: UNIPROT:O83803; UNIPARC:UPI000013666B; GB:AE001253; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:
A:Superfamily: Bacillus arginine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 80.0%; Score 32; DB 2; Length 589;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 473 RISSLLKKV 481

RESULT 9

T50316
hypotheical Armadillo/beta-catenin domain protein [imported] - fission yeast (Schizosac
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: T50316
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, F
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25061

Query Match 80.0%; Score 32; DB 2; Length 589;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

A:Accession: T50316
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-664 <MCD>
A:Cross-references: UNIPROT:Q9P7W7; UNIPARC:UPI000006B097; EMBL:AL136536; PIDN:CAB66447.1
A:Experimental source: strain 972h(-); cosmid c1703
C:Genetics:
A:Gene: SPDB:SPBC1703.03c
A:Map position: 2
A:Introns: 43/3

Query Match 80.0%; Score 32; DB 2; Length 664;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 624 RLQNMVKKI 632

RESULT 10

H85470
hypotheical protein AT4g39750 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85470
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85470
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-912 <STO>
A:Cross-references: UNIPROT:Q9LDK6; UNIPARC:UPI00000A9562; GB:NC_001268; NID:g7270959; P1
C:Genetics:
A:Gene: AT4g39750
A:Map position: 4

Query Match 77.5%; Score 31; DB 2; Length 912;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 403 RFSSMIRKI 411

RESULT 11

T05012
hypotheical protein T19P19.140 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05012
R:Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.; N
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15394
A:Accession: T05012
A:Molecule type: DNA
A:Residues: 1-925 <BEV>
A:Cross-references: UNIPROT:Q9LDK6; UNIPARC:UPI000017AFB3; EMBL:AL022605
A:Experimental source: cultivar Columbia; BAC clone T19P19
C:Genetics:
A:Map position: 4
A:Introns: 142/3; 193/1; 551/1
A:Note: T19P19.140

Query Match 77.5%; Score 31; DB 2; Length 925;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 403 RFSSMIRKI 411

Db 416 RFSSMIRKI 424

RESULT 12

T02473
hypothetical protein At2g45740 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F4118.28
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C:Accession: T02473; C94894
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C94894
A:Status: preliminary
A:Map position: 2
A:Gene: At2g45740; F4118.28
C:Genetics:
A:Cross-references: UNIPARC:UPI000017AF99; GB:AE002093; NID:G3386621; PIDN:AAC28551.1; G
A:Introns: 65/3; 90/3; 115/3; 142/3; 167/3

Query Match 75.0%; Score 30; DB 2; Length 239;

Best Local Similarity 66.7%; Pred. No. 54;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 148 RLSSSMKKI 156

RESULT 13

T32363
hypothetical protein C08E3.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32363
R:Miller, N.; Kramer, J.; Keppler, D.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid C08E3.
A:Reference number: Z21155
A:Accession: T32363
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-240 <MIL>
A:Cross-references: UNIPROT:O17203; UNIPARC:UPI000007F654; EMBL:AF025457; PIDN:AAB70970.
A:Experimental source: strain Bristol N2; clone C08E3
C:Genetics:
A:Gene: CESP:C08E3.12
A:Map position: 2
A:Introns: 167/3

Query Match 75.0%; Score 30; DB 2; Length 240;

Best Local Similarity 66.7%; Pred. No. 54;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 193 RPSMLKKV 201

RESULT 14

156519
taipoxin-associated calcium binding protein-49 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56519
R:Dodds, D.; Schlingens, A.K.; Lu, S.Y.; Perin, M.S.
J. Neurochem. 64, 2339-2344, 1995
A:Title: Novel reticular calcium binding protein is purified on taipoxin columns.
A:Reference number: I56519; MUID:95239201; PMID:7722520
A:Accession: I56519
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-318 <RES>
A:Cross-references: UNIPROT:Q62703; UNIPARC:UPI0000133470; EMBL:U15734; NID:G606967; PIDN

C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand
F:62-94/Domain: calmodulin repeat homology <EF1>
F:120-152/Domain: calmodulin repeat homology <EF2>
F:187-219/Domain: calmodulin repeat homology <EF3>
F:228-260/Domain: calmodulin repeat homology <EF4>
F:264-296/Domain: calmodulin repeat homology <EF5>

Query Match 75.0%; Score 30; DB 2; Length 318;

Best Local Similarity 55.6%; Pred. No. 71;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 66 RLQSIKKI 74

RESULT 15

JC5402
vitamin D receptor associated factor 1 - mouse
N:Alternate names: ERC-55 protein
C:Species: Mus musculus (house mouse)
C>Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5402
R:Imai, T.; Matsuda, K.; Shimojima, T.; Hashimoto, T.; Masuhiro, Y.; Kitamoto, T.; Sugita
Biochem. Biophys. Res. Commun. 233, 765-769, 1997
A:Title: ERC-55, a binding protein for the papilloma virus E6 oncoprotein, specifically i
A:Reference number: JC5402; MUID:97312489; PMID:9168930
A:Accession: JC5402
A:Molecule type: mRNA
A:Residues: 1-319 <IMA>
A:Cross-references: UNIPROT:O70341; UNIPARC:UPI0000177892
C:Comment: This protein acts as a vitamin D receptor-specific cofactor modulating its fur
C:Superfamily: reticulocalbin; calmodulin repeat homology
C:Keywords: EF hand
F:63-95/Domain: calmodulin repeat homology <EF1>
F:99-131/Domain: calmodulin repeat homology <EF2>
F:151-183/Domain: calmodulin repeat homology <EF3>
F:188-220/Domain: calmodulin repeat homology <EF4>
F:229-261/Domain: calmodulin repeat homology <EF5>
F:265-297/Domain: calmodulin repeat homology <EF6>

Query Match 75.0%; Score 30; DB 2; Length 319;

Best Local Similarity 55.6%; Pred. No. 72;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 67 RLQSIKKI 75

Search completed: March 11, 2006, 00:40:46

Job time : 16.1111 secs

RESULT 2			
KLK7_HUMAN	KLK7_HUMAN	STANDARD;	PRT; 253 AA.
ID	KLK7_HUMAN		
AC	P49862; Q8NSN9; Q8NFV7;		
DC	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum		
DE	chymotryptic enzyme) (hSCCE).		
GN	Name=KLK7; Synonyms=PRSS6, SCCE;		
OS	Homo sapiens (Human) .		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei		

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
 RP TISSUE=Skin;
 RX MEDLINE=94308225; PubMed=8034709;
 RA Hanson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
 RA Egelrud T.,
 RT Cloning, expression, and characterization of stratum corneum
 RT chymotryptic enzyme. A skin-specific human serine proteinase.";
 RL J. Biol. Chem. 269:19420-19426(1994).
 RN [2]
 RC NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
 RP TISSUE=Keratinocyte;
 RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
 RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
 RA Diamandis E.P.,
 RT The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
 RT enzyme is a new member of the human kallikrein gene family - genomic
 RT characterization, mapping, tissue expression and hormonal
 RT regulation.";
 RL Gene 254:119-128(2000).
 RN [3]
 RC NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Mose P., Paepfer B., Wang K.,
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Hanson L., Baekman A., Ny A., Edlund M., Edholm E., Tornell J.,
 RA Wallbrandt P., Egelrud T.,
 RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
 RT mice; a model for chronic itchy dermatitis.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
 RP AND TISSUE SPECIFICITY.
 RC TISSUE=Ovarian carcinoma;
 RX MEDLINE=22623266; PubMed=12738725;
 RA Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.,
 RA Diatchenko L., Marcusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Tohnyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP CHARACTERIZATION.

RX MEDLINE=95314630; PubMed=7794273;
 RA Skytt A., Stroemqvist M., Egelrud T.,
 RT "Primary substrate specificity of recombinant human stratum corneum
 RT chymotryptic enzyme.";
 RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
 CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
 CC structures in the cornified layer of the skin in the continuous
 CC shedding of cells from the skin surface. Specific for amino acid
 CC residues with aromatic side chains in the P1 position. SCCE
 CC cleaves insulin B chain at 6-Leu|-Cys-7, 16-Tyr|-Leu-17, 25-
 CC Phe|-Tyr-26, and 26-Tyr|-Thr-27. Could play a role in the
 CC activation of precursors to inflammatory cytokines.
 CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
 CC also observed at the apical membrane and in cytoplasm at the
 CC invasive front.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=P49862-1; Sequences=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=P49862-2; Sequences=VSP_013581;
 CC -!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
 CC expressed by keratinocytes in the epidermis. Also expressed in the
 CC brain, mammary gland, cerebellum, spinal cord and kidney. Lower
 CC levels in salivary glands, uterus, thymus, thyroid, placenta,
 CC trachea and testis. Up-regulated in ovarian carcinoma, especially
 CC late-stage serous carcinoma, compared with normal ovaries and
 CC benign adenomas (at the protein level).
 CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
 CC cell line.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; L33404; AAC37551.1; -; mRNA.
 DR EMBL; AF166330; AAD49718.1; -; Genomic DNA.
 DR EMBL; AF243527; AAG33360.1; -; Genomic DNA.
 DR EMBL; AF332583; AAK69624.1; -; Genomic DNA.
 DR EMBL; AF411214; AAN03662.1; -; mRNA.
 DR EMBL; AF411215; AAN03663.1; -; mRNA.
 DR EMBL; BC032005; AAH32005.1; -; mRNA.
 DR PIR; A53968; A53968.
 DR HSP; P00760; IEZX.
 DR MEROPS; S01.300; -.
 DR Ensembl; ENSG00000169035; Homo sapiens.
 DR HGNC; HGNC:6368; KLK7.
 DR H-InvDB; HIX0015373; -.
 DR MIM; 604438; -.
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
 DR GO; GO:0008544; P:epidermis development; TAS.
 DR InterPro; IPR001254; Peptidase S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM0020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;
 KW Hydroxylase; Protease; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 22
 FT PROPEP 23 29 Activation peptide.
 FT CHAIN 30 253 Kallikrein 7.
 FT DOMAIN 30 250 Peptidase S1.
 FT ACT_SITE 70 70 Charge relay system (By similarity).
 FT ACT_SITE 112 112 Charge relay system (By similarity).
 FT ACT_SITE 205 205 Charge relay system (By similarity).

```

FT CARBOHYD 246 246 N-linked (GlcNAc... ) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 /FTId=VSP_013581.
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A668 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 123 RLSSMVKKV 131
|||||
|

RESULT 3
Q6VPM5 ANOGA
ID Q6VPM5_ANOGA PRELIMINARY; PRT; 202 AA.
AC Q6VPM5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Odorant receptor 1 (Fragment).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=4ARR, Yaounde, and L3-5;
RA Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY334006; AAR01131.1; -; Genomic DNA.
DR EMBL; AY334007; AAR01132.1; -; Genomic DNA.
DR EMBL; AY334005; AAR01130.1; -; Genomic DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005549; F:odorant binding; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007608; P:perception of smell; IEA.
DR InterPro; IPR004117; 7tm6_olftrecept.
KW Pfam; PF02949; 7tm6; 1.
KX Receptor.
FT NON_TER 1
FT NON_TER 202
FT SEQUENCE 202 AA; 23639 MW; E4F6334A7FC8E8A0 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 202;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 185 RLSSMVKKL 193
|||||
|

RESULT 4
Q7QIV3 ANOGA
ID Q7QIV3_ANOGA PRELIMINARY; PRT; 259 AA.
AC Q7QIV3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000011096.
GN ORFNames=ENSANG000000008607;
OS Anopheles gambiae str. PEST.

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008807; EAA04012.2; -; Genomic DNA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_TYP.
DR Pfam; PF00560; LRR 1; 5.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_TYP; 5.
KW Leucine-rich repeat; Repeat.
SQ SEQUENCE 259 AA; 28975 MW; EFB47C010FDEF6A4 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 259;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 77 RVASMVKKI 85
|||||
|

RESULT 5
Q9S2Q8 STRCO
ID Q9S2Q8_STRCO PRELIMINARY; PRT; 282 AA.
AC Q9S2Q8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative endo alpha-1,4 polygalactosaminidase.
GN OrderedLocustNames=SCO2178; ORFNames=SCSP7.23c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21596410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417.141-147(2002).
DR EMBL; AL939111; CAB51262.1; -; Genomic DNA.
DR PIR; T35294; T35294.
KW Complete proteome.
SQ SEQUENCE 282 AA; 30789 MW; BEECFE1743703A33 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 282;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 RLSSMVKK 8
Db      265 RLSSMLKK 272

RESULT 6
Q7P141_CHRVO
ID      Q7P141_CHRVO PRELIMINARY;      PRT;      297 AA.
AC      Q7P141;
DT      01-MAR-2004 (TREMBLrel. 26, Created)
DT      01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Hypothetical protein.
GN      OrderedLocusNames=C03073;
OS      Chromobacterium violaceum.
OC      Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC      Neisseriaceae; Chromobacterium.
OX      NCBI_TaxID=536;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=ATCC 12472 / DSM 30191;
RX      MEDLINE=2282980; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA      Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA      Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA      Alves-Gomes J.A., Andrade E.M., Axtaripe J., de Araujo M.F.F.,
RA      Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA      Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA      Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA      Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA      Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
RA      Crezynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA      Paninatti P., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA      Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R.,
RA      Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangierio T.B.,
RA      Grattapaglia D., Griard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA      Leoi L.C.T., Lima L.F.A., Loureiro M.P., Lyra M.C.C.P.,
RA      Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
RA      di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA      Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA      Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA      Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA      Ramalho-Neco C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA      Santos E.B.P., Santos F.R., Schneider M.P.C., Seunarez H.N.,
RA      Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA      Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA      Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA      Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT      "The complete genome sequence of Chromobacterium violaceum reveals
RT      remarkable and exploitable bacterial adaptability";
RL      Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR      EMBL; AB016911; AAO58051.1; -; Genomic_DNA.
DR      InterPro; IPR002790; DUF88.
DR      Pfam; PF01936; DUF88; 1.
DR      ProDom; PD010896; DUF88; 1.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE 297 AA; 3242 MW; FCD02708D8087690 CRC64;

Query Match      82.5%; Score 33; DB 2; Length 297;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      225 RLSQMVKKL 233

RESULT 7
COQ2_YEAST
ID      COQ2_YEAST      STANDARD;      PRT;      372 AA.
AC      P32378; Q6B113;
DT      01-OCT-1993 (Rel. 27, Created)
DT      01-OCT-1993 (Rel. 27, Last sequence update)

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10-MAY-2005 (Rel. 47, Last annotation update)
Para-hydroxybenzoate-polyphenyltransferase, mitochondrial precursor
(EC 2.5.1.-) [PHB:polyphenyltransferase]
Name=COQ2; OrderedLocusNames=YNR041C; ORFNames=N3419;
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=92156158; PubMed=1740455;
RA Ashby M.N., Kutsunai S.Y., Ackerman S., Tzagoloff A., Edwards P.A.;
RT "COQ2 is a candidate for the structural gene encoding para-
hydroxybenzoate:polyphenyltransferase.";
RL J. Biol. Chem. 267:4128-4136(1992).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP MEDLINE=97313269; PubMed=9169873;
RA Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albertmann K.,
RA Philippsen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K.,
RA Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,
RA Beinhauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,
RA Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F.,
RA Doignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,
RA Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,
RA Goffeau A., Gueldener U., Herbert C.J., Heumann K., Heuss-Neitzel D.,
RA Hilbert H., Hinni K., Iraqui Housaini I., Jacquet M., Jimenez A.,
RA Joniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,
RA Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C.,
RA Messenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M.,
RA Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Plantia R.J.,
RA Pohl T.M., Runkle B., Rebeschung C., Remacha M.A., Revuelta J.L.,
RA Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,
RA Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhaeselt P.,
RA Vierendeels F., Visser S., Voet M., Volckaert G., Wach A.,
RA Wambutt R., Wedler H., Zollner A., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV
and its evolutionary implications.";
RL Nature 387:93-98(1997).
[3]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RP STRAINS=S288C;
RA Marsischky G., Rols A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Congra L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;
RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the prenylation of para-hydroxybenzoate with
an all-trans polyphenyl group.
CC -!- PATHWAY: Coenzyme Q biosynthesis; second step.
CC -!- INTERACTION: Q05946:UTP13; NDEXP=1; IntAct=EBI-4919, EBI-34702;
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -!- SIMILARITY: Belongs to the ubia prenyltransferase family.
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC EMBL; M81698; AAA34507.1; -; Genomic DNA.
CC EMBL; Z71656; CAA96321.1; -; Genomic DNA.
CC EMBL; AY693097; AAT93116.1; -; Genomic DNA.
CC PIR; S20056; S20056.
CC InterAct; P32378; -;
CC GenomOnline; I43386; -;
CC Ensembl; YNR041C; Saccharomyces cerevisiae.
CC SGD; S000005324; COQ2.


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DR GO: GO:0005743; C-mitochondrial inner membrane; TAS.
DR GO: GO:0005386; F-carrier activity; TAS.
DR GO: GO:0019440; F-isoprenoid binding; TAS.
DR GO: GO:0004659; F-prenyltransferase activity; IMP.
DR GO: GO:0006743; P-pubiquinone metabolism; IMP.
DR InterPro: IPR000537; Ubia_prenyltrans.
DR InterPro: IPR006370; Ubia_proteo.
DR Pfam: PF01040; Ubia; 1.
DR TIGRfam: TIGR01474; ubia_proteo; 1.
DR PROSITE: PS00943; Ubia; 1.
KW Complete proteome; Isoprene biosynthesis; Mitochondrion; Transferase;
FT TRANSIT 1 22 Mitochondrion (Potential).
FT CHAIN 23 372 Para-hydroxybenzoate--
FT TRANSMEM 92 112 polyphenyltransferase.
FT TRANSMEM 114 133 1 (Potential).
FT TRANSMEM 170 191 2 (Potential).
FT TRANSMEM 193 210 3 (Potential).
FT TRANSMEM 229 249 4 (Potential).
FT TRANSMEM 298 318 5 (Potential).
FT REGION 134 156 6 (Potential).
FT COMPIAS 29 49 Alkyl polyphenyl diphosphate-binding
FT CONFLICT 273 273 site (Potential).
FT CONFLICT 273 273 Ser-rich.
FT CONFLICT 273 273 A -> T (in Ref. 3).
FT SEQUENCE 372 AA; 41001 MW; 4D9738CE248B4AD6 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 372;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 326 RLFSMIKKV 334

RESULT 8
ORI_ANOGA
ID ORI_ANOGA STANDARD; PRT; 417 AA.
AC Q8WTE7; Q7Q1T3;
DC 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Odorant receptor Ori (Agor1).
GN Name=Ori;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.
RC STRAIN=G3;
RX MEDLINE=21593012; PubMed=11724964; DOI=10.1073/pnas.261432998;
RA Fox A.N., Pitts R.J., Robertson H.M., Carlson J.R., Zwiebel L.J.;
RT "Candidate odorant receptors from the malaria vector mosquito
RT Anopheles gambiae and evidence of down-regulation in response to blood
RT feeding.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:14693-14697(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PEST;
RG Anopheles genome sequencing consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION, AND INDUCTION.
RX PubMed=14724626; DOI=10.1038/427212a;
RA Hallen E.A., Fox A.N., Zwiebel L.J., Carlson J.R.;
RT "Olfaction: mosquito receptor for human-sweat odorant.";
RL Nature 427:212-213(2004).
RN [4]
RP IDENTIFICATION, AND TISSUE SPECIFICITY.
RX PubMed=12364795; DOI=10.1126/science.1076196;

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RA Hill C.A., Fox A.N., Pitts R.J., Kent L.B., Tan P.L., Chrystal M.A.,
RA Cravchik A., Collins F.H., Robertson H.M., Zwiebel L.J.;
RT "G protein-coupled receptors in Anopheles gambiae.";
RL Science 298:176-178(2002).
CC -!- FUNCTION: Plays a critical role in the anthropophilic host-seeking
CC behavior; establishes the host preference to transmit malaria. May
CC participate in the phenomenon of decreased host-seeking behavior
CC in disease vector mosquitoes after blood feeding.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Female-specific antennae and maxillary palp
CC expression.
CC -!- INDUCTION: Strong response to the odorant 4-methylphenol, a
CC component of human sweat, when expressed in odorant receptor
CC deficient Drosophila. In vivo, decreased expression in antennae
CC after a blood meal.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor Dr-or
CC family.
CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 44 of February 2004;
CC WWW="http://www.expasy.org/spotlight/back_issues/sptl044.shtml".
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
CC EMBL; AF364130; AAL35506.1; -; Genomic DNA.
CC EMBL; AAAB01008980; EAA13838.1; -; Genomic DNA.
CC Ensembl; ENSANG00000007844; Anopheles gambiae.
CC GO; GO:0016021; C:integral to membrane; NAS.
CC GO; GO:0005549; F:odorant binding; IDA.
CC GO; GO:0004984; F:olfactory receptor activity; IDA.
CC GO; GO:0042048; P:olfactory behavior; IDA.
CC GO; GO:0007608; P:perception of smell; IDA.
CC InterPro: IPR004117; 7tm6_olfrrecept.
CC Pfam: PF02949; 7tm6; 1.
KW G-protein coupled receptor; Multigene family; Olfaction; Receptor;
KW Sensory transduction; Transducer; Transmembrane.
FT TOPO_DOM 1 2 Extracellular (Potential).
FT TRANSMEM 3 23 1 (Potential).
FT TOPO_DOM 24 45 Cytoplasmic (Potential).
FT TRANSMEM 46 66 2 (Potential).
FT TOPO_DOM 67 73 Extracellular (Potential).
FT TRANSMEM 74 94 3 (Potential).
FT TOPO_DOM 95 133 Cytoplasmic (Potential).
FT TRANSMEM 134 154 4 (Potential).
FT TOPO_DOM 155 178 Extracellular (Potential).
FT TRANSMEM 179 199 5 (Potential).
FT TOPO_DOM 200 284 Cytoplasmic (Potential).
FT TRANSMEM 285 305 6 (Potential).
FT TOPO_DOM 306 317 Extracellular (Potential).
FT TRANSMEM 318 338 7 (Potential).
FT TOPO_DOM 339 417 Cytoplasmic (Potential).
FT SEQUENCE 417 AA; 48520 MW; F6D07D7BD93D37F2 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 417;
Best Local Similarity 77.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 219 RLGSVMKKL 227

RESULT 9
Q8FR58 CANGA
ID Q8FR58 CANGA PRELIMINARY; PRT; 530 AA.
AC Q6FR58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|P40215|Saccharomyces cerevisiae YMR145c NDHL.
DE OrderedLocusNames=CAGL0100748g;
GN

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OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boirame A., Boyer J., Battelico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller R.,
RA Niclaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissensbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR380955; CAG60223.1; -; Genomic DNA.
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001327; FAD_pyr_redox.
DR Pfam; PF00070; Pyr_redox; 1.
KW Complete proteome.
SQ SEQUENCE 530 AA; 59726 MW; 9BF95A03A0347248 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 530;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 316 RLKTVKKV 324
||:|||||

RESULT 10
ID YM23 YEAST STANDARD; PRT; 560 AA.
AC P40215;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical 62.8 kDa protein in RPS16A-TIF34 intergenic region.
GN OrderedLocNames=YM145C; ORFNames=YM9375.14C;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetales; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye K., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S.V., Whitehead S., Barrett B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII.";
RL Nature 387:90-93(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=S288c;
RA Marischky G., Rolfs A., Richardson A., Kane M., Baqui M., Tavcher E.,
RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle J., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;

RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC removed.
CC -----
CC EMBL; Z47071; CAA87359.1; -; Genomic_DNA.
CC EMBL; AY632785; AAT92804.1; -; Genomic_DNA.
CC PIR; S50401; S50401.
CC IntAct; P40215; -.
CC GeronOnline; 142815; -.
CC Ensemble; YMR145C; Saccharomyces cerevisiae.
CC SGD; S000004753; NDEL1.
CC GO; GO:0005739; C:mitochondrion; IDA.
CC GO; GO:0003954; P:NADH dehydrogenase activity; IDA.
CC GO; GO:0019685; P:ethanol fermentation; IMP.
CC GO; GO:0006116; P:NADH oxidation; IDA.
CC InterPro; IPR001327; FAD_pyr_redox.
CC Pfam; PF00070; Pyr_redox; 1.
CC KW Complete proteome; FAD; Flavoprotein; Hypothetical protein; NAD;
CC Oxidoreductase; Ubiquinone.
CC SEQUENCE 560 AA; 62774 MW; 10B1795E12E29C34 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 560;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 347 RLKTVKKV 355
||:|||||

RESULT 11
Q616B7 ECOLI PRELIMINARY; PRT; 107 AA.
AC Q616B7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
OS Escherichia coli.
OG Plasmid R388.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Anbutsu H., Tauda M.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB182370; BAD24124.1; -; Genomic_DNA.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 107 AA; 12021 MW; 1E128007B7367B5B CRC64;

Query Match 80.0%; Score 32; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
DB 52 RVSSNVKSV 60
||:|||||

RESULT 12
Q899C6 CLOTE PRELIMINARY; PRT; 169 AA.
AC Q899C6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

DE Anaerobic ribonucleoside-triphosphate reductase activating protein
 (EC 1.97.1.1-).
 GN OrderedLocusNames=CTC00258;
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Massachusetts / E88;
 RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
 RA Brueggemann H., Baumeister S., Fricke W.F., Wiezer A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 RT tetanus disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321 (2003).
 DR EMBL; AB015936; AAC34903.1; -; Genomic DNA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; IEA.
 DR InterPro; IPR001989; Radical activat.
 DR InterPro; IPR007197; Radical SAM.
 DR Pfam; PF04055; Radical SAM; I.
 DR PROSITE; PS01087; RADICAL_ACTIVATING; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 169 AA; 19292 MW; CC7AB2511D3844C1 CRC64;
 Query Match 80.0%; Score 32; DB 2; Length 169;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLSSWVKK 8
 DB 85 RLASMIKK 92
 RESULT 13
 QGAIB5 DESPS
 ID Q6AIB5 DESPS PRELIMINARY; PRT; 288 AA.
 AC Q6AIB5;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Probable UTP-glucose-1-phosphate uridylyltransferase.
 GN OrderedLocusNames=DPPB68;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=LSV54 / DSM 12343;
 RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Kuepp A., Frickey T., Rattel T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902 (2004).
 DR EMBL; CR522871; CAG37932.1; -; Genomic DNA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0003983; F:UTP-glucose-1-phosphate uridylyltransferase. . .; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR GO; GO:0006011; P:UDP-glucose metabolism; IEA.
 DR InterPro; IPR005771; Galu trans.
 DR InterPro; IPR005835; NTP transferase.
 DR Pfam; PF00483; NTP transferase; 1.
 DR TIGRFAMs; TIGR01099; galu; 1.
 KW Complete proteome; Nucleotidyltransferase; Transferase.
 SQ SEQUENCE 288 AA; 31782 MW; FID28AC4A04EE3CB CRC64;

Query Match 80.0%; Score 32; DB 2; Length 288;
 Best Local Similarity 87.5%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLSSWVKK 8
 DB 184 RLSSWVEK 191
 RESULT 14
 Q7NVJ5 CHRVO
 ID Q7NVJ5 CHRVO PRELIMINARY; PRT; 330 AA.
 AC Q7NVJ5;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Probable membrane lipoprotein.
 GN OrderedLocusNames=CV2347;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.P.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogio M., Bonatto S.,
 RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasek T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunarez H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
 DR EMBL; AB016918; AAQ60019.1; -; Genomic DNA.
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR InterPro; IPR003760; Bmp.
 DR Pfam; PF02608; Bmp; 1.
 DR Complete proteome; Lipoprotein.
 SQ SEQUENCE 330 AA; 35382 MW; 2AFAB050961AF87F CRC64;

Query Match 80.0%; Score 32; DB 2; Length 330;
 Best Local Similarity 87.5%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LSSWVKV 9
 DB 247 LSSWVKV 254

RESULT 15
 YUFN_BACSU

ID YUFN BACSU STANDARD; PRT; 350 AA.
AC O05252;
DT 15-DEC-1998 (Rel. 37, Last Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical lipoprotein yufN precursor.
GN Name=yufN; OrderedLocNames=BSU31540;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RX MEDLINE=97419515; PubMed=9274030;
RA Oudega B., Koningshoeft A., Pohl T.M., Weitzenecker T.,
RA Hilbert H., Duesterhoeft A., Hahne J., Weitzenecker T.,
RT "Analysis of the Bacillus subtilis genome: cloning and nucleotide
RT sequence of a 62 kb region between 275 degrees (rrnB) and 284 degrees
RT (pat).";
RL Microbiology 143:2769-2774 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=168;
RX MEDLINE=9804033; PubMed=9384377; DOI=10.1038/36786;
RA Kunz F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.-Y., Glaser P., Goffeau A., Goltightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.-W., Levine A., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -!- SIMILARITY: Belongs to the BMP lipoprotein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z39337; CAB07936.1; -; Genomic DNA.
CC EMBL; Z99120; CAB15143.1; -; Genomic DNA.
CC FIC; C70009; C70009.
CC Subtilist; BG12349; yufN.
CC InterPro; IPR003760; Bmp.
CC InterPro; IPR000437; Prok_lipoprot_s.
CC Pfam; PF02608; Bmp; 1.

DR PROSITE; PS00013; PROKAR LIPOPROTEIN; FALSE_NEG.
KW Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
KW Palmitate; Signal.
FT SIGNAL 1 13 Probable.
FT CHAIN 14 350 Hypothetical lipoprotein yufN.
FT LIPID 14 14 N-palmitoyl cysteine (Probable).
FT LIPID 14 14 S-diacylglycerol cysteine (Probable).
SQ SEQUENCE 350 AA; 37349 MW; 16D5176A52A99284 CRC64;
Query Match 80.0%; Score 32; DB 1; Length 350;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LSSMVKKV 9
DB 269 LSSMVKKV 276
Search completed: March 11, 2006, 00:38:38
Job time : 100.333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083a-32

Perfect score: 40

Sequence: 1 RLSSMVKKV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5-COMB.pep:*
2: /cgn2_6/prodata/1/iaa/6-COMB.pep:*
3: /cgn2_6/prodata/1/iaa/H-COMB.pep:*
4: /cgn2_6/prodata/1/iaa/PCUS-COMB.pep:*
5: /cgn2_6/prodata/1/iaa/R8-COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	2	US-09-502-600-32
2	40	100.0	9	2	US-09-918-243-32
3	40	100.0	144	2	US-09-618-259-4
4	40	100.0	154	2	US-09-261-416-7
5	40	100.0	161	2	US-09-261-416-8
6	40	100.0	224	2	US-08-944-483-33
7	40	100.0	225	1	US-08-557-146-12
8	40	100.0	225	1	US-09-027-337-4
9	40	100.0	225	1	US-09-154-344-12
10	40	100.0	225	1	US-09-644-600-4
11	40	100.0	225	1	US-09-654-600A-4
12	40	100.0	253	1	US-08-557-146-2
13	40	100.0	253	1	US-08-824-874-3
14	40	100.0	253	1	US-09-154-344-2
15	40	100.0	253	1	US-08-930-188-2
16	40	100.0	253	2	US-09-210-084-3
17	40	100.0	253	2	US-09-764-762-3
18	40	100.0	253	4	PCT-US96-04294-2
19	40	100.0	265	2	US-09-949-016-7716
20	36	90.0	9	2	US-09-502-600-110
21	36	90.0	9	2	US-09-918-243-110
22	31	77.5	9	2	US-09-502-600-79
23	31	77.5	9	2	US-09-502-600-87
24	31	77.5	9	2	US-09-918-243-79
25	31	77.5	9	2	US-09-918-243-87
26	30	75.0	156	2	US-09-328-352-7506
27	29	72.5	571	2	US-09-690-942-15

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28 29 72.5 582 1 US-08-261-086-2 Sequence 2, Appli
29 29 72.5 582 1 US-08-261-086-4 Sequence 4, Appli
30 29 72.5 582 1 US-08-261-086-6 Sequence 6, Appli
31 28 70.0 90 2 US-09-248-796A-23383 Sequence 23383, A
32 28 70.0 154 2 US-09-328-352-7990 Sequence 7990, Ap
33 28 70.0 174 2 US-09-248-796A-18044 Sequence 18044, A
34 28 70.0 214 2 US-09-583-110-3154 Sequence 3154, Ap
35 28 70.0 217 2 US-09-107-433-4867 Sequence 4867, Ap
36 28 70.0 218 2 US-09-270-767-49085 Sequence 49085, A
37 28 70.0 250 2 US-09-107-532A-4737 Sequence 4737, Ap
38 28 70.0 289 2 US-09-134-001C-3650 Sequence 3650, Ap
39 28 70.0 341 2 US-09-134-001C-3650 Sequence 3650, Ap
40 28 70.0 357 2 US-09-710-279-1360 Sequence 1360, Ap
41 28 70.0 405 2 US-09-134-000C-5465 Sequence 5465, Ap
42 28 70.0 448 2 US-09-871-212-8 Sequence 8, Appli
43 28 70.0 459 2 US-09-491-785-2 Sequence 2, Appli
44 28 70.0 459 2 US-09-710-279-2462 Sequence 2462, Ap
45 28 70.0 464 2 US-09-134-001C-4562 Sequence 4562, Ap

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ALIGNMENTS

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RESULT 1
US-09-502-600-32
; Sequence 32, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-502-600-32

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Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

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RESULT 2
US-09-918-243-32
; Sequence 32, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-918-243-32

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
||| ||| |||
DB 1 RLSSMVKKV 9

RESULT 3
US-09-618-259-4
; Sequence 4, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (sccc) catalytic domain
US-09-618-259-4

Query Match 100.0%; Score 40; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
||| ||| |||
DB 60 RLSSMVKKV 68

RESULT 4
US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: chymotryptic enzyme (Sccc) homologous to similar
; OTHER INFORMATION: domain in TADG-12
US-09-261-416-7

Query Match 100.0%; Score 40; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
||| ||| |||
DB 69 RLSSMVKKV 77

RESULT 5
US-09-261-416-8
; Sequence 8, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 8
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of hepsin (Heps)
; OTHER INFORMATION: homologous to similar domain in TADG-12
US-09-261-416-8

Query Match 100.0%; Score 40; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
||| ||| |||
DB 75 RLSSMVKKV 83

RESULT 6
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

Query Match 100.0%; Score 40; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183. US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match 100.0%; Score 40; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 94 RLSSMVKKV 102

RESULT 7
US-08-557-146-12
Sequence 12, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 40; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

Db 95 RLSSMVKKV 103

RESULT 8
US-09-027-337-4
Sequence 4, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotooshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 225
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Query Match 100.0%; Score 40; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 95 RLSSMVKKV 103

RESULT 9
US-09-154-344-12
Sequence 12, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-09-154-344-12

Query Match      100.0%; Score 40; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      95 RLSSMVKKV 103

RESULT 10
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; FILE REFERENCE: D6084CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; PRIOR FILING DATE: 2000-08-23
; PRIOR FILING DATE: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-644-600-4

Query Match      100.0%; Score 40; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      95 RLSSMVKKV 103

RESULT 11
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      123 RLSSMVKKV 131

RESULT 12
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      123 RLSSMVKKV 131

RESULT 13
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
```


STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-08-824-874-3

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||||
Db 123 RLSSMVKKV 131

RESULT 14
US-09-154-344-2
Sequence 2, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2
Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
|||||
Db 123 RLSSMVKKV 131

RESULT 15
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bialock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RLSSMVKKV 9
| | | | |
Db 123 RLSSMVKKV 131

Search completed: March 11, 2006, 01:24:24
Job time : 22.2222 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-32

Perfect score: 40

Sequence: 1 RLSSMVKKV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	3	US-09-918-243-32
2	40	100.0	9	3	US-09-905-083-32
3	40	100.0	9	4	US-10-372-521-32
4	40	100.0	9	5	US-10-437-963-155539
5	40	100.0	30	5	US-10-831-075-32
6	40	100.0	144	3	US-09-796-294-4
7	40	100.0	144	4	US-10-461-787-4
8	40	100.0	224	3	US-09-789-210-33
9	40	100.0	224	4	US-10-262-511-104
10	40	100.0	225	4	US-10-600-187-4
11	40	100.0	247	4	US-10-262-511-102
12	40	100.0	250	4	US-10-262-511-92
13	40	100.0	252	4	US-10-262-511-94
14	40	100.0	253	3	US-09-888-615-98
15	40	100.0	253	3	US-09-764-762-3
16	40	100.0	253	4	US-10-071-214-2
17	40	100.0	253	4	US-10-071-214-48
18	40	100.0	253	4	US-10-264-283-90
19	40	100.0	253	4	US-10-295-027-498
20	40	100.0	253	4	US-10-173-999-48
21	40	100.0	253	4	US-10-408-765A-639
22	40	100.0	253	5	US-10-643-795A-95
23	40	100.0	253	5	US-10-948-518-95
24	40	100.0	253	5	US-10-868-490A-1
25	40	100.0	257	4	US-10-344-394-38
26	36	90.0	9	3	US-09-918-243-110
27	36	90.0	9	3	US-09-905-083-110

Sequence 110, App
Sequence 110, App
Sequence 244024,
Sequence 155539,
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 61611, A
Sequence 49273, A
Sequence 43367, A
Sequence 59862, A
Sequence 53750, A
Sequence 63676, A
Sequence 76609, A
Sequence 79, Appl
Sequence 87, Appl
Sequence 79, Appl
Sequence 87, Appl

ALIGNMENTS

RESULT 1

US-09-918-243-32

; Sequence 32, Application US/09918243

; Patent No. US20020142317A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santini, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CJP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 32

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 123-131 of the SCCE protein

US-09-918-243-32

Query Match 100.0%; Score 40; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9

|||||

Db 1 RLSSMVKKV 9

RESULT 2

US-09-905-083-32

; Sequence 32, Application US/09905083

; Patent No. US20020146708A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CJP/C/Div

; CURRENT APPLICATION NUMBER: US/09/905,083

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 09/502,600

; PRIOR FILING DATE: 2000-02-11

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 32

; LENGTH: 9

; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-905-083-32

Query Match      100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 3
US-10-372-521-32
; Sequence 32, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-10-372-521-32

Query Match      100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 4
US-10-831-075-32
; Sequence 32, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-10-831-075-32

Query Match      100.0%; Score 40; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 1 RLSSMVKKV 9

RESULT 5
US-10-831-075-137
; Sequence 137, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 137
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 110-139 of the SCCE protein
US-10-831-075-137

Query Match      100.0%; Score 40; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 14 RLSSMVKKV 22

RESULT 6
US-09-796-294-4
; Sequence 4, Application US/09796294
; Patent No. US20020037581A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4

Query Match      100.0%; Score 40; DB 3; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches          9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 60 RLSSMVKKV 69
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RESULT 7
US-10-461-787-4
; Sequence 4, Application US/10461787
; Publication No. US20030199010A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. US20030199010A1 Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/10/461,787
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/09/618,259
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (sccc) catalytic domain
US-10-461-787-4

Query Match 100.0%; Score 40; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 RLSSMVKKV 9
Db 60 RLSSMVKKV 68
|||||

RESULT 8
US-09-789-210-33
; Sequence 33, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
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NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183. US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33

Query Match 100.0%; Score 40; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RLSSMVKKV 9
Db 94 RLSSMVKKV 102
|||||
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RESULT 9
US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
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; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104

Query Match      100.0%; Score 40; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLSSMVKKV 9
Db      109 RLSSMVKKV 117

RESULT 10
US-10-600-187-4
; Sequence 4, Application US/10600187
; Publication No. US20040086910A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064C1P/D
; CURRENT APPLICATION NUMBER: US/10/600,187
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/654,600A
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; 09/027,337
; PRIOR FILING DATE: 1999-10-20
; 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-10-600-187-4

Query Match      100.0%; Score 40; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLSSMVKKV 9
Db      95 RLSSMVKKV 103

RESULT 11
US-10-262-511-102
; Sequence 102, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 102
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-102

Query Match      100.0%; Score 40; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RLSSMVKKV 9
Db      109 RLSSMVKKV 117

RESULT 12
US-10-262-511-92
; Sequence 92, Application US/10262511
; Publication No. US2004003823A1
; GENERAL INFORMATION:
```

; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SEQ ID NO 92
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-92

Query Match 100.0%; Score 40; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
| | | | |
Db 120 RLSSMVKKV 128

RESULT 13
US-10-262-511-94

; Sequence 94, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 94
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-94

Query Match 100.0%; Score 40; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
| | | | |
Db 122 RLSSMVKKV 130

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-32

Perfect score: 40

Sequence: 1 RLSSMWKVV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_New.*
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2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB pep.*
3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	181	6	US-10-412-748-19
2	40	100.0	253	6	US-10-412-748-11
3	40	100.0	253	6	US-10-412-748-14
4	40	100.0	253	6	US-10-412-748-17
5	40	100.0	253	7	US-11-037-243-98
6	30	75.0	220	7	US-11-096-568A-29743
7	30	75.0	236	7	US-11-096-568A-29742
8	30	75.0	334	7	US-11-096-568A-32412
9	30	75.0	385	7	US-11-096-568A-32411
10	30	75.0	390	7	US-11-096-568A-32410
11	30	75.0	457	6	US-11-208-308-13
12	30	75.0	524	6	US-11-208-308-4
13	30	75.0	524	7	US-11-208-308-11
14	30	75.0	524	7	US-11-208-308-12
15	29	72.5	187	7	US-11-096-568A-24167
16	29	72.5	235	7	US-11-096-568A-24166
17	29	72.5	247	7	US-11-096-568A-24165
18	29	72.5	631	7	US-11-087-099-4595
19	28	70.0	185	7	US-11-087-099-12061
20	28	70.0	235	7	US-11-087-099-9520
21	28	70.0	235	7	US-11-087-099-11057
22	28	70.0	236	7	US-11-098-686-10100
23	28	70.0	238	7	US-11-087-099-3228
24	28	70.0	249	7	US-11-087-099-6428
25	28	70.0	319	6	US-10-510-941-4
Sequence 19, Appl					Sequence 11, Appl
Sequence 11, Appl					Sequence 14, Appl
Sequence 14, Appl					Sequence 17, Appl
Sequence 17, Appl					Sequence 98, Appl
Sequence 98, Appl					Sequence 29743, A
Sequence 29743, A					Sequence 29742, A
Sequence 29742, A					Sequence 32412, A
Sequence 32412, A					Sequence 32411, A
Sequence 32411, A					Sequence 32410, A
Sequence 32410, A					Sequence 13, Appl
Sequence 13, Appl					Sequence 4, Appl
Sequence 4, Appl					Sequence 11, Appl
Sequence 11, Appl					Sequence 12, Appl
Sequence 12, Appl					Sequence 24167, A
Sequence 24167, A					Sequence 24166, A
Sequence 24166, A					Sequence 24165, A
Sequence 24165, A					Sequence 4595, Ap
Sequence 4595, Ap					Sequence 12061, A
Sequence 12061, A					Sequence 9520, Ap
Sequence 9520, Ap					Sequence 11057, Ap
Sequence 11057, Ap					Sequence 10100, A
Sequence 10100, A					Sequence 3228, Ap
Sequence 3228, Ap					Sequence 6428, Ap
Sequence 6428, Ap					Sequence 4, Appl

RESULT 1

US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1

GENERAL INFORMATION:

; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; TYPE: PRT
; ORGANISM: Human
; LENGTH: 181
; US-10-412-748-19

Query Match 100.0%; Score 40; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RLSSMWKVV 9

Db 51 RLSSMWKVV 59

RESULT 2

US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1

GENERAL INFORMATION:

; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; TYPE: PRT
; US-10-412-748-11

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      123 RLSSMVKKV 131

RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      123 RLSSMVKKV 131

RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      123 RLSSMVKKV 131

RESULT 5
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      123 RLSSMVKKV 131

RESULT 6
US-11-096-568A-29743
; Sequence 29743, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29743
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(220)
; OTHER INFORMATION: Ceres Seq. ID no. 4927738
US-11-096-568A-29743

Query Match      75.0%; Score 30; DB 7; Length 220;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RLSSMVKKV 9
Db      132 RLSSMVKKI 140

RESULT 7
US-11-096-568A-29742
; Sequence 29742, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 29742
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(236)
; OTHER INFORMATION: Ceres Seq. ID no. 4927737
US-11-096-568A-29742

Query Match 75.0%; Score 30; DB 7; Length 236;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLSSMVKKV 9
Db 148 RLSSMKKI 156
|||||

RESULT 8
US-11-096-568A-32412
; Sequence 32412, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32412
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(334)
; OTHER INFORMATION: Ceres Seq. ID no. 13592964
US-11-096-568A-32412

Query Match 75.0%; Score 30; DB 7; Length 334;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSMVKK 8
Db 316 LSSMIKK 322
|||||

RESULT 9
US-11-096-568A-32411
; Sequence 32411, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32411
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (1)..(385)
; OTHER INFORMATION: Ceres Seq. ID no. 13592963
US-11-096-568A-32411

Query Match 75.0%; Score 30; DB 7; Length 385;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSMVKK 8
Db 367 LSSMIKK 373
|||||

RESULT 10
US-11-096-568A-32410
; Sequence 32410, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32410
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(390)
; OTHER INFORMATION: Ceres Seq. ID no. 13592962
US-11-096-568A-32410

Query Match 75.0%; Score 30; DB 7; Length 390;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LSSMVKK 8
Db 372 LSSMIKK 378
|||||

RESULT 11
US-11-208-308-13
; Sequence 13, Application US/11208308
; Publication No. US20060041952A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Zhihong C.
; TITLE OF INVENTION: P450 Polynucleotides, Polypeptides, and
; FILE REFERENCE: 18207-006001
; CURRENT APPLICATION NUMBER: US/11/208,308
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: 60/603,533
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(457)
; OTHER INFORMATION: Public GI no. 4006922
US-11-208-308-13

Query Match 75.0%; Score 30; DB 7; Length 457;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy 1 RLSSMVKKV 9
Db 199 RLKMKVKV 207

RESULT 12
US-10-507-106-4
; Sequence 4, Application US/10507106
; Publication NO. US20050246797A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Agency
; TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
; FILE REFERENCE: 26352U (P503-311pCt)
; CURRENT APPLICATION NUMBER: US/10/507,106
; CURRENT FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-507-106-4

Query Match 75.0%; Score 30; DB 6; Length 524;
Best Local Similarity 77.8%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 266 RLKMKVKV 274

RESULT 13
US-11-208-308-11
; Sequence 11, Application US/11208308
; Publication No. US20060041952A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Zhihong C.
; TITLE OF INVENTION: P450 Polynucleotides, Polypeptides, and
; FILE REFERENCE: 18207-006001
; CURRENT APPLICATION NUMBER: US/11/208,308
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: 60/603,533
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(524)
; OTHER INFORMATION: Public GI no. 13878393
US-11-208-308-11

Query Match 75.0%; Score 30; DB 7; Length 524;
Best Local Similarity 77.8%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 266 RLKMKVKV 274

RESULT 14
US-11-208-308-12
; Sequence 12, Application US/11208308
; Publication No. US20060041952A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Zhihong C.
; TITLE OF INVENTION: P450 Polynucleotides, Polypeptides, and
```

```
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 18207-006001
; CURRENT APPLICATION NUMBER: US/11/208,308
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: 60/603,533
; PRIOR FILING DATE: 2004-08-20
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(524)
; OTHER INFORMATION: Public GI no. 18419825
US-11-208-308-12

Query Match 75.0%; Score 30; DB 7; Length 524;
Best Local Similarity 77.8%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 266 RLKMKVKV 274

RESULT 15
US-11-096-568A-24167
; Sequence 24167, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24167
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(187)
; OTHER INFORMATION: Ceres Seq. ID no. 12419624
US-11-096-568A-24167

Query Match 72.5%; Score 29; DB 7; Length 187;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RLSSMVKKV 9
Db 152 RLSECVKKI 160

Search completed: March 11, 2006, 01:38:39
Job time : 9 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	4 AAE08238	Aae08238 Human str
2	40	100.0	9	8 ADR68794	Adr68794 Human str
3	40	100.0	136	4 ABG23378	Abg23378 Novel hum
4	40	100.0	198	6 ADA05736	Ada05736 Human NOV
5	40	100.0	198	8 ADN62900	Adn62900 Human NOV
6	40	100.0	250	6 ADA05732	Ada05732 Human NOV
7	40	100.0	250	8 ADN62896	Adn62896 Human NOV
8	40	100.0	253	2 AAR05383	Aar05383 Human str
9	40	100.0	253	2 AAW05383	Aaw05383 Human amy
10	40	100.0	253	5 ABB84421	Abb84421 Human SCC
11	40	100.0	253	5 ABB84406	Abb84406 Human SCC
12	40	100.0	253	5 AAU82740	Aau82740 Amino aci
13	40	100.0	253	6 ABU07440	Abu07440 Protein d
14	40	100.0	253	6 ABU07471	Abu07471 Protein d
15	40	100.0	253	6 ABR58471	Abr58471 Human str
16	40	100.0	253	7 ADB80484	Adb80484 Ovarian c
17	40	100.0	253	7 ADJ68833	Adj68833 Human hea
18	40	100.0	253	7 ADN39180	Adn39180 Cancer/tu
19	40	100.0	253	8 ADL06515	Adl06515 Human tum
20	40	100.0	253	8 ADN04182	Adn04182 Antipori
21	40	100.0	253	8 ADR72880	Adr72880 Human ova
22	40	100.0	253	9 ADY67588	Ady67588 Human kal
23	40	100.0	253	9 AEC00353	Aec00353 Human kal
24	40	100.0	257	3 AAB21326	Aab21326 Human HSC

25	38	95.0	812	7	ABO65558	Abo65558 Klebsiell
26	36	90.0	9	4	AAE08240	Aae08240 Human str
27	36	90.0	9	4	AAE08241	Aae08241 Human str
28	36	90.0	9	8	ADR68796	Adr68796 Human str
29	36	90.0	9	8	ADR68797	Adr68797 Human str
30	35	87.5	61	4	AAO12472	Aao12472 Human pol
31	35	87.5	142	4	AAB63580	Aab63580 Human gas
32	35	87.5	156	4	AAB63578	Aab63578 Human gas
33	35	87.5	159	4	AAB63582	Aab63582 Human gas
34	34	85.0	23	4	ABB43858	Abb43858 Peptide #
35	34	85.0	23	4	AAM37771	Aam37771 Peptide #
36	34	85.0	23	4	AAM64837	Aam64837 Human bra
37	34	85.0	23	4	ABG59233	Abg59233 Human liv
38	34	85.0	23	5	ABG46617	Abg46617 Human pep
39	34	85.0	115	7	ADF59165	Adf59165 Human pol
40	34	85.0	187	8	ADX94464	Adx94464 Plant ful
41	34	85.0	201	5	ABB78636	Abb78636 Rat OST10
42	34	85.0	369	8	ADL91113	Adl91113 Bovine lu
43	34	85.0	369	8	ADL91117	Adl91117 Bovine lu
44	34	85.0	369	8	ADL91127	Adl91127 Bovine lu
45	34	85.0	371	2	AAR75642	Aar75642 Bovine co

ALIGNMENTS

RESULT 1

AAE08238
ID AAE08238 standard; peptide; 9 AA.

XX AC AAE08238;

XX XX 01-NOV-2001 (first entry)

XX DE Human stratum corneum chymotrypsin enzyme peptide #3 (residues 5-13).

XX KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
XX KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
XX KW antisense therapy; malignant hyperplasia.

XX OS Homo sapiens.

XX XX WO200159158-A1.

XX XX 16-AUG-2001.

XX PF 07-FEB-2001; 2001WO-US003977.

XX XX 11-FEB-2000; 2000US-00502600.

XX XX (UYAR-) UNIV ARKANSAS.

XX PI O'brien TJ;

XX XX WPI; 2001-514676/56.

XX DR Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

XX PS Claim 25; Page 102; 127pp; English.

XX CC The invention relates to diagnosing cancer especially ovarian cancer, by
XX CC screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are
XX CC considered to be an integral part of tumour growth and metastasis, and
XX CC therefore, markers indicative of their presence or absence are useful for
XX CC the diagnosis of cancer. The method is useful for diagnosing cancer,
XX CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used
XX CC to treat a cancer selected from ovarian, breast, lung, colon, prostate
XX CC and other cancers in which SCCE is overexpressed. The present sequence is
XX CC human SCCE peptide

XX XX Sequence 9 AA;

SQ

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLILL 9
Db 1 LLLPLQLILL 9

RESULT 2
ADR68794
ID ADR68794 standard; peptide; 9 AA.
XX
AC ADR68794;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:33.
XX
XX serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
XX Homo sapiens.
OS
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005134.
PF
XX 21-FEB-2003; 2003US-00372521.
PR
XX (UYAR-) UNIV ARKANSAS.
PA
XX
PI O'Brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/63.
XX
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX Claim 5; SEQ ID NO 33; 117pp; English.
PS
XX The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLILL 9
Db 1 LLLPLQLILL 9

RESULT 3
ABG23378

ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR N-PSDB; AAS87565.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 136 AA;

Query Match 100.0%; Score 40; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLILL 9
Db 11 LLLPLQLILL 19

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX

09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET J.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJJ/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIW/) JI W.
PA (MILL/) MILLER C E.
PA (RASI/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet J, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spyttek KA, Edinger SR, Ellerman K, Malvankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR WPI: 2004-213931/20.
DR N-PSDB; ADN62899.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX

PS Claim 1; SEQ ID NO 96; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, immune disorders,
CC disorders, Alzheimer's Disease, Parkinson's Disorder, neurodegenerative
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 198 AA;

Query Match 100.0%; Score 40; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 6
ADA05732
ID ADA05732 standard; protein; 250 AA.
XX
AC ADA05732;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18a protein SEQ ID NO:92.
XX
KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
OS
XX Homo sapiens.
XX
PN WO2003029424-A2.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031373.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkete RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05731.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 169-170; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nontropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 40; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLLPLQLLL 9
Db 2 LLLPLQLLL 10
RESULT 7
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX
AC ADN62896;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18a.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 09-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPVT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPL/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
WPI: 2004-213931/20.
DR N-PSDB; ADN62895.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 92; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient with
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

XX SQ Sequence 250 AA;

Query Match 100.0%; Score 40; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 2 LLLPLQILL 10
|||||

RESULT 8

AAR67888
ID AAR67888 standard; protein; 253 AA.

XX AC AAR67888;

XX DT 25-MAR-2003 (revised)

XX DT 09-AUG-1995 (first entry)

XX DE Human stratum corneum chymotrophic recombinant enzyme (SCCE) .

XX KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
XX KW callosities; keratosis pilaris; ichthyoses; eczema.

XX OS Homo sapiens.

XX PN WO9500651-A1.

XX PD 05-JAN-1995.

XX PF 20-JUN-1994; 94WO-IB000166.

XX PR 18-JUN-1993; 93DK-00000725.

XX PA (SYMB-) SYMBICOM AB.

XX PI Egelrud T, Hansson L;

XX DR WPI: 1995-052088/07.

XX DR N-PSDB; AAQ81203.

XX PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
XX PT related vectors, transformed cells and polypeptides, useful for treating
XX PT skin disorders, e.g. acne or psoriasis, and for identification of
XX PT specific inhibitors.

XX PS Disclosure; Page 97; 137pp; English.

XX CC The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
XX CC and skin care products, especially to treat and prevent acne, xeroderma,
XX CC or other hyperkeratotic conditions (e.g. callosities or keratosis
XX CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
XX CC recombinantly following mammal, insect, plant, or microorganism
XX CC transformation with plasmid pBS07. (Updated on 25-MAR-2003 to correct PN
XX CC field.)

XX SQ Sequence 253 AA;

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13
|||||

RESULT 9

AAW05383
ID AAW05383 standard; protein; 253 AA.
XX
AC AAW05383;
XX
DT 31-DEC-1996 (first entry)
XX
DE Human amyloid precursor protein protease.
XX
KW Amyloid precursor protein protease; Alzheimer's disease; diagnosis; therapy.
KW
XX Homo sapiens.
OS
XX
PN WO9631122-A1.
XX
PD 10-OCT-1996.
XX
PF 02-APR-1996; 96WO-US004294.
XX
PR 04-APR-1995; 95US-00416257.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Dixon EP, Johnstone BM, Little SP;
XX
DR WPI; 1996-464694/46.
DR
DR N-PSDB; AAT39783.
XX
XX New isolated human amyloid precursor protein protease - used to develop
PT prods. for the treatment or diagnosis of associated conditions, esp.
PT Alzheimer's disease.
XX
PS Claim 1; Page 44-45; 55pp; English.
XX
CC Human amyloid precursor protein protease (AAW05383) is involved in the
CC processing or clearance of amyloid precursor protein to form beta-amyloid
CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
CC obt'd. from a human lung library. Recombinant protease can be produced in
CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
CC (partic. AV-120 host cells). It is used to develop products for the design
CC and testing of cpds. useful for treating or preventing conditions
CC associated with beta-amyloid peptide, esp. Alzheimer's disease
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13
RESULT 10
ABB84421
ID ABB84421 standard; peptide; 253 AA.
XX
AC ABB84421;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human SCCE protein N-terminal fragment SEQ ID 48.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.
XX
PN WO200262135-A2.

15-AUG-2002.
08-FEB-2002; 2002WO-IB001300.
09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
Egelrud T, Hansson L;
WPI; 2002-643380/69.
Transgenic mammal or its embryo useful as model for human disease, has
heterologous nucleotide sequence coding for stratum corneum chymotryptic
enzyme operably linked to promoter that drives its expression in skin.
Example 6; Page 37; 74pp; English.
This invention describes a novel non-human transgenic mammal or mammalian
embryo having integrated within its genome, a heterologous nucleotide
sequence comprising at least a significant part of a nucleotide sequence
coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
operably linked to a promoter that drives expression of heterologous scce
or its variant in skin. The product of the invention is useful as a model
for the study of disease with the aim of improving treatment, to relieve
or ameliorate a pathogenic condition, for development or testing of a
cosmetic or a pharmaceutical formulation, and for the development of a
diagnostic method. It can also be used as a model for a skin disease or
skin cancer. The invention is also useful for screening or identifying a
compound or composition effective for the prevention or treatment of an
abnormal or unwanted phenotype, and for screening or identifying a
compound or composition effective for the prevention or treatment of
inflammatory skin diseases selected from diseases consisting of epidermal
hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
with epidermal hyperkeratosis. The mammal of the invention is also useful
as a model for further studies of itch mechanisms and the testing of
potential compounds and compositions for relieve of various skin diseases
where itch is a component. This sequence represents the N-terminal
fragment of the human stratum corneum chymotryptic enzyme, SCCE
synonymous with human kallikrein 7 (KLK7), used in the development of the
transgenic mammals described in the invention
Sequence 253 AA;
Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13
RESULT 11
ABB84406
ID ABB84406 standard; protein; 253 AA.
XX
AC ABB84406;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human SCCE protein.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.

XX WO200262135-A2.
PN 15-AUG-2002.
XX 08-FEB-2002; 2002WO-IB001300.
XX 09-FEB-2001; 2001CA-02332655.
PR 09-FEB-2001; 2001DK-00000218.
XX (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX Egelrud T, Hansson L;
XX WPI; 2002-643380/69.
DR N-PSDB; ABQ76226.
XX Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX Claim 10; Page 58-59; 74pp; English.
XX This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a
CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents the human stratum
CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
CC with human kallikrein 7 (KLK7) and is used in the development of the
CC transgenic mammals described in the invention
XX Sequence 253 AA;
SQ Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13
RESULT 12
AAU82740
ID AAU82740 standard; protein; 253 AA.
XX AAU82740;
XX 23-APR-2002 (first entry)
DT Amino acid sequence of novel human protease #39.
DE Human; protease; cancer; immune-related disorder; cardiovascular disease;
XX neuronal-associated disease; metabolic disorder; inflammatory disorder;
KW nervous system disorder; sexual dysfunction; pain; mood disorder;
XX

KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
XX ocular disease; cytostatic; enzyme.
OS Homo sapiens.
XX WO200200860-A2.
XX 03-JAN-2002.
XX 26-JUN-2001; 2001WO-US020171.
XX 26-JUN-2000; 2000US-0214047P.
XX (SUGE-) SUGEN INC.
XX Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepel S;
PI Charyczak G;
XX WPI; 2002-139913/18.
DR N-PSDB; ABK31782.
XX Nucleic acids encoding novel human proteases, useful for useful for
PT treating diseases and disorders such as cancers, immune-related diseases
PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
PT disorders.
XX Claim 6; Fig 2N; 313pp; English.
XX The present invention relates to the isolation of novel human proteases,
CC and the nucleic acids encoding them. The sequences of the invention are
CC useful for treating diseases and disorders such as cancers (e.g. breast,
CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
CC disorders, cognitive disorders, hypotension, hypertension, psychotic
CC disease) and dyskinesias. The nucleic acids and polypeptides are also
CC useful for treating viral infections caused by human immunodeficiency
CC virus (HIV), and non-viral infections such as ocular disease (e.g.
CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
CC human proteases of the invention
XX Sequence 253 AA;
SQ Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13
RESULT 13
ABU07440
ID ABU07440 standard; protein; 253 AA.
XX ABU07440;
XX 28-JAN-2003 (first entry)
DT Protein differentially regulated in prostate cancer #43.
DE Prostate cancer; gene expression; differential regulation;
XX molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
XX Homo sapiens.
XX


```

QY      1 LLLPLQILL 9
Db      5 LLLPLQILL 13

RESULT 15
ABR58471
ID ABR58471 standard; protein; 253 AA.
XX
XX AC ABR58471;
XX
XX DT 07-JUL-2003 (first entry)
XX
XX DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
XX
XX KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX
XX OS Homo sapiens.
XX
XX PN WO2003029468-A1.
XX
XX PD 10-APR-2003.
XX
XX PF 02-OCT-2002; 2002WO-US031467.
XX
XX PR 02-OCT-2001; 2001US-0327135P.
XX
XX PR 30-MAY-2002; 2002US-0384531P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Algate PA, Mannion J;
XX
XX DR WPI; 2003-372001/35.
XX
XX PT New polynucleotide and polypeptide useful for diagnosing and/or treating
XX cancer, particularly ovarian cancer, and as a vaccine.
XX
XX PS Claim 2; Page 157-158; 169pp; English.
XX
XX CC The invention relates to a novel isolated polynucleotide. The
XX polynucleotides of the invention have cytostatic activity, and may have a
XX use in gene therapy, and in a vaccine. The composition and methods are
XX useful in diagnosing and/or treating cancer, particularly ovarian cancer.
XX The composition may also be used as a vaccine to prevent cancer. The
XX present sequence is used in the exemplification of the invention
XX
SQ Sequence 253 AA;

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LLLPLQILL 9
Db      5 LLLPLQILL 13

Search completed: March 11, 2006, 00:24:13
Job time : 88.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQLLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: piri:*
2: piri2:*
3: piri3:*
4: piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	253	2 A53968	serine proteinase
2	36	90.0	146	2 H75201	hypothetical prote
3	34	85.0	277	2 H84314	cytochrome aa3 con
4	34	85.0	369	2 S33603	surfactant protein
5	34	85.0	371	1 JN0450	conglutinin precu
6	34	85.0	371	2 I45878	conglutinin - bovi
7	34	85.0	754	2 AE0614	probable competenc
8	34	85.0	845	2 D97163	cation transport p
9	33	82.5	196	2 G65039	hypothetical prote
10	33	82.5	282	2 E70890	hypothetical prote
11	33	82.5	370	2 A46334	daunorubicin resis
12	33	82.5	398	2 C91063	hypothetical prote
13	33	82.5	413	2 AC0834	probable membrane
14	33	82.5	426	2 C83103	hypothetical prote
15	33	82.5	470	2 A90083	hypothetical prote
16	33	82.5	475	1 A69149	O-antigen transpor
17	33	82.5	653	2 A46362	amyloid precursor-
18	32	80.0	198	2 S25656	T-cell surface gly
19	32	80.0	235	1 RWHUT8	T-cell surface gly
20	32	80.0	238	1 LNR7MA	mannose-binding le
21	32	80.0	247	1 KYHUCM	chymase (EC 3.4.21
22	32	80.0	249	2 F91095	type III secretion
23	32	80.0	249	2 B85941	hypothetical prote
24	32	80.0	264	2 C97402	probable acyltrans
25	32	80.0	264	2 AC2620	1-acyl-sn-glycerol
26	32	80.0	266	2 JC7300	tax-responsive ele
27	32	80.0	267	2 JC4857	hepatocarcinogenes
28	32	80.0	491	2 JC6197	stromelysin 3 (EC
29	32	80.0	492	2 A44399	stromelysin 3 (EC

30	32	80.0	543	2 AI2088	Na+/H+-exchanging
31	32	80.0	1306	1 A31759	peptidyl-dipeptida
32	31	77.5	100	2 A38685	apolipoprotein C-I
33	31	77.5	155	2 A31278	interleukin-2 prec
34	31	77.5	159	2 G75555	conserved hypotet
35	31	77.5	184	2 S10125	alpha-2u-globulin
36	31	77.5	189	2 T43766	hypothetical prote
37	31	77.5	244	2 F69260	nitrate ABC transp
38	31	77.5	249	2 T35589	probable secreted
39	31	77.5	269	2 T38931	hypothetical prote
40	31	77.5	303	2 C84914	hypothetical prote
41	31	77.5	322	2 A98157	probable permease
42	31	77.5	372	2 AH3130	ABC transporter, m
43	31	77.5	392	2 D83934	hypothetical prote
44	31	77.5	447	2 C84306	hypothetical prote
45	31	77.5	493	2 A71875	hypothetical prote

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:g521214; PIDN:7
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

RESULT 2

H75201
hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75201
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: H75201
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <RAW>
A;Cross-references: UNIPROT:Q9V2D5; UNIPARC:UPI0000063243; GB:AJ248283; GB:AL096836; NID
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0088
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

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Query Match      90.0%; Score 36; DB 2; Length 146;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 67 LLLPLQIII 75

RESULT 3
H84314
cytochrome aa3 controlling protein [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84314
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.;
; Leichauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A>Title: Genome sequence of Halobacterium species NRC-1
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84314
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-277 <STO>
A:Cross-references: UNIPROT:Q9HP13; UNIPARC:UPI0000063931; GB:AE004437; NID:g10581096; E
C:Genetics:
A:Gene: ccp

Query Match      85.0%; Score 34; DB 2; Length 277;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 97 VLLPLQVIL 105

RESULT 4
S33603
surfactant protein D - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S33603
R:Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A>Title: Structural similarity between bovine conglutinin and bovine lung surfactant pro
A:Reference number: S33603; MUID:93170856; PMID:8436402
A:Accession: S33603
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-369 <DIM>
A:Cross-references: UNIPARC:UPI0000177932
C:Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:248-367/Domain: C-type lectin homology <LCH>

Query Match      85.0%; Score 34; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 2 LLLPLSVLL 10

RESULT 5
JN0450
conglutinin precursor - bovine
N:Alternate names: C3b-binding protein
N:Contains: conglutinin-N
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

```

```

C:Accession: JN0450; JC2396; S33235; A23740; S36879; S35044; I46010; A29416; S34054
R:Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A>Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
A:Reference number: JN0450; MUID:93213261; PMID:8460993
A:Accession: JN0450
A:Molecule type: mRNA
A:Residues: 1-371 <SUZ>
A:Cross-references: UNIPROT:P23805; UNIPARC:UPI0000127EB3; DDBJ:D14085; NID:g285643; PID:
A:Experimental source: liver
R:Kawasaki, N.; Itoh, N.; Kawasaki, T.
Biochem. Biophys. Res. Commun. 198, 597-604, 1994
A>Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamme
A:Reference number: JC2396; MUID:94128104; PMID:8297370
A:Accession: JC2396
A:Molecule type: mRNA
A:Residues: 1-371 <KAZ>
A:Cross-references: UNIPARC:UPI0000127EB3
A>Note: The authors translated the codon GAT for residues 250 and 270 as Glu
R:Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
Biochem. J. 292, 157-162, 1993
A>Title: The cDNA cloning of conglutinin and identification of liver as a primary site of
A:Reference number: S3235; MUID:93277452; PMID:7684896
A:Accession: S3235
A:Molecule type: mRNA
A:Residues: 1-172, 'H', 174-217, 'A', 219-271, 'V', 273-371 <LUJ>
A:Cross-references: UNIPARC:UPI000016C2E3; EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PII
A:Experimental source: liver
R:Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarna, T.B.
J. Biol. Chem. 266, 2715-2723, 1991
A>Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin fa
A:Reference number: A23740; MUID:91131556; PMID:1993651
A:Accession: A23740
A:Molecule type: protein
A:Residues: 21-209, 'S', 211-371 <LEB>
A:Cross-references: UNIPARC:UPI000014DF2A
R:Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Biochem. Biophys. 305, 533-540, 1993
A>Title: Differentiation of conglutination activity and sugar-binding activity of conglu
A:Reference number: S36879; MUID:93384312; PMID:8373191
A:Accession: S36879
A:Molecule type: protein
A:Residues: 21-54; 75-86, 'X', 88-89, 'X', 91, 'X', 93-94; 208-209, 'X', 211-227 <KAW>
A:Cross-references: UNIPARC:UPI00001741A3; UNIPARC:UPI00001741A4; UNIPARC:UPI00001741A5
A:Experimental source: serum
R:Lu, J.; Wiedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
Eur. J. Biochem. 215, 793-799, 1993
A>Title: Structural similarity between lung surfactant protein D and conglutinin. Two di
A:Reference number: S35044; MUID:93358905; PMID:8354286
A:Accession: S35044
A:Molecule type: protein
A:Residues: 75-86, 'X', 88-89, 'X', 91, 'I', 'I' <LUA>
A:Cross-references: UNIPARC:UPI00001741A6
A:Experimental source: lung
R:Young, N.M.; Leon, M.A.
Biochem. Biophys. Res. Commun. 143, 645-651, 1987
A>Title: The carbohydrate specificity of conglutinin and its homology to proteins in the
A:Reference number: A29416; MUID:87184551; PMID:3566740
A:Contents: annotation
R:Malhotra, R.; Laursen, S.B.; Willis, A.C.; Sim, R.B.
Biochem. J. 293, 15-19, 1993
A>Title: Research Communication. Localization of the receptor-binding site in the collect
A:Reference number: S34054; MUID:93319501; PMID:8328957
A:Contents: annotation
R:Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarna, T.B.; Tauber, A.I.; Sastry,
J. Immunol. 153, 173-180, 1994
A>Title: Bovine conglutinin Gene exon structure reveals its evolutionary relationship to
A:Reference number: I46010; MUID:94267222; PMID:8207234
A:Accession: I46010
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-371 <LIO>
A:Cross-references: UNIPARC:UPI0000127EB3; EMBL:U06860; NID:G507183; PIDN:AAB60624.1; PII

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C;Comment: This protein mediates the agglutination of erythrocytes with antibody and complement. This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamin C;Genetics:

A;Gene: CGN1
 A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
 C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 C;Keywords: calcium binding; glycoprotein; hydroxyllysine; hydroxyproline
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-371/Product: conglutinin #status predicted <MAT>
 F;46-214/Region: collagen-like
 F;75-371/Product: conglutinin-N #status predicted <MA2>
 F;248-369/Domain: C-type lectin homology <LCH>
 F;63,87,99,135,141,159,162,198,210/Binding site: carbohydrate (Lys) (covalent) #status predicted <LCH>
 F;63,87,99,135,141,159,162,198,210/Modified site: 5-hydroxylysine (Lys) #status experimental
 F;78,96,108,111,129,132,147,153,171,195/Modified site: 4-hydroxyproline (Pro) #status experimental
 F;337/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 85.0%; Score 34; DB 1; Length 371;
 Best Local Similarity 77.8%; Pred. No. 45;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 2 LLLPLSVLL 10

RESULT 6
 I45878
 conglutinin - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
 C;Accession: I45878
 R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, Gene 141, 277-281, 1994
 A;Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization of the cDNA
 A;Reference number: I45878; MUID:94215917; PMID:8163202
 A;Accession: I45878
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-371 <LIO>
 A;Cross-references: UNIPROT:P23805; UNIPARC:UPI000016C2E0; GB:L18871; NID:g495012; PIDN: I45878
 C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 F;248-369/Domain: C-type lectin homology <LCH>

Query Match 85.0%; Score 34; DB 2; Length 371;
 Best Local Similarity 77.8%; Pred. No. 45;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 2 LLLPLSVLL 10

RESULT 7
 AE0614
 probable competence-related protein STY0984 [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: This species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
 C;Accession: AE0614
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P. Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; et al.
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AE0614
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-754 <PAR>
 A;Cross-references: UNIPARC:UPI000005A06F; GB:AL513382; PIDN:CAD05383.1; PID:g16502146; C;Genetics:

A;Gene: STY0984
 C;Superfamily: competence protein ComEC

Query Match 85.0%; Score 34; DB 2; Length 754;
 Best Local Similarity 77.8%; Pred. No. 92;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 371 LLLPLQVAL 379

RESULT 8

D97163
 cation transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: D97163
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: D97163
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-845 <KUR>
 A;Cross-references: UNIPROT:Q97H76; UNIPARC:UPI00000CA412; GB:AE001437; PIDN:AAK80095.1; A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC2137

Query Match 85.0%; Score 34; DB 2; Length 845;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQILL 9
 ||||| :||
 Db 670 LLLPLQILL 677

RESULT 9

G65039
 hypothetical protein b2612 - Escherichia coli (strain K-12)
 C;Species: Escherichia coli
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 C;Accession: G65039
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Colwell, R.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: G65039
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-136 <BLAT>
 A;Cross-references: UNIPARC:UPI000016ED74; GB:AE000347; GB:U00096; NID:g2367142; PIDN:AAK80095.1; A;Experimental source: strain K-12, substrain MG1655

Query Match 82.5%; Score 33; DB 2; Length 196;
 Best Local Similarity 77.8%; Pred. No. 37;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 ||||| :||
 Db 123 LLLPLQILL 131

RESULT 10

E70890
 hypothetical protein Rv1978 - Mycobacterium tuberculosis (strain H37Rv)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

```
C:Accession: E70890
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: E70890
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-282 <COL>
A: Cross-references: UNIPROT: O53979; UNIPARC: UPI00001652BF; GB: AL123456; NID
A: Experimental source: strain H37Rv
C: Geneticks:
A: Gene: Rv1978

Query Match      82.5%; Score 33; DB 2; Length 282;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
   |||||:
Db 196 LLLPLHLL 204

RESULT 11
AB3334
daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain 1
C: Species: Brucella melitensis
C: Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C: Accession: AB3334
R: DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Muier, C.; Los, T.; Ivanova,
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
; Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A: Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A: Reference number: AD3252; PMID: 11756688
A: Accession: AB3334
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-370 <KUR>
A: Cross-references: UNIPROT: Q8YHY9; UNIPROT: Q8FZX1; UNIPARC: UPI0000057D7A; GB: AE008917;
A: Experimental source: strain 16M
C: Geneticks:
A: Gene: BMEI0656
A: Map position: I

Query Match      82.5%; Score 33; DB 2; Length 370;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQIL 8
   :|||:|
Db 293 ILLPLQVL 300

RESULT 12
C91063
hypothetical protein ECs3475 [imported] - Escherichia coli (strain O157:H7, substrain RI
C: Species: Escherichia coli
C: Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C: Accession: C91063
R: Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A: Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A: Reference number: A99629; MUID: 21156231; PMID: 11258796
A: Accession: C91063
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-398 <HAY>
A: Cross-references: UNIPROT: Q8X9C3; UNIPARC: UPI00001654C8; GB: BA000007; PIDN: BAB36998.1;
A: Experimental source: strain O157:H7, substrain RIMD 0509952
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C: Geneticks:
A: Gene: ECs3475
C: Superfamily: yfjD protein

Query Match      82.5%; Score 33; DB 2; Length 398;
Best Local Similarity 77.8%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
   |||||:
Db 101 LLAPLQILM 109

RESULT 13
AC0834
probable membrane protein corB [imported] - Salmonella enterica subsp. enterica serovar
C: Species: Salmonella enterica subsp. enterica serovar Typhi
A: Note: this species has also been called Salmonella typhi
C: Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C: Accession: AC0834
R: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A: Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A: Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A: Reference number: AB0502; MUID: 21534947; PMID: 11677608
A: Accession: AC0834
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-413 <PAR>
A: Cross-references: UNIPARC: UPI000005A2E0; GB: AL513382; PIDN: CAD05858.1; PID: g16503833;
C: Geneticks:
A: Gene: corB
C: Superfamily: hypothetical protein HI1017

Query Match      82.5%; Score 33; DB 2; Length 413;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
   |||||:
Db 116 LLAPLQILM 124

RESULT 14
CB3103
hypothetical protein PA4338 [imported] - Pseudomonas aeruginosa (strain PA01)
C: Species: Pseudomonas aeruginosa
C: Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C: Accession: CB3103
R: Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A: Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A: Reference number: AB2950; MUID: 20437337; PMID: 10984043
A: Accession: CB3103
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-426 <STO>
A: Cross-references: UNIPROT: Q9HW63; UNIPARC: UPI0000005CC9; GB: AE004850; GB: AE004091; NID:
A: Experimental source: strain PA01
C: Geneticks:
A: Gene: PA4338

Query Match      82.5%; Score 33; DB 2; Length 426;
Best Local Similarity 77.8%; Pred. No. 81;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
   |||||:
Db 301 LLLPAQLLL 309
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RESULT 15
 A90083
 hypothetical protein orf470 [imported] - Guillardia theta nucleomorph
 C:Species: nucleomorph Guillardia theta
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: A90083
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Red
 Nature 410, 1091-1096, 2001
 A:Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: A90083
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-470 <DOU>
 A:Cross-references: UNIPROT:Q9SEA5; UNIPARC:UPI0000092883; GB:AF165818; NID:g6690603; PI
 C:Genetics:
 A:Gene: orf470
 A:Map position: 1
 A:Genome: nucleomorph
 C:Keywords: nucleomorph

Query Match 82.5%; Score 33; DB 2; Length 470;
 Best Local Similarity 66.7%; Pred. No. 89;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
 Db 253 MLLPLEILI 261

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05_80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	40	100.0	66	Q6DTY1_HUMAN	Q6dtY1 homo sapien
2	40	100.0	253	1 KLK7_HUMAN	P49862 homo sapien
3	39	97.5	545	Q5N0S0_SYNP6	Q5n0s0 synchococc
4	38	95.0	73	Q8VCA9_MOUSE	Q8vca9 mus musculu
5	38	95.0	104	Q8R5D6_MOUSE	Q8r5d6 mus musculu
6	38	95.0	138	Q6PXE2_MOUSE	Q6pke2 mus musculu
7	38	95.0	201	1 FK311_MOUSE	Q9dlm7 mus musculu
8	38	95.0	246	Q585W6_9TRYP	Q585w6 trypanosoma
9	38	95.0	361	1 INHA_TRIVU	Q77755 trichosurus
10	37	92.5	208	Q21527_CLEGA	Q21527 clethrionom
11	36	90.0	146	Q9V2D5_PYRAB	Q9v2d5 pyrococcus
12	36	90.0	205	Q65323_ORYSA	Q65323 oryza sativ
13	35	87.5	181	Q6N896_RHOPA	Q6n896 rhodopeudo
14	35	87.5	1084	Q41B17_GIBZE	Q41b17 gibberella
15	35	87.5	1527	Q6PPA4_LEITA	Q6ppa4 leishmania
16	34	85.0	96	Q5XFW5_RAT	Q5xfw5 rattus norv
17	34	85.0	162	Q91T40_LSDV	Q91t40 lumpy skin
18	34	85.0	162	Q91W24_LSDV	Q91w24 lumpy skin
19	34	85.0	205	Q5V730_HALMA	Q5v730 halocaula
20	34	85.0	241	Q5V727_HALMA	Q5v727 halocaula
21	34	85.0	251	Q5N5T6_SYNP6	Q5n5t6 synchococc
22	34	85.0	277	Q9HP13_HALSA	Q9hpi3 halobacteri
23	34	85.0	369	1 SFTPD_BOVIN	P35246 bos taurus
24	34	85.0	369	2 Q863AI_BOVIN	Q863ai bos taurus
25	34	85.0	371	1 CL46_BOVIN	Q8mhz9 bos taurus
26	34	85.0	371	1 CONG_BOVIN	P23805 bos taurus
27	34	85.0	371	2 Q58CU7_BOVIN	Q58cu7 bos taurus
28	34	85.0	373	2 Q749Q7_GEOSL	Q749q7 geobacter s
29	34	85.0	754	2 Q8Z8Q2_SALTI	Q8z8q2 salmonella
30	34	85.0	754	2 Q8ZQC3_SALTY	Q8zqc3 salmonella
31	34	85.0	775	2 Q7N6C7_PHOLL	Q7n6c7 photorhabdu

32	34	85.0	845	2	Q97H76_CLOAB	Q97h76 clostridium
33	33	82.5	68	2	Q6KG65_9CAUD	Q6kg65 bacterioph
34	33	82.5	109	2	Q8BJK7_MOUSE	Q8bjk7 mus musculu
35	33	82.5	189	2	Q7M8B8_WOLSU	Q7m8b8 wolfinella s
36	33	82.5	196	2	Q9X620_SALTY	Q9x620 salmonella
37	33	82.5	196	2	Q9D226_MOUSE	Q9d226 mus musculu
38	33	82.5	282	2	Q53979_MYCTU	Q53979 mycobacteri
39	33	82.5	282	2	Q7T268_MYCBO	Q7t268 mycobacteri
40	33	82.5	294	2	Q7D7M8_MYCTU	Q7d7m8 mycobacteri
41	33	82.5	302	2	Q6GNT6_XENLA	Q6gnt6 xenopus lae
42	33	82.5	307	2	Q4NVN1_9DELT	Q4nvn1 anaeromykob
43	33	82.5	370	2	Q8FZX1_BRUSU	Q8fzx1 bruceella su
44	33	82.5	370	2	Q8YHY9_BRUME	Q8yhy9 bruceella me
45	33	82.5	374	2	Q57CF5_BRUAB	Q57cf5 bruceella ab

ALIGNMENTS

RESULT 1
Q6DTY1_HUMAN
ID Q6DTY1_HUMAN PRELIMINARY; PRT; 66 AA.
AC Q6DTY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T., Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646152; AAT66047.1; -; mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 40; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
|||
Db 5 LLLPLQILL 13

RESULT 2
KLK7_HUMAN
ID_KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (BC 3.4.21.-) (hk7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
RA Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum
RT chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

RN RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
 RC TISSUE=keratinocyte; DOI=10.1016/S0378-1119(00)00280-8;
 RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
 RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
 RA Diamandis E.P.;
 RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
 RT enzyme is a new member of the human kallikrein gene family - genomic
 RT characterization, mapping, tissue expression and hormonal
 RT regulation.";
 RL Gene 254:119-128(2000).
 RN [3]
 RN RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Paepfer B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 RN RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Hansson L., Baackman A., Ny A., Edlund M., Edholm E., Tornell J.,
 RA Wallbrandt P., Egelrud T.;
 RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
 RT mice; a model for chronic itchy dermatitis.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
 RP AND TISSUE SPECIFICITY.
 RC TISSUE=Ovarian carcinoma;
 RX MEDLINE=22623266; PubMed=12738725;
 RA Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.;
 RT "Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer
 RT produces novel variants with potential as cancer biomarkers.";
 RL Clin. Cancer Res. 9:1710-1720(2003).
 RN [6]
 RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RN RP CHARACTERIZATION.
 RX MEDLINE=95314630; PubMed=7794273;
 RA Skytt A., Stroemqvist M., Egelrud T.;
 RT "Primary substrate specificity of recombinant human stratum corneum
 RT chymotryptic enzyme.";
 RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
 CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
 CC structures in the cornified layer of the skin in the continuous
 CC shedding of cells from the skin surface. Specific for amino acid
 CC residues with aromatic side chains in the P1 position. SCCE
 CC cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-
 CC Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the
 CC activation of precursors to inflammatory cytokines.

CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
 CC also observed at the apical membrane and in cytoplasm at the
 CC invasive front.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=P49862-1; Sequences=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=P49862-2; Sequences=VSP_013581;
 CC -!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
 CC expressed by keratinocytes in the epidermis. Also expressed in the
 CC brain, mammary gland, cerebellum, spinal cord and kidney. Lower
 CC levels in salivary glands, uterus, thymus, thyroid, placenta,
 CC trachea and testis. Up-regulated in ovarian carcinoma, especially
 CC late-stage serous carcinoma, compared with normal ovaries and
 CC benign adenomas (at the protein level).
 CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
 CC cell line.
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; L33404; AAC37551.1; -; mRNA.
 DR EMBL; AF166330; AAD49718.1; -; Genomic_DNA.
 DR EMBL; AF243527; AAG33360.1; -; Genomic_DNA.
 DR EMBL; AF332583; AAK69624.1; -; Genomic_DNA.
 DR EMBL; AF411214; AAN03662.1; -; mRNA.
 DR EMBL; AF411215; AAN03663.1; -; mRNA.
 DR EMBL; BC032005; AAH32005.1; -; mRNA.
 DR PIR; A53968; A53968.
 DR HSSP; P00760; 1E2X.
 DR MEROPS; S01.300; -.
 DR Ensembl; ENSG00000169035; Homo sapiens.
 DR HGNC; HGNC:6388; KLK7.
 DR H-InvDB; HIX0015373; -.
 DR MIM; 604438; -.
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
 DR GO; GO:0008544; P:epidermis development; TAS.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1a.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;
 KW Hydroxylase; Protease; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 22
 FT PROPEP 23 29 Activation peptide.
 FT CHAIN 30 253 Kallikrein 7.
 FT DOMAIN 30 250 Peptidase S1.
 FT ACT_SITE 70 70 Charge relay system (By similarity).
 FT ACT_SITE 112 112 Charge relay system (By similarity).
 FT ACT_SITE 205 205 Charge relay system (By similarity).
 FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
 FT DISULFID 36 137 By similarity.
 FT DISULFID 55 71 By similarity.
 FT DISULFID 144 211 By similarity.
 FT DISULFID 176 190 By similarity.
 FT DISULFID 201 226 By similarity.
 FT DISULFID ? 239 By similarity.
 FT VARSPPLIC 1 72 Missing (in isoform 2).
 FT CONFLICT 226 226 /FTId=VSP_013581.
 FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A668 CRC64;

Query Match 100.0%; Score 40; DB 1; Length 253;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
 DB 5 LLLPLQLLL 13
 |||||

RESULT 3

QSNOS0 SYNTP6
 ID QSNOS0 SYNTP6 PRELIMINARY; PRT; 545 AA.
 AC QSNOS0;
 DT 01-FEB-2005 (TReMBLrel. 29, Created)
 DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
 DE 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Probable Na+/H+-exchanging protein.
 GN OrderedLocusNames=ncyl910.c;
 OS Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=269084;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCC6301;
 RA Sugita M.;
 RT "Complete genome structure of the unicellular cyanobacterium Anacystis nidulans 6301 (Synechococcus sp. PCC6301).";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP008231; BAD80100.1; -; Genomic DNA.
 DR GO; GO:0006950; P:response to stress; IEA.
 DR InterPro; IPR006153; Na_Hporter.
 DR InterPro; IPR006015; Usp.
 DR InterPro; IPR006016; UspA.
 DR Pfam; PF00999; Na_H Exchanger; 1.
 DR Pfam; PF00582; Usp_1.
 DR PRINTS; PR01438; UNRSLSSTRESS.
 KW Complete proteome.

SQ SEQUENCE 545 AA; 58143 MW; 2DB84E920CD7DEDC CRC64;
 Query Match 97.5%; Score 39; DB 2; Length 545;
 Best Local Similarity 98.9%; Pred. No. 64;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
 DB 193 LLLPLQLLL 201
 |||||

RESULT 4

Q8VCA9 MOUSE
 ID Q8VCA9 MOUSE PRELIMINARY; PRT; 73 AA.
 AC Q8VCA9;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Fkbp11 protein.
 GN Name=Fkbp11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]

NUCLEOTIDE SEQUENCE.

RP STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021345; AH21345.1; -; mRNA.
 DR MGI; MGI:1913370; Fkbp11.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 SQ SEQUENCE 73 AA; 7819 MW; 938F53399BF3C11 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 73;
 Best Local Similarity 88.9%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
 DB 6 LLLPLQLLL 14
 |||||

RESULT 5

Q8RSD6 MOUSE
 ID Q8RSD6 MOUSE PRELIMINARY; PRT; 104 AA.
 AC Q8RSD6;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Fkbp11 protein.
 GN Name=Fkbp11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]

```
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH I2;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RL EMBL; (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR SUBMIT; BC022900; AAH22900.1; -; mRNA.
DR HSSP; P18203; 1FKL.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR PROSITE; PS50059; FKBP_PPIASE; 1.
SQ SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
Db 6 LLLPLQLLL 14

RESULT 6
Q6PKE2_MOUSE PRELIMINARY; PRT; 138 AA.
AC Q6PKE2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Fkbp11 protein.
NCBI_TaxID=10090;
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kertanen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Trichman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grooman J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002311; AAH02311.1; -; mRNA.
DR MGI; MGI:1913370; Fkbp11.

DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR PROSITE; PS50059; FKBP_PPIASE; 1.
SQ SEQUENCE 138 AA; 15105 MW; C138B8B08FDDF59D CRC64;

Query Match 95.0%; Score 38; DB 2; Length 138;
Best Local Similarity 88.9%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
Db 6 LLLPLQLLL 14

RESULT 7
FKB11_MOUSE STANDARD; PRT; 201 AA.
AC Q9DIM7; O9CRE4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
DE trans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
DE (FKBP-19).
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA MGI; MGI:1913370; Fkbp11.
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carlinici P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: PPIases accelerate the folding of proteins during
CC protein synthesis.
CC -I- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -I- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC -I- SIMILARITY: Contains 1 PPIase FKBP-type domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
CC EMBL; AK003331; BAB22719.1; -; mRNA.
CC EMBL; AK019132; BAB31559.1; -; mRNA.
CC EMBL; BC037596; AAK37596.1; -; mRNA.
CC HSSP; P20071; ITCC.
CC Ensembl; ENSMUSG0000003355; Mus musculus.
CC MGI; MGI:1913370; Fkbp11.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC InterPro; IPR001179; FKBP_PPIase.
CC Pfam; PF00254; FKBP_C; 1.
CC PROSITE; PS0059; FKBP_PPIASE; 1.
CC Isomerase; Rotamase; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 201 FK506 binding protein 11.
FT DOMAIN 57 144 PPIase FKBP-type.
FT CONFLICT 53 53 S -> F (in Ref. 1; BAB31559).
FT CONFLICT 198 198 S -> R (in Ref. 1; BAB31559).
SQ SEQUENCE 201 AA; 22137 MW; 94D955C57264BD82 CRC64;

Query Match 95.0%; Score 38; DB 1; Length 201;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
DB 6 LLLPLQLLL 14
|:|||||:|

RESULT 8
Q585W6_9TRYP PRELIMINARY; PRT; 246 AA.
AC Q585W6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=Tb27.6.3680;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTa10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
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RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTa10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTa10.1;
RA Haas B., Blandin G., El-Sayed N.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009259; AAX80785.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 246 AA; 27875 MW; 706DD83BA6BB46AB CRC64;

Query Match 95.0%; Score 38; DB 2; Length 246;
Best Local Similarity 88.9%; Pred. No. 47;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
DB 163 LMLPLQLLL 171
|:|||||:|

RESULT 9
INHA_TRIVU STANDARD; PRT; 361 AA.
AC Q77755;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Inhibin alpha chain precursor.
GN Name=INHA;
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99027340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
RA Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
RA Greenwood P.J., McNatty K.;
RT "cDNA sequence analysis, gene expression and protein localisation of
RT the inhibin alpha subunit of Australian brushtail possum (Trichosurus
RT vulpecula).";
RL J. Mol. Endocrinol. 21:141-152(1998).
CC -I- FUNCTION: Inhibins and activins inhibit and activate,
CC respectively, the secretion of follitropin by the pituitary gland.
CC Inhibins/activins are involved in regulating a number of diverse
CC functions such as hypothalamic and pituitary hormone secretion,
CC gonadal hormone secretion, germ cell development and maturation,
CC erythroid differentiation, insulin secretion, nerve cell survival,
CC embryonic axial development or bone growth, depending on their
CC subunit composition. Inhibins appear to oppose the functions of
CC activins.
CC -I- SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin A
CC is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
CC beta-B.
CC -I- PTM: Proteolytic processing yields a number of bioactive forms,
CC consisting either solely of the mature alpha chain, of the most N-
CC terminal propeptide linked through a disulfide bond to the mature
CC alpha chain, or of the entire proprotein.
CC -I- SIMILARITY: Belongs to the TGF-beta family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL; AF033340; AAC63945.1; -: mRNA.
DR GO; GO:0003576; Cetraxcellular region; ISS.
DR GO; GO:0001706; F:activin inhibitor activity; ISS.
DR GO; GO:0005125; F:cytokine activity; ISS.
DR GO; GO:0008083; F:growth factor activity; ISS.
DR GO; GO:0005179; F:hormone activity; ISS.
DR GO; GO:0005515; F:hormone binding; ISS.
DR GO; GO:0007050; F:cell cycle arrest; ISS.
DR GO; GO:0030154; F:cell differentiation; ISS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0003218; P:erythrocyte differentiation; ISS.
DR GO; GO:0042541; P:hemoglobin biosynthesis; ISS.
DR GO; GO:0008917; P:induction of apoptosis; ISS.
DR GO; GO:0045578; P:negative regulation of B cell differentiation; ISS.
DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.
DR GO; GO:0046882; P:negative regulation of follicle-stimulating. .; ISS.
DR GO; GO:0045077; P:negative regulation of interferon-gamma bio. .; ISS.
DR GO; GO:0045650; P:negative regulation of macrophage different. .; ISS.
DR GO; GO:0042326; P:negative regulation of phosphorylation; ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0001541; P:ovarian follicle development; ISS.
DR GO; GO:0046881; P:positive regulation of follicle-stimulating. .; ISS.
DR InterPro; IPR002405; Inhibin_alpha.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF_beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein; Growth_Factor; Hormone; Signal.
FT SIGNAL 1 21 By similarity.
FT PROPEP 22 64 By similarity.
FT PROPEP 65 230 Inhibin alpha N-terminal region (By
FT CHAIN 231 361 Inhibin alpha chain.
FT SITE 64 65 Cleavage (By similarity).
FT SITE 230 231 Cleavage (By similarity).
FT CARBOHYD 48 48 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 266 266 N-linked (GlcNAc. .) (By similarity).
FT DISULFID 260 323 By similarity.
FT DISULFID 289 358 By similarity.
FT DISULFID 293 360 By similarity.
FT DISULFID 322 322 Interchain (By similarity).
SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDA87D CRC64;

Query Match 95.0%; Score 38; DB 1; Length 361;
Best Local Similarity 88.9%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 4 LLLPLQLL 12

RESULT 10
O21527 CLEGA PRELIMINARY; PRT; 208 AA.
AC O21527
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN Name=ND4;
OS Clethrionomys gapperi (Southern red-backed vole).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Arvicolinae; Clethrionomys.
OX NCBI_TaxID=56223;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98152303; PubMed=9491603;
RA Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
RT "Molecular systematics and paleobiogeography of the South American
RL Mol. Biol. Evol. 15:35-49 (1998).
DR EMBL; U83808; AAB87168.1; -: Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0042773; F:ATP synthesis coupled electron transport; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.
DR InterPro; IPR003918; NADH_oxred4.
DR InterPro; IPR000260; Oxidored_q5_N.
DR Pfam; PF01059; Oxidored_q5_N; 1.
DR PRINTS; PR01437; NUOXDRDTASE4.
DR KW Mitochondrion.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;

Query Match 92.5%; Score 37; DB 2; Length 208;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 98 LLLPLQILL 106

RESULT 11
Q9V2D5 PYRAB PRELIMINARY; PRT; 146 AA.
AC Q9V2D5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PYRAB01390; ORFNames=PAB0088;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=13622808;
RX DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi."
RL Mol. Microbiol. 47:1495-1512 (2003).
DR EMBL; AJ248283; CAB49063.1; -: Genomic_DNA.
DR PIR; H75201; H75201.
DR InterPro; IPR008537; DUF819.
DR Pfam; PF05684; DUF819; 1.
DR KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 146 AA; 16092 MW; 7182941371258C1F CRC64;

Query Match 90.0%; Score 36; DB 2; Length 146;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 67 LLLPLQIII 75

RESULT 12
Q65323 ORYSA PRELIMINARY; PRT; 205 AA.
AC Q65323
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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Endonuclease V protein-like.
 GN Names=OSUNB0065C04.45;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 6, BAC
 RT clone:OSJNB0065C04.45";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF004744; BAD45874.1; -; Genomic_DNA.
 DR Gramene; O65323; -;
 DR GO; GO:0004519; F:endonuclease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0000287; F:magnesium ion binding; IEA.
 DR GO; GO:0006281; P:DNA repair; IEA.
 DR InterPro; IPR007581; Endonuc V.
 DR Pfam; PF04493; Endonuclease_5; 1.
 KW Endonuclease.
 SQ SEQUENCE 205 AA; 22733 MW; 6FBFE7178FC9BEFF CRC64;
 Query Match 90.0%; Score 36; DB 2; Length 205;
 Best Local Similarity 77.8%; Pred. No. 96;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLLPLQLLL 9
 Db 176 LLLPLQLLL 184
 RESULT 13
 ID Q6NB96 RHOPA PRELIMINARY; PRT; 181 AA.
 AC Q6NB96;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RP0932;
 OS Rhodopsudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopsudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lanerding J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopsudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572595; CAE26376.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 181 AA; 19632 MW; CDB44D8210E565D1 CRC64;
 Query Match 87.5%; Score 35; DB 2; Length 181;
 Best Local Similarity 87.5%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLLPLQLLL 9
 Db 24 LLLPLQLLL 31

RESULT 14
 ID Q4IB17 GIBZE PRELIMINARY; PRT; 1064 AA.
 AC Q4IB17;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=FG05591.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearliano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramaeamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAC001000229; EAA73727.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 1064 AA; 117828 MW; 2174A5BE94DEB5F CRC64;
 Query Match 87.5%; Score 35; DB 2; Length 1064;
 Best Local Similarity 88.9%; Pred. No. 7.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LLLPLQLLL 9
 Db 862 LLLPLNILL 870
 RESULT 15
 ID Q6PPA4 LEITA PRELIMINARY; PRT; 1527 AA.
 AC Q6PPA4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE P-glycoprotein D.
 GN Name=PGPD;
 OS Leishmania tarentolae (Sauroleishmania tarentolae).
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania;
 OC Lizard Leishmania.
 OX NCBI_TaxID=5689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Leprohon P.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY589043; AAT02643.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0018887; F:ATPase activity; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_membrane_1.
 DR InterPro; IPR011440; ABC_TM_transp.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS09229; ABC_TMIF; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 SQ SEQUENCE 1527 AA; 167945 MW; E942681FFC675AAE CRC64;

Query Match 87.5%; Score 35; DB 2; Length 1527;
 Best Local Similarity 77.8%; Pred. No. 1e+03;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQLL 9
 Db 424 LFLPLQVLL 432

Search completed: March 11, 2006, 00:38:42
 Job time : 99.3333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	2	US-09-502-600-33
2	40	100.0	9	2	US-09-918-243-33
3	40	100.0	253	1	US-08-557-146-2
4	40	100.0	253	1	US-08-824-874-3
5	40	100.0	253	1	US-09-154-344-2
6	40	100.0	253	2	US-08-330-188-2
7	40	100.0	253	2	US-09-210-084-3
8	40	100.0	253	2	US-09-764-762-3
9	40	100.0	253	4	PCT-US96-04294-2
10	40	100.0	265	2	US-09-949-016-7716
11	38	95.0	812	2	US-09-489-039A-12075
12	36	90.0	9	2	US-09-502-600-35
13	36	90.0	9	2	US-09-502-600-36
14	36	90.0	9	2	US-09-918-243-35
15	36	90.0	9	2	US-09-918-243-36
16	33	82.5	190	1	US-08-339-152A-19
17	33	82.5	190	1	US-08-007-999B-6
18	33	82.5	190	1	US-08-689-276A-6
19	33	82.5	447	2	US-09-252-991A-24312
20	33	82.5	634	1	US-08-339-152A-17
21	33	82.5	653	1	US-08-339-152A-16
22	33	82.5	653	1	US-08-007-999B-3
23	33	82.5	653	1	US-08-689-276A-3
24	32	80.0	21	2	US-08-753-007A-24
25	32	80.0	21	2	US-09-398-496-24
26	32	80.0	22	2	US-08-977-378-22
27	32	80.0	102	2	US-10-104-047-2266

28 80.0 235 1 US-07-940-605A-12 Sequence 12, Appl
29 80.0 235 1 US-08-690-096-12 Sequence 12, Appl
30 80.0 295 2 US-09-270-767-39889 Sequence 33889, A
31 80.0 295 2 US-09-270-767-55106 Sequence 55106, A
32 80.0 302 2 US-09-393-634-37 Sequence 37, Appl
33 80.0 376 2 US-08-751-512-8 Sequence 8, Appl
34 80.0 436 2 US-09-489-039A-11785 Sequence 11785, A
35 80.0 492 1 US-07-794-393-4 Sequence 4, Appl
36 80.0 492 1 US-08-001-711-4 Sequence 4, Appl
37 80.0 837 2 US-09-489-039A-12646 Sequence 12646, A
38 80.0 1306 2 US-08-989-299-7 Sequence 7, Appl
39 80.0 1306 2 US-09-407-427-7 Sequence 7, Appl
40 80.0 1306 2 US-09-635-501-7 Sequence 7, Appl
41 77.5 91 2 US-09-605-703B-1574 Sequence 1574, Ap
42 77.5 129 2 US-09-513-999C-4177 Sequence 4177, Ap
43 77.5 134 2 US-09-621-976-3902 Sequence 3902, Ap
44 77.5 142 2 US-09-248-796A-21399 Sequence 21399, A
45 77.5 180 2 US-09-270-767-42872 Sequence 42872, A

ALIGNMENTS

RESULT 1
US-09-502-600-33
; Sequence 33, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US/09/502,600A
; PRIOR FILING DATE: 09/039,211
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-502-600-33

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 2
US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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;
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match      100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
DB 5 LLLPLQILL 13

RESULT 6
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLPLQILL 9
DB 5 LLLPLQILL 13
RESULT 7
US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
DB 5 LLLPLQILL 13

RESULT 8
US-09-764-762-3
Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5

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/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 317A Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/764,762
/ FILING DATE: 16-Jan-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/210,084
/ FILING DATE: <Unknown>
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: Genbank
/ CLONE: 532504
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 9
PCT-US96-04294-2
/ Sequence 2, Application PC/TUS9604294
/ GENERAL INFORMATION:
/ APPLICANT: Dixon, Eric P.
/ APPLICANT: Johnstone, Edward M.
/ APPLICANT: Little, Sheila P.
/ TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
/ TITLE OF INVENTION: RELATED NUCLEIC ACIDS
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Eli Lilly and Company
/ STREET: Lilly Corporate Center
/ CITY: Indianapolis
/ STATE: Indiana
/ COUNTRY: United States of America
/ ZIP: 46285
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US96/04294
/ FILING DATE:
/ CLASSIFICATION:
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/416,257
/ FILING DATE: 04-APR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bialock, Donna K.
/ REGISTRATION NUMBER: 38,082
/ REFERENCE/DOCKET NUMBER: X9239
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 317-277-1090
/ TELEFAX: 317-276-3861
/
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US96-04294-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 10
US-09-949-016-7716
/ Sequence 7716, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7716
/ LENGTH: 265
/ TYPE: PRT
/ ORGANISM: Human
/ US-09-949-016-7716

Query Match 100.0%; Score 40; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 17 LLLPLQILL 25

RESULT 11
US-09-489-039A-12075
/ Sequence 12075, Application US/09489039A
/ Patent No. 6610836
/ GENERAL INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A
/ CURRENT FILING DATE: 2000-01-27
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; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12075
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12075

Query Match 95.0%; Score 38; DB 2; Length 812;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 9
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DB 429 LLLPLQLLL 437

RESULT 12
US-09-502-600-35
; Sequence 35, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-502-600-35

Query Match 90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQLLL 9
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DB 1 LLLPLQLLL 8

RESULT 13
US-09-502-600-36
; Sequence 36, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-502-600-36

Query Match 90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLLPLQLLL 8
| | | | | | | |
DB 2 LLLPLQLLL 9

RESULT 14
US-09-918-243-35
; Sequence 35, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35

Query Match 90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQLLL 9
| | | | | | | |
DB 1 LLLPLQLLL 8

RESULT 15
US-09-918-243-36
; Sequence 36, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36

Query Match 90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQLLL 8
| | | | | | | |
DB 2 LLLPLQLLL 9

Search completed: March 11, 2006, 01:24:24
Job time : 21.2222 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	9	3 US-09-918-243-33	Sequence 33, Appl
2	40	100.0	9	3 US-09-905-083-33	Sequence 33, Appl
3	40	100.0	9	3 US-10-372-521-33	Sequence 33, Appl
4	40	100.0	9	5 US-10-831-075-33	Sequence 33, Appl
5	40	100.0	136	5 US-10-450-763-53737	Sequence 53737, A
6	40	100.0	198	4 US-10-262-511-96	Sequence 96, Appl
7	40	100.0	250	4 US-10-262-511-92	Sequence 92, Appl
8	40	100.0	253	3 US-09-888-615-98	Sequence 98, Appl
9	40	100.0	253	3 US-09-764-762-3	Sequence 3, Appl
10	40	100.0	253	4 US-10-071-214-2	Sequence 2, Appl
11	40	100.0	253	4 US-10-071-214-48	Sequence 48, Appl
12	40	100.0	253	4 US-10-264-283-90	Sequence 90, Appl
13	40	100.0	253	4 US-10-295-027-498	Sequence 498, App
14	40	100.0	253	4 US-10-173-999-48	Sequence 48, Appl
15	40	100.0	253	4 US-10-408-765A-639	Sequence 639, Appl
16	40	100.0	253	5 US-10-643-795A-95	Sequence 95, Appl
17	40	100.0	253	5 US-10-948-518-95	Sequence 95, Appl
18	40	100.0	253	5 US-10-868-490A-1	Sequence 1, Appl
19	40	100.0	257	4 US-10-344-394-38	Sequence 38, Appl
20	38	95.0	70	4 US-10-424-599-207950	Sequence 207950,
21	36	90.0	9	3 US-09-918-243-35	Sequence 35, Appl
22	36	90.0	9	3 US-09-918-243-36	Sequence 36, Appl
23	36	90.0	9	3 US-09-905-083-35	Sequence 35, Appl
24	36	90.0	9	3 US-09-905-083-36	Sequence 36, Appl
25	36	90.0	9	4 US-10-372-521-35	Sequence 35, Appl
26	36	90.0	9	4 US-10-372-521-36	Sequence 36, Appl
27	36	90.0	9	5 US-10-831-075-35	Sequence 35, Appl

28 36 90.0 187 5 US-10-831-075-36 Sequence 36, Appl
29 36 90.0 187 4 US-10-437-963-110905 Sequence 110905,
30 35 87.5 99 4 US-10-425-115-348070 Sequence 348070,
31 35 87.5 173 4 US-10-437-963-119305 Sequence 119305,
32 34 85.0 23 3 US-09-864-761-46097 Sequence 46097, A
33 34 85.0 61 4 US-10-425-115-218429 Sequence 218429, A
34 34 85.0 187 4 US-10-425-114-57128 Sequence 57128, A
35 34 85.0 201 3 US-09-956-622A-39 Sequence 39, Appl
36 34 85.0 229 4 US-10-425-115-227327 Sequence 227327,
37 34 85.0 369 5 US-10-820-155-60 Sequence 60, Appl
38 34 85.0 369 5 US-10-820-155-64 Sequence 64, Appl
39 34 85.0 369 5 US-10-820-155-74 Sequence 74, Appl
40 34 85.0 371 5 US-10-820-155-3 Sequence 3, Appl
41 34 85.0 371 5 US-10-820-155-4 Sequence 4, Appl
42 34 85.0 371 5 US-10-820-155-24 Sequence 24, Appl
43 34 85.0 371 5 US-10-820-155-54 Sequence 54, Appl
44 34 85.0 845 4 US-10-282-122A-51875 Sequence 51875, A
45 33 82.5 46 4 US-10-424-599-265948 Sequence 265948,

ALIGNMENTS

RESULT 1
US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match 100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 2
US-09-905-083-33
; Sequence 33, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-905-083-33

Query Match          100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 3
US-10-372-521-33
; Sequence 33, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-10-372-521-33

Query Match          100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 4
US-10-831-075-33
; Sequence 33, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-10-831-075-33

Query Match          100.0%; Score 40; DB 5; Length 9;
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 1 LLLPLQILL 9

RESULT 5
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match          100.0%; Score 40; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 11 LLLPLQILL 19

RESULT 6
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
```

```

: APPLICANT: Gorman, Linda
: APPLICANT: Zerhusen, Bryan D.
: APPLICANT: Anderson, David W.
: APPLICANT: Zhong, Mei
: APPLICANT: Catterton, Elina
: APPLICANT: Ji, Weizhen
: APPLICANT: Miller, Charles E.
: APPLICANT: Rastelli, Luca
: APPLICANT: Stone, David J.
: APPLICANT: Pena, Carol E. A.
: APPLICANT: Shenoy, Suresh G.
: APPLICANT: Shinkets, Richard A.
: APPLICANT: Rothenberg, Mark E.
: APPLICANT: Leach, Martin D.
: APPLICANT: Agee, Michele L.
: APPLICANT: Berghs, Constance
: TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: 21402-462C
: CURRENT APPLICATION NUMBER: US/10/262,511
: CURRENT FILING DATE: 2003-05-28
: PRIOR APPLICATION NUMBER: 60/326,483
: PRIOR FILING DATE: 2001-10-02
: PRIOR APPLICATION NUMBER: 60/373,815
: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: 60/327,917
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/381,642
: PRIOR FILING DATE: 2002-05-17
: PRIOR APPLICATION NUMBER: 60/328,029
: PRIOR FILING DATE: 2002-10-09
: PRIOR APPLICATION NUMBER: 60/381,038
: PRIOR FILING DATE: 2002-05-16
: PRIOR APPLICATION NUMBER: 60/328,056
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/373,260
: PRIOR FILING DATE: 2002-04-17
: PRIOR APPLICATION NUMBER: 60/373,826
: PRIOR FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: 60/327,435
: PRIOR FILING DATE: 2001-10-05
: Remaining Prior Application data removed - See File Wrapper or PALM
: NUMBER OF SEQ ID NOS: 439
: SOFTWARE: CuraSeqList version 0.1
: SEQ ID NO 92
: LENGTH: 250
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-262-511-92

Query Match 100.0%; Score 40; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LLLPLQILL 9
Db 2 LLLPLQILL 10

RESULT 8
US-09-888-615-98
: Sequence 98, Application US/09888615
: Patent No. US20020064856A1
: GENERAL INFORMATION:
: APPLICANT: FLOWMAN, GREGORY
: APPLICANT: WHYTE, DAVID
: APPLICANT: CAENEPEEL, SEAN
: APPLICANT: CHARYDCZAK, GLEN
: APPLICANT: MANNING, GERARD
: APPLICANT: SUDARSANAM, SUCHA
: TITLE OF INVENTION: NOVEL PROTEASES
: FILE REFERENCE: 038602/1214
: CURRENT APPLICATION NUMBER: US/09/888,615
: CURRENT FILING DATE: 2001-06-26

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; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
| | | | |
Db 5 LLLPLQILL 13

RESULT 9

US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
| | | | |
Db 5 LLLPLQILL 13

RESULT 10

US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart

; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 253

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
| | | | |
Db 5 LLLPLQILL 13

RESULT 11

US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart

; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48
; LENGTH: 253

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from

; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
| | | | |
Db 5 LLLPLQILL 13

RESULT 12

US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US2003014494A1

GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 13
US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 14
US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US2004000563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; FILE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 15
US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Fred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLLPLQILL 9
 |||||
Db 5 LLLPLQILL 13

Search completed: March 11, 2006, 01:37:22
Job time : 69.4444 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083a-33
Perfect score: 40
Sequence: 1 LLLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
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2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pbp.*
3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pbp.*
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5: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pbp.*
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	253	6	US-10-412-748-11
2	40	100.0	253	6	US-10-412-748-11
3	40	100.0	253	6	US-10-412-748-17
4	40	100.0	253	7	US-11-037-243-98
5	34	85.0	71	7	US-11-096-568A-27354
6	34	85.0	71	7	US-11-096-568A-27391
7	34	85.0	85	7	US-11-096-568A-27353
8	34	85.0	85	7	US-11-096-568A-27390
9	33	82.5	125	7	US-11-096-568A-23862
10	32	80.0	102	7	US-11-072-512-2266
11	32	80.0	202	7	US-11-098-686-10163
12	32	80.0	1302	6	US-10-995-561-1024
13	31	77.5	278	6	US-10-131-826A-136
14	31	77.5	278	6	US-10-973-115B-136
15	31	77.5	461	6	US-10-878-556A-162
16	31	77.5	463	6	US-10-131-826A-360
17	31	77.5	463	6	US-10-973-115B-360
18	31	77.5	463	7	US-11-154-673-9
19	31	77.5	469	6	US-10-821-234-1151
20	31	77.5	498	7	US-11-051-720-1355
21	31	77.5	505	7	US-11-051-720-1357
22	31	77.5	506	7	US-11-154-673-2
23	31	77.5	519	7	US-11-051-720-1350
24	31	77.5	541	7	US-11-051-720-1351
25	31	77.5	544	7	US-11-245-400-7

26	31	77.5	544	7	US-11-051-720-1352	Sequence 1352, Ap
27	31	77.5	550	7	US-11-154-673-8	Sequence 8, Appli
28	31	77.5	588	7	US-11-051-720-1356	Sequence 1356, Ap
29	31	77.5	593	7	US-11-154-673-3	Sequence 3, Appli
30	31	77.5	597	7	US-11-051-720-1354	Sequence 1354, Ap
31	31	77.5	619	7	US-11-051-720-1353	Sequence 1353, Ap
32	31	77.5	625	7	US-11-154-673-7	Sequence 7, Appli
33	31	77.5	650	7	US-11-051-720-1439	Sequence 1439, Ap
34	31	77.5	673	6	US-10-063-703-16	Sequence 16, Appl
35	31	77.5	673	7	US-11-102-240-16	Sequence 30, Appl
36	31	77.5	758	7	US-11-245-400-30	Sequence 26, Appl
37	31	77.5	1493	7	US-11-183-136-26	Sequence 3255, Ap
38	30	75.0	256	7	US-11-072-512-3255	Sequence 2450, Ap
39	30	75.0	311	6	US-10-793-626-2450	Sequence 5, Appli
40	30	75.0	333	7	US-11-181-234-5	Sequence 7, Appli
41	30	75.0	333	7	US-11-181-234-7	Sequence 2854, Ap
42	30	75.0	342	6	US-10-793-626-2854	Sequence 4, Appli
43	30	75.0	478	7	US-11-092-353-4	Sequence 26217, A
44	30	75.0	558	7	US-11-096-568A-26217	Sequence 881, App
45	29	72.5	146	7	US-11-000-463-881	

ALIGNMENTS

RESULT 1
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
; US-10-412-748-11

Query Match	100.0%	Score 40;	DB 6;	Length 253;
Best Local Similarity	100.0%	Pred. No. 1.6;		
Matches	9;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	LLLPLQILL 9		
DB	5	LLLPLQILL 13		
RESULT 2				
US-10-412-748-14				
; Sequence 14, Application US/10412748				
; Publication No. US20060035219A1				
; GENERAL INFORMATION:				
; APPLICANT: Queensland University of Technology				
; APPLICANT: Clements, Judith A				
; TITLE OF INVENTION: Aberrant Kallikrein Expression				
; FILE REFERENCE: DAV1172.003AUS				
; CURRENT APPLICATION NUMBER: US/10/412,748				
; CURRENT FILING DATE: 2003-04-09				
; PRIOR APPLICATION NUMBER: AU PS1616/02				
; PRIOR FILING DATE: 2002-04-09				
; NUMBER OF SEQ ID NOS: 41				
; SOFTWARE: PatentIn version 3.2				
; SEQ ID NO 14				
; LENGTH: 253				
; TYPE: PRT				

; ORGANISM: Human
US-10-412-748-14

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 3

US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A.
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 4

US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match 100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 5 LLLPLQILL 13

RESULT 5

US-11-096-568A-27354
; Sequence 27354, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27354
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 5677704
US-11-096-568A-27354

Query Match 85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 5.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 8
Db 1 LLLPLQILL 8

RESULT 6

US-11-096-568A-27391
; Sequence 27391, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27391
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391

Query Match 85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 5.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQILL 8
Db 1 LLLPLQILL 8

RESULT 7

US-11-096-568A-27353
; Sequence 27353, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.

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/ TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
/ TITLE OF INVENTION: Therby
/ FILE REFERENCE: 2750-1592PUS2
/ CURRENT APPLICATION NUMBER: US/11/096,568A
/ CURRENT FILING DATE: 2005-04-01
/ NUMBER OF SEQ ID NOS: 34471
/ SEQ ID NO 27353
/ LENGTH: 85
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(85)
/ OTHER INFORMATION: Ceres Seq. ID no. 5677703
US-11-096-568A-27353

Query Match      85.0%; Score 34; DB 7; Length 85;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQL 8
Db 15 MLLPLQL 22

RESULT 8
US-11-096-568A-27390
/ Sequence 27390, Application US/11096568A
/ Publication No. US20060048240A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexandrov, Nikolai et al.
/ TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
/ TITLE OF INVENTION: Therby
/ FILE REFERENCE: 2750-1592PUS2
/ CURRENT APPLICATION NUMBER: US/11/096,568A
/ CURRENT FILING DATE: 2005-04-01
/ NUMBER OF SEQ ID NOS: 34471
/ SEQ ID NO 27390
/ LENGTH: 85
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (1)..(85)
/ OTHER INFORMATION: Ceres Seq. ID no. 13500183
US-11-096-568A-27390

Query Match      85.0%; Score 34; DB 7; Length 85;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQL 8
Db 15 MLLPLQL 22

RESULT 9
US-11-096-568A-23862
/ Sequence 23862, Application US/11096568A
/ Publication No. US20060048240A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexandrov, Nikolai et al.
/ TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
/ TITLE OF INVENTION: Therby
/ FILE REFERENCE: 2750-1592PUS2
/ CURRENT APPLICATION NUMBER: US/11/096,568A
/ CURRENT FILING DATE: 2005-04-01
/ NUMBER OF SEQ ID NOS: 34471
/ SEQ ID NO 23862
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Zea mays subsp. mays
/ FEATURE:
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/ NAME/KEY: misc.feature
/ LOCATION: (1)..(125)
/ OTHER INFORMATION: Ceres Seq. ID no. 12415965
US-11-096-568A-23862

Query Match      82.5%; Score 33; DB 7; Length 125;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQL 9
Db 82 LLLPLQL 90

RESULT 10
US-11-072-512-2266
/ Sequence 2266, Application US/11072512
/ Publication No. US20060029945A1
/ GENERAL INFORMATION:
/ APPLICANT: ISOGAI, TAKAO
/ APPLICANT: SUGIYAMA, TOMOYASU
/ APPLICANT: OTSUKI, TETSUJI
/ APPLICANT: WAKAMATSU, AI
/ APPLICANT: SATO, HIROYUKI
/ APPLICANT: ISHII, SHIZUKO
/ APPLICANT: YAMAMOTO, JUN-ICHI
/ APPLICANT: ISONO, YUUKO
/ APPLICANT: HIO, YURI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKA, ICHIRO
/ APPLICANT: SEKI, NAOHIKO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTOYUKI
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: 084335-0191
/ CURRENT APPLICATION NUMBER: US/11/072,512
/ CURRENT FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: US 60/350,978
/ PRIOR FILING DATE: 2002-01-25
/ PRIOR APPLICATION NUMBER: JP 2001-379298
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2266
/ LENGTH: 102
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-072-512-2266

Query Match      80.0%; Score 32; DB 7; Length 102;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQL 9
Db 16 LLLPLQL 24

RESULT 11
US-11-098-686-10163
/ Sequence 10163, Application US/11098686
/ Publication No. US2006002496A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
/ TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
/ FILE REFERENCE: 09531-128001
/ CURRENT APPLICATION NUMBER: US/11/098,686
/ CURRENT FILING DATE: 2005-04-04
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; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10163
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10163
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Query Match      80.0%; Score 32; DB 7; Length 202;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 LLLPLQILL 9
Db 146 LLLPLTILI 154
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RESULT 12

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US-10-995-561-1024
; Sequence 1024, Application US/10995561
; Publication No. US20050272054A1
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; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1024
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; LENGTH: 1302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1024
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Query Match      80.0%; Score 32; DB 6; Length 1302;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 LLLPLQILL 9
Db 12 LLLPLPLL 20
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RESULT 13

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US-10-131-826A-136
; Sequence 136, Application US/10131826A
; Publication No. US20050245730A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
```

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 136
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; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-136
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Query Match      77.5%; Score 31; DB 6; Length 278;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 LLLPLQILL 9
Db 13 LLLPLLLL 21
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RESULT 14

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US-10-973-115B-136
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; Sequence 136, Application US/10973115B
; Publication No. US20060040351A1
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; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
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; TITLE OF INVENTION: SAME
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
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; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 136
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-973-115B-136
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Query Match 77.5%; Score 31; DB 6; Length 278;
Best Local Similarity 77.8%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 13 LLLPLLLL 21
```

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RESULT 15
US-10-878-556A-162
; Sequence 162, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/ncbl_human
; DATABASE ENTRY DATE: 1993-07-01
US-10-878-556A-162
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Query Match 77.5%; Score 31; DB 6; Length 461;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLLPLQILL 9
Db 11 LLLPLLLL 19
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Search completed: March 11, 2006, 01:38:40
Job time : 9 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLINERWVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	100.0	9	4	AAE08239	Aae08239 Human str
2	47	100.0	9	8	ADR68795	Adr68795 Human str
3	47	100.0	97	6	ADA05740	Ada05740 Human NOV
4	47	100.0	97	8	ADN62904	Adn62904 Human NOV
5	47	100.0	136	4	ABG23378	Abg23378 Novel hum
6	47	100.0	181	6	ADA05738	Ada05738 Human NOV
7	47	100.0	181	6	ADN62902	Adn62902 Human NOV
8	47	100.0	198	6	ADA05736	Ada05736 Human NOV
9	47	100.0	198	8	ADN62900	Adn62900 Human NOV
10	47	100.0	224	6	ADA05744	Ada05744 Human NOV
11	47	100.0	224	8	ADN62908	Adn62908 Human NOV
12	47	100.0	224	9	ADV21100	Adv21100 Human str
13	47	100.0	225	4	AAB98502	Ab98502 Human Str
14	47	100.0	247	6	ADA05742	Ada05742 Human NOV
15	47	100.0	247	8	ADN62906	Adn62906 Human NOV
16	47	100.0	250	6	ADA05732	Ada05732 Human NOV
17	47	100.0	250	8	ADN62896	Adn62896 Human NOV
18	47	100.0	252	6	ADA05734	Ada05734 Human NOV
19	47	100.0	252	8	ADN62898	Adn62898 Human NOV
20	47	100.0	253	2	AAR67888	Aar67888 Human str
21	47	100.0	253	2	AAW05383	Aaw05383 Human amy
22	47	100.0	253	5	ABB84421	Abb84421 Human SCC
23	47	100.0	253	5	ABB84406	Abb84406 Human SCC
24	47	100.0	253	5	AAU82740	Aau82740 Amino aci

25	47	100.0	253	6	ABU07440	Abu07440 Protein d
26	47	100.0	253	6	ABU07471	Abu07471 Protein d
27	47	100.0	253	6	ABR58471	AbR58471 Human str
28	47	100.0	253	7	ADB80484	AdB80484 Ovarian c
29	47	100.0	253	7	ADJ68833	Adj68833 Human hea
30	47	100.0	253	7	ADN39180	Adn39180 Cancer/an
31	47	100.0	253	8	ADL06515	Adl06515 Human tum
32	47	100.0	253	8	ADN04182	Adn04182 Antipsori
33	47	100.0	253	8	ADR72880	Adr72880 Human ova
34	47	100.0	253	9	ADY67588	Ady67588 Human kal
35	47	100.0	253	9	AEC00353	Aec00353 Human kal
36	47	100.0	257	3	AAB21326	Aab21326 Human HSC
37	43	91.5	9	4	AAE08245	Aae08245 Human str
38	43	91.5	9	4	AAE08255	Aae08255 Human str
39	43	91.5	9	8	ADR68801	Adr68801 Human str
40	43	91.5	9	8	ADR68811	Adr68811 Human str
41	40	85.1	243	5	ABB84419	Abb84419 Bovine SC
42	40	85.1	249	5	ABB84420	Abb84420 Porcine S
43	39	83.0	212	2	AAZ28590	Aay28590 Human Fac
44	39	83.0	228	7	AAE39994	Aae39994 Human adi
45	39	83.0	228	8	ADN04134	Adn04134 Antipsori

ALIGNMENTS

RESULT 1
AAE08239
ID AAE08239 standard; peptide; 9 AA.
XX AAE08239;
AC AAE08239;
XX
XX
XX 01-NOV-2001 (first entry)
XX Human stratum corneum chymotrypsin enzyme peptide #3 (residues 58-66) .
DE
DE Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisease therapy; malignant hyperplasia.
XX
XX Homo sapiens.
XX
XX
PN WO200159158-A1.
XX
XX 16-AUG-2001.
XX
XX 07-FEB-2001; 2001WO-US003977.
XX
XX 11-FEB-2000; 2000US-00502600.
XX (UYAR-) UNIV ARKANSAS.
XX O'brien TJ;
XX WPI; 2001-514676/56.
XX Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
XX Claim 25; Page 103; 127pp; English.
XX
XX The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate CC and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 1 VLVNERWVL 9

RESULT 2
ADR68795
ID ADR68795 standard; peptide; 9 AA.
AC ADR68795;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:34.
XX
XX serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
XX WO2004075723-A2.
XX
XX 10-SEP-2004.
XX
XX 20-FEB-2004; 2004WO-US005134.
PF
XX 21-FEB-2003; 2003US-00372521.
PR
XX (UYAR-) UNIV ARKANSAS.
PA
XX
XX O'Brien TJ, Cannon MJ, Santin A;
PI
XX WPI; 2004-653294/63.
DR
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX Claim 5; SEQ ID NO 34; 117pp; English.
PS
XX The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
XX Sequence 9 AA;
SQ

Query Match 100.0%; Score 47; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 1 VLVNERWVL 9

RESULT 3
ADA05740

ID ADA05740 standard; protein; 97 AA.
XX
AC ADA05740;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human NOV18e protein SEQ ID NO:100.
XX
XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; neurotropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS Homo sapiens.
XX
XX WO2003029424-A2.
PN
XX 10-APR-2003.
PD
XX 02-OCT-2002; 2002WO-US031373.
PF
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 09-OCT-2001; 2001US-032749P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381042P.
PR 28-MAY-2002; 2002US-0381642P.
PR 29-MAY-2002; 2002US-0383656P.
PR 25-JUN-2002; 2002US-0383831P.
PR 01-OCT-2002; 2002US-0391335P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Otcuturajan M, Sytek KA, Edinger SR, Ellerman K, Malvankar UM;
PI Part T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eissen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR
XX N-PSDB; ADA05739.
DR
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 171; 586pp; English.
PS
XX

CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipaeamic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 97 AA;

Query Match 100.0%; Score 47; DB 6; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
 DB 39 VLVNERWVL 47
 |||||

RESULT 4
 ADN62904
 ID ADN62904 standard; protein; 97 AA.
 AC ADN62904;
 DT 01-JUL-2004 (first entry)
 XX Human NOV18e.
 DE
 XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
 XX
 XX 26-FEB-2004.
 PD
 XX 01-OCT-2002; 2002US-00262511.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 12-OCT-2001; 2001US-0328056P.
 PR 15-OCT-2001; 2001US-0328949P.
 PR 17-OCT-2001; 2001US-0329414P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 28-MAY-2002; 2002US-0381642P.
 PR 29-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZESH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENNA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGE E M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 WPI: 2004-213931/20.
 DR N-PSDB; ADN62903.
 DR
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,

PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 100; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ

Sequence 97 AA;

Query Match 100.0%; Score 47; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|||
DB 39 VLVNERWVL 47

RESULT 5
ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;

DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #23369.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX

OS Homo sapiens.

XX WO200175067-A2.

PN 11-OCT-2001.

PD 30-MAR-2001; 2001WO-US008631.

PF 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS87565.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 53737; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 136 AA;

Query Match 100.0%; Score 47; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|||
DB 64 VLVNERWVL 72

RESULT 6
ADA05738
ID ADA05738 standard; protein; 181 AA.

XX
AC ADA05738;

XX 06-NOV-2003 (first entry)

DE Human NOV18d protein SEQ ID NO:98.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

PD 02-OCT-2002; 2002WO-US031373.

PF 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328449P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 17-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerkhusen BD, Anderson DM, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI: 2003-381626/36.
DR N-PSDB; ADA05737.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 171; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
XX Sequence 181 AA;
Query Match 100.0%; Score 47; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLVNERWVL 9
Db 39 VLVNERWVL 47
RESULT 7
ADN62902
ID ADN62902 standard; protein; 181 AA.
XX
XX AC ADN62902;
XX DT 01-JUL-2004 (first entry)
XX DE Human NOV18d.
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX OS Homo sapiens.
XX PN US2004038223-A1.
XX PD 26-FEB-2004.
XX PF 01-OCT-2002; 2002US-00262511.
XX PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 09-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 18-OCT-2001; 2001US-0330142P.
PR 22-OCT-2001; 2001US-0330309P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPVT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENN/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGRE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP1/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62901.
DR
XX
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
XX
PS Claim 1; SEQ ID NO 98; 395pp; English.
XX
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent.
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.

SQ Sequence 181 AA;

Query Match 100.0%; Score 47; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLVNERWVL 9
Db 39 VLVNERWVL 47
|||||||

RESULT 8

ADA05736
ID ADA05736 standard; protein; 198 AA.

XX
AC ADA05736;

DT 06-NOV-2003 (first entry)

XX Human NOV18c protein SEQ ID NO:96.

XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipemic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX WO2003029424-A2.

XX 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 09-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 18-OCT-2001; 2001US-0330309P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0339266P.

PR 24-OCT-2001; 2001US-0343629P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 17-APR-2002; 2002US-0373260P.

PR 19-APR-2002; 2002US-0373815P.

PR 19-APR-2002; 2002US-0373826P.

PR 19-APR-2002; 2002US-0373884P.

PR 22-APR-2002; 2002US-0374977P.

PR 16-MAY-2002; 2002US-0381037P.

PR 16-MAY-2002; 2002US-0381038P.

PR 16-MAY-2002; 2002US-0381042P.

PR 17-MAY-2002; 2002US-0381642P.

PR 28-MAY-2002; 2002US-0383656P.

PR 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.

PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.

PA

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05735.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acid can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC present invention.
XX
XX SQ Sequence 198 AA;

Query Match 100.0%; Score 47; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 58 VLVNERWVL 66
|||||||

RESULT 9
ADN62900
ID ADN62900 standard; protein; 198 AA.
XX
AC ADN62900;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18c.
XX

KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX Homo sapiens.
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374377P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381642P.
XX 29-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383931P.
XX 25-JUN-2002; 2002US-0391335P.
XX
XX (SMIT/) SMITHSON G.
XX (MILL/) MILLET I.
XX (PEYM/) PEYMAN J A.
XX (KEKU/) KEKUDA R.
XX (JUGU/) JU J.
XX (LILL/) LI L.
XX (GUOX/) GUO X.
XX (PATT/) PATTURAJAN M.
XX (SPYT/) SPYTEK K A.
XX (EDIN/) EDINGER S R.
XX (ELLE/) ELLERMAN K.
XX (MALY/) MALLYANKAR U M.
XX (ORTT/) ORT T.
XX (GORM/) GORMAN L.
XX (ZERH/) ZERHUSEN B D.
XX (ANDE/) ANDERSON D W.
XX (ZHON/) ZHONG M.
XX (CATT/) CATTERTON E.
XX (JIWW/) JI W.
XX (MILL/) MILLER C E.
XX (RAST/) RASTELLI L.
XX (STON/) STONE D J.
XX (PENA/) PENA C E A.
XX (SHEN/) SHENOY S G.
XX (SHIM/) SHIMKETS R A.
XX (ROTH/) ROTHENBERG M E.
XX (LEAC/) LEACH M D.
XX (AGEE/) AGE M L.
XX (BERG/) BERGH S C.

PA (DIPI/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2004-213931/20.
 DR N-PSDB; ADM62899.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 47; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. NO. 2.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLVNERWVL 9
 DB 58 VLVNERWVL 66
 RESULT 10
 ADA05744
 ID ADA05744 standard; protein; 224 AA.
 XX
 AC ADA05744;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18g protein SEQ ID NO:104.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;

KW antiparkinsonian; antilipaemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381039P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 (CURA-) CURAGEN CORP.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2003-381626/36.
 DR N-PSDB; ADA05743.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; Page 172; 586pp; English.
 XX
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to

CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipidemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders, such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 224 AA;

Query Match 100.0%; Score 47; DB 6; Length 224;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
 DB 44 VLVNERWVL 52
 |||||

RESULT 11
 ADN62908
 ID ADN62908 standard; protein; 224 AA.
 XX
 AC ADN62908;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV18g.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 XX US2004038223-A1.
 XX
 PD 26-FEB-2004.
 XX
 XX 01-OCT-2002; 2002US-00262511.
 XX
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.

PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 17-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJJ/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATI/) PATURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhuseen BD, Anderson DW, Pena CE, Sheno S G;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Zeng M, Sheno S G;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agge ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 WPI; 2004-213931/20.
 DR N-PSDB; ADN62907.
 DR
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO 104; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our

CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX

SQ Sequence 224 AA;
 Query Match 100.0%; Score 47; DB 8; Length 224;
 Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 VLVNERWVL 9
 Db 44 VLVNERWVL 52
 |||||

RESULT 12

ADV21100
 ID ADV21100 standard; protein; 224 AA.

AC ADV21100;

XX 24-FEB-2005 (first entry)

XX Human stratum corneum chymotrypsin protein.

DE Protein purification; PS133 protein; serine protease; prostate disease;
 KW andrology; genitourinary disease; prostatic cancer; cytostatic;
 KW protein therapy; chymotrypsin; enzyme.

XX Homo sapiens.

PH Key Location/Qualifiers

FT Domain 26..42 /note = Catalytically functional motif

FT Domain 83..87 /note = Catalytically functional motif

FT Domain 174..179 /note = Catalytically functional motif

XX US2004241646-A1.

XX 02-DEC-2004.

XX 20-FEB-2001; 2001US-00789210.

XX 06-OCT-1997; 97US-00944483.

XX (COHE/) COHEN M.

PA (COLP/) COLPITTS T L.

PA (FRIE/) FRIEDMAN P N.

PA (GRAN/) GRANADOS E.

PA (KLAS/) KLAS M R.

PA (RUSSEL/) RUSSELL J C.

PA (STEW/) STEWART K D.

PA (STRO/) STROUPE S D.
 XX Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;
 PI Russell JC, Stewart KD, Stroupe SD;
 XX WPI; 2005-011614/01.
 DR GENBANK; L33404.
 XX New isolated polypeptides, useful for detecting, diagnosing, staging,
 PT monitoring, prognosticating, preventing or treating, or determining
 PT predisposition to diseases or conditions of the prostate such as prostate
 PT cancer.
 XX Example 1; SEQ ID NO 33; 96pp; English.
 PS The invention relates to PS133 protein, a member of the human serine
 CC protease family and its corresponding nucleic acid sequence. PS133
 CC polypeptide is useful for detecting, diagnosing, staging, monitoring,
 CC prognosticating, preventing or treating or determining predisposition to
 CC diseases or conditions of the prostate such as prostatic cancer. The
 CC present sequence is the human stratum corneum chymotrypsin protein. This
 CC sequence is used to align with PS133 consensus protein.
 XX

SQ Sequence 224 AA;

Query Match 100.0%; Score 47; DB 9; Length 224;

Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

QY 1 VLVNERWVL 9

Db 29 VLVNERWVL 37

RESULT 13

AAB98502
 ID AAB98502 standard; protein; 225 AA.

XX AAB98502;

XX 03-AUG-2001 (first entry)

XX Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.

XX Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;

XX tumour antigen-derived gene 15; serine protease;

XX Stratum Corneum Chymotryptic Enzyme; SCCE.

XX Homo sapiens.

XX WO200129056-A1.

XX 26-APR-2001.

XX 20-OCT-2000; 2000WO-US029095.

XX 20-OCT-1999; 99US-00421213.

XX (UYAR-) UNIV ARKANSAS.

XX O'brien TJ, Tanimoto H;

XX WPI; 2001-381031/40.

XX Novel extracellular serine protease, termed tumor antigen-derived gene 15
 PT protein overexpressed in carcinomas and DNA encoding it, for diagnosis,
 PT treatment, prevention of cancer, particularly breast, ovarian cancer.
 XX Example 10; Fig 1; 130pp; English.

XX The present invention relates to human tumour antigen-derived gene 15
 CC (TADG-15) protein and coding sequence (see AAB98500). TADG-
 CC 15 is an extracellular serine protease. It was found that TADG-15 is over

CC -expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20
 CC residues that lack TADG-15 protease activity are useful for vaccinating
 CC an individual against TADG-15, having, suspected of having or at risk of
 CC getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic
 CC or therapeutic target in cancer. The present sequence was used in a
 CC sequence homology alignment with the catalytic domain of TADG-15
 XX
 SQ Sequence 225 AA;

Query Match 100.0%; Score 47; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
 DB 30 VLVNERWVL 38
 |||||

RESULT 14
 ADA05742
 ID ADA05742 standard; protein; 247 AA.

XX
 AC ADA05742;

DT 06-NOV-2003 (first entry)

XX
 DE Human NOV18f protein SEQ ID NO:102.

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX
 OS Homo sapiens.

XX
 PN WO2003029424-A2.

XX
 PD 10-APR-2003.

XX
 PF 02-OCT-2002; 2002WO-US031373.

XX
 PR 02-OCT-2001; 2001US-0326483P.

XX
 PR 05-OCT-2001; 2001US-0327435P.

XX
 PR 05-OCT-2001; 2001US-0327449P.

XX
 PR 09-OCT-2001; 2001US-0327917P.

XX
 PR 09-OCT-2001; 2001US-0328029P.

XX
 PR 09-OCT-2001; 2001US-0328044P.

XX
 PR 09-OCT-2001; 2001US-0328056P.

XX
 PR 12-OCT-2001; 2001US-0328849P.

XX
 PR 15-OCT-2001; 2001US-0329414P.

XX
 PR 17-OCT-2001; 2001US-0330142P.

XX
 PR 18-OCT-2001; 2001US-0330309P.

XX
 PR 22-OCT-2001; 2001US-0341058P.

XX
 PR 24-OCT-2001; 2001US-0339266P.

XX
 PR 24-OCT-2001; 2001US-0343629P.

XX
 PR 29-OCT-2001; 2001US-0349575P.

XX
 PR 01-NOV-2001; 2001US-0346357P.

XX
 PR 17-APR-2002; 2002US-0373260P.

XX
 PR 19-APR-2002; 2002US-0373815P.

XX
 PR 19-APR-2002; 2002US-0373817P.

XX
 PR 19-APR-2002; 2002US-0373826P.

XX
 PR 19-APR-2002; 2002US-0373884P.

XX
 PR 22-APR-2002; 2002US-0374977P.

XX
 PR 16-MAY-2002; 2002US-0381037P.

XX
 PR 16-MAY-2002; 2002US-0381038P.

XX
 PR 16-MAY-2002; 2002US-0381042P.

XX
 PR 17-MAY-2002; 2002US-0381642P.

XX
 PR 28-MAY-2002; 2002US-0383656P.

XX
 PR 29-MAY-2002; 2002US-0383831P.

XX
 PR 25-JUN-2002; 2002US-0391335P.

XX
 PR 01-OCT-2002; 2002US-00262511.

XX
 PA (CURA-) CURAGEN CORP.

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ott T, Gorman L, Zehusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX
 DR WPI: 2003-381626/36.

DR
 N-PSDB; ADA05741.

XX
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX
 PS Claim 1; Page 172; 586pp; English.

XX
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.

XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 47; DB 6; Length 247;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9

DB 44 VLVNERWVL 52

RESULT 15

ADN62906

ID ADN62906 standard; protein; 247 AA.

XX
 AC ADN62906;

XX
 DT 01-JUL-2004 (first entry)

XX DE Human NOV18f.
 XX KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX OS Homo sapiens.
 XX US2004038223-A1.
 XX 26-FEB-2004.
 XX 01-OCT-2002; 2002US-00262511.
 XX 02-OCT-2001; 2001US-0326483P.
 XX 05-OCT-2001; 2001US-0327435P.
 XX 09-OCT-2001; 2001US-0327449P.
 XX 09-OCT-2001; 2001US-0327917P.
 XX 09-OCT-2001; 2001US-0328029P.
 XX 09-OCT-2001; 2001US-0328044P.
 XX 09-OCT-2001; 2001US-0328056P.
 XX 12-OCT-2001; 2001US-0328849P.
 XX 15-OCT-2001; 2001US-0329414P.
 XX 17-OCT-2001; 2001US-0330142P.
 XX 18-OCT-2001; 2001US-0330309P.
 XX 22-OCT-2001; 2001US-0341058P.
 XX 24-OCT-2001; 2001US-0339266P.
 XX 24-OCT-2001; 2001US-0343629P.
 XX 29-OCT-2001; 2001US-0349575P.
 XX 01-NOV-2001; 2001US-0346357P.
 XX 17-APR-2002; 2002US-0373260P.
 XX 19-APR-2002; 2002US-0373815P.
 XX 19-APR-2002; 2002US-0373817P.
 XX 19-APR-2002; 2002US-0373826P.
 XX 22-APR-2002; 2002US-0373884P.
 XX 22-APR-2002; 2002US-0374977P.
 XX 16-MAY-2002; 2002US-0381037P.
 XX 16-MAY-2002; 2002US-0381038P.
 XX 16-MAY-2002; 2002US-0381042P.
 XX 17-MAY-2002; 2002US-0381642P.
 XX 28-MAY-2002; 2002US-0383656P.
 XX 29-MAY-2002; 2002US-0383831P.
 XX 25-JUN-2002; 2002US-0391335P.
 XX (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWV/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.

PA (LEAC/) LEACH M D.
 PA (AGEE/) AGE E M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPIPPO V A.
 PA (RISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghe C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI; 2004-213931/20.
 DR N-PSDB; ADN62905.
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX Claim 1; SEQ ID NO 102; 395pp; English.
 XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 247 AA;

Query Match 100.0%; Score 47; DB 8; Length 247;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWYL 9
 |||||
 Db 44 VLVNERWYL 52

Search completed: March 11, 2006, 00:24:13
 Job time : 86.6667 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWVL 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	253	2 A53968	serine proteinase
2	39	83.0	246	1 DBHU	complement factor
3	38	80.9	232	1 KQPG	tissue kallikrein
4	38	80.9	260	2 I56559	neuropsin - mouse
5	38	80.9	417	2 T25594	hypothetical prote
6	37	78.7	250	2 T01779	trypsin (EC 3.4.21
7	37	78.7	250	2 S31384	trypsin (EC 3.4.21
8	37	78.7	258	1 S44184	chymotrypsin (EC 3
9	37	78.7	259	1 S49129	chymotrypsin (EC 3
10	37	78.7	1421	2 T05892	hypothetical prote
11	36	76.6	72	2 F82825	hypothetical prote
12	36	76.6	258	2 A45161	serine proteinase
13	36	76.6	426	2 D42519	A20R protein - vac
14	36	76.6	426	2 T37408	probable 49.1K pro
15	36	76.6	426	2 C72166	A22R protein - var
16	36	76.6	426	2 T28563	hypothetical prote
17	36	76.6	426	2 C36850	A21R protein - var
18	36	76.6	516	2 T47075	hypothetical prote
19	35	74.5	178	2 T25570	hypothetical prote
20	35	74.5	231	2 S31778	trypsin (EC 3.4.21
21	35	74.5	242	2 S31776	trypsin (EC 3.4.21
22	35	74.5	242	2 S31775	trypsin (EC 3.4.21
23	35	74.5	242	2 S49489	trypsin (EC 3.4.21
24	35	74.5	247	1 A25852	trypsin (EC 3.4.21
25	35	74.5	257	1 JC2479	venombin B (EC 3.4
26	35	74.5	258	2 G02959	haptoglobin - rhes
27	35	74.5	258	2 I36945	haptoglobin Hp - c
28	35	74.5	258	2 I36947	haptoglobin Hpp -
29	35	74.5	274	2 I47078	coagulation factor

30	35	74.5	274	2 E70472	ribosomal protein
31	35	74.5	282	2 A83757	hypothetical prote
32	35	74.5	329	1 HPDG	haptoglobin precu
33	35	74.5	345	2 I36941	haptoglobin - chim
34	35	74.5	346	2 I36942	haptoglobin - chim
35	35	74.5	347	1 HPHU1	haptoglobin precu
36	35	74.5	347	2 G00006	haptoglobin blac
37	35	74.5	348	1 HPHUR	haptoglobin-relate
38	35	74.5	349	2 I36944	haptoglobin - chim
39	35	74.5	406	1 HPHU2	haptoglobin precu
40	35	74.5	410	2 T46034	branched-chain-ami
41	35	74.5	416	1 KFBO	coagulation factor
42	35	74.5	421	1 S11674	acrosin (EC 3.4.21
43	35	74.5	453	2 G96695	hypothetical prote
44	35	74.5	505	2 C86443	unknown protein [i
45	35	74.5	539	2 S54045	probable membrane

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hanson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym.
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:9521214; PIDN:7
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

RESULT 2

DBHU
complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
N;Alternate names: adipsin; C3 convertase activator
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40197; A00936; A60571; S66645
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;
J. Biol. Chem. 267, 9210-9213, 1992
A;Title: Human adipsin is identical to complement factor D and is expressed at high level
A;Reference number: A40197; MUID:92250520; PMID:1374388
A;Accession: A40197
A;Molecule type: mRNA
A;Residues: 1-246 <WHI>
A;Cross-references: UNIPROT:P00746; UNIPARC:UPI0000172AE4; GB:M94526
R;Niemann, M.A.; Bhow, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
A;Title: Amino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
A;Accession: A00936

A:Molecule type: protein
A:Residues: 19-44,'G',46-51,'Q',53-75,'TH',78,'P',80-83,'XXXITIE',90-172,86-91,185-235,'
A:Cross-references: UNIPARC:UPI0000172AE5
A:Note: a few residues were assigned from the previously published sequence of Reid et al
R:Miyaata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya
Mol. Immunol. 27, 637-644, 1990
A:Title: Molecular and functional identification and purification of complement component
A:Reference number: A60571; MUID:90370044; PMID:2395435
A:Accession: A60571
A:Molecule type: protein
A:Residues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>
A:Cross-references: UNIPARC:UPI0000172AE6
R:Balke, N.; Holtkamp, U.; Hoerl, W.H.; Teschesche, H.
FEBS Lett. 371, 300-302, 1995
A:Title: Inhibition of degradation of human polymorphonuclear leukocytes by complement
A:Reference number: S66645; MUID:96013156; PMID:7556615
A:Accession: S66645
A:Status: preliminary
A:Molecule type: protein
A:Residues: 19-44,'C',46-48 <BAL>
A:Cross-references: UNIPARC:UPI0000172AE7
C:Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
C:Genetics:
A:Gene: GDB:DF
A:Cross-references: GDB:132645; OMIM:134350
A:Map position: Xpter-Xqter
C:Superfamily: trypsin; trypsin homology
C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-246/Product: complement factor D (fragment) #status experimental <MAT>
F:19-241/Domain: trypsin homology <TRY>
F:44-60,141-207,172-188,197-222/disulfide bonds: #status predicted
F:59,105,201/Active site: His, Asp, Ser #status predicted

Query Match 83.0%; Score 39; DB 1; Length 246;
Best Local Similarity 88.9%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
||| :|||
DB 47 VLVNERWVL 55

RESULT 3
KQPG
tissue kallikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)
N:Alternate names: glandular kallikrein; kininogenin
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C:Accession: A00938; A92895
R:Tschesche, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, M.;
Adv. Exp. Med. Biol. 120, 245-260, 1979
A:Title: The primary structure of porcine glandular kallikreins.
A:Reference number: A90015
A:Accession: A00938
A:Molecule type: protein
A:Residues: 1-49,'GWL',53-134,'D',136-156,'H',158,'B',160-224,'B',226-232 <TSC>
A:Cross-references: UNIPARC:UPI0000172AB9
A:Note: the residue identified as 225-Aex is bound to carbohydrate; therefore, we have
R:Bode, W.; Chen, Z.; Bartels, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunik, H.
J. Mol. Biol. 164, 237-282, 1983
A:Title: Refined 2 angstrom X-ray crystal structure of porcine pancreatic kallikrein A,
t. structure and its comparison with bovine trypsin.
A:Reference number: A92895; MUID:83189107; PMID:6551452
A:Contents: X-ray crystallography, 2 angstroms
A:Accession: A92895
A:Molecule type: protein
A:Residues: 1-224,'B',226-232 <BOD>
A:Cross-references: UNIPARC:UPI0000172ABA
C:Comment: The protein consists of two chains, A and B, held together by disulfide bonds
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release I
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; pancreas; serine proteinase

F:1-224/Domain: trypsin homology <TRY>
F:1-80/Product: tissue kallikrein chain A #status experimental <MPTA>
F:79-82/Region: autolysis loop
F:91-232/Product: tissue kallikrein chain B #status experimental <MPTB>
F:7-144,26-42,121-190,155-169,180-205/disulfide bonds: #status experimental
F:41,89,184/Active site: His, Asp, Ser #status experimental
F:78/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:225/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 80.9%; Score 38; DB 1; Length 232;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
||| :|||
DB 29 VLVNERWVL 37

RESULT 4
I56559
neurospain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: I56559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishin
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease gene
A:Reference number: I56559; MUID:95348817; PMID:7623137
A:Accession: I56559
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: UNIPROT:O61955; UNIPARC:UPI0000292C5; GB:D30785; NID:G1648847; PIDN:
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Query Match 80.9%; Score 38; DB 2; Length 260;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
||| :|||
DB 61 VLVGDRWVL 69

RESULT 5
T25594
hypothetical protein C32E8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25594
R:Gattung, S.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid C32E8.
A:Reference number: Z20056
A:Accession: T25594
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-417 <GAT>
A:Cross-references: UNIPROT:P91123; UNIPARC:UPI000017B7F4; EMBL:U88308; PIDN:AAB42324.1;
A:Experimental source: strain Bristol N2; clone C32E8
C:Genetics:
A:Gene: CESP:C32E8.6
A:Map position: 1
A:Introns: 22/3; 51/2; 92/1; 297/1; 354/1

Query Match 80.9%; Score 38; DB 2; Length 417;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERW 7
||| :|||
DB 219 VLVNERW 225

```
A;Description: Cloning of blood meal induced serine protease genes of the mosquito Anopheles
A;Reference number: S35412
A;Accession: S49130
A;Molecule type: DNA
A;Residues: 1-165,'R',167-193,'FPD',197-258 <MU2>
A;Cross-references: UNIPARC:UPI000016B7D4; EMBL:Z18888; NID:G509416; PIDN:CAA79326.1; PII
C;Genetics:
A;Introns: 78/2; 209/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-32/Domain: activation peptide #status predicted <PRO>
F;33-258/Product: chymotrypsin 2 #status predicted <MAT>
F;33-250/Domain: trypsin homology <TRY>
F;59-75,182-198,208-232/Disulfide bonds: #status experimental
F;74,119,212/Active site: His, Asp, Ser #status predicted

Query Match      78.7%; Score 37; DB 1; Length 258;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
DB      63 LLNDRWVL 70

RESULT 9
S49129
chymotrypsin (EC 3.4.21.1) 1 precursor - African malaria mosquito
N;Alternate names: chymotrypsin-like proteinase ANCHYM1
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
A;Accession: S44185
R;Mueller, H.
submitted to the EMBL Data Library, November 1992
A;Description: Cloning of blood meal induced serine protease genes of the mosquito Anopheles
A;Reference number: S35412
A;Accession: S49129
A;Molecule type: mRNA
A;Residues: 1-259 <MUE>
A;Cross-references: UNIPROT:Q27289; UNIPARC:UPI0000128651; EMBL:Z18887; NID:G509414; PIDN
A;Experimental source: strain Suakoko
A;Keywords: hydrolase; protein digestion; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-32/Domain: activation peptide #status predicted <PRO>
F;33-259/Product: chymotrypsin 1 #status predicted <MAT>
F;33-250/Domain: trypsin homology <TRY>
F;59-75,182-198,208-232/Disulfide bonds: #status experimental
F;74,119,212/Active site: His, Asp, Ser #status predicted

Query Match      78.7%; Score 37; DB 1; Length 259;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
DB      63 LLNDRWVL 70

RESULT 10
T05892
chymotrypsin (EC 3.4.21.1) 2 precursor - African malaria mosquito
N;Alternate names: chymotrypsin-like proteinase ANCHYM2
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
A;Accession: S44184
R;Mueller, H.M.; Catteruccia, F.; Crisanti, A.
submitted to the EMBL Data Library, April 1994
A;Description: An Anopheles gambiae locus containing the sequences of two closely related
A;Reference number: S44184
A;Accession: S44184
A;Molecule type: DNA
A;Residues: 1-258 <MUE>
A;Cross-references: UNIPROT:Q17025; UNIPARC:UPI0000128657; EMBL:Z32645; NID:G474026; PIDN
R;Mueller, H.
submitted to the EMBL Data Library, November 1992
```


Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|:|:
Db 130 VLLNNEWIM 138

RESULT 15

C72166
A22R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C>Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C:Accession: C72166
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: C72166
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <SHC>
A:Cross-references: UNIPROT:Q89166; UNIPARC:UPI0000061D50; GB:Y16780; NID:G5830555; PIDN
A:Experimental source: strain Garcia-1966
C:Genetics:
A:Gene: A22R
C:Superfamily: vaccinia virus probable 49.IX protein

Query Match 76.6%; Score 36; DB 2; Length 426;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|:|:
Db 130 VLLNNEWIM 138

Search completed: March 11, 2006, 00:40:49
Job time : 15.1111 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	47	100.0	253	1	KLK7_HUMAN	P49862 homo sapien
2	40	85.1	455	2	Q9FFR7_ARATH	Q9ffr7 arabidopsis
3	39	83.0	100	2	Q9MYV8_BOVIN	Q9myv8 bos taurus
4	39	83.0	235	2	Q4K9V0_PSEF5	Q4k9v0 pseudomonas
5	39	83.0	249	2	Q8JFQ7_GADMO	Q8jf07 gadus morhu
6	39	83.0	254	2	Q5M8G2_XENTR	Q5m8g2 xenopus tro
7	39	83.0	690	2	Q5F3N3_CHICK	Q5f3n3 gallus gall
8	38	80.9	223	2	Q9XY58_CTEFE	Q9xy58 ctencoccephal
9	38	80.9	234	2	Q7SZE2_AKCA	Q7sze2 agkistrodon
10	38	80.9	235	2	Q66PG8_FUGRU	Q66pg8 fugu rubrip
11	38	80.9	246	1	KLK_PIG	P00752 sus scrofa
12	38	80.9	252	2	Q5M508_XENTR	Q5m508 xenopus tro
13	38	80.9	260	1	NRPN_MOUSE	Q61955 mus musculus
14	38	80.9	260	1	NRPN_RAT	Q88780 rattus norv
15	38	80.9	262	2	Q7ZOG5_9DIPT	Q7z0g5 phlebotomus
16	38	80.9	313	2	Q8T3B8_CABEL	Q8t3b8 caenorhabdi
17	38	80.9	377	2	Q9SNY9_SOLTU	Q9sn99 solanum tub
18	38	80.9	418	2	Q9SNY9_SOLTU	Q9sn99 solanum tub
19	38	80.9	461	2	P91123_CABEL	P91123 caenorhabdi
20	38	80.9	791	2	Q7NUH8_CHRVO	Q7nuh8 chromobacte
21	37	78.7	60	2	Q4RC62_TETNG	Q4rc62 tetraodon n
22	37	78.7	184	2	Q67PW1_SYMYH	Q67pw1 symbiobacte
23	37	78.7	229	2	Q5QX46_IDILO	Q5qx46 idiomarina
24	37	78.7	233	2	Q9PT51_AKCHA	Q9pt51 agkistrodon
25	37	78.7	234	2	Q8UUJ1_AKCA	Q8uu1 agkistrodon
26	37	78.7	243	2	Q9VEM7_DROME	Q9vem7 drosophila
27	37	78.7	249	2	Q9W6K0_9PERC	Q9w6k0 notothenia
28	37	78.7	249	2	Q92046_DISMA	Q92046 disostichu
29	37	78.7	249	2	Q788V0_DISMA	Q788v0 disostichu
30	37	78.7	250	1	TRYF_PLEPL	P35034 pleuronecte
31	37	78.7	250	2	Q93265_PSEAM	Q93265 pseudopleur

32	37	78.7	254	2	Q97098_ANOQA	Q97098 anopheles a
33	37	78.7	255	2	Q97100_ANODA	Q97100 anopheles d
34	37	78.7	257	1	VSP4_TRIMU	Q91510 trimeresu
35	37	78.7	257	1	VSP5_TRIMU	Q91511 trimeresu
36	37	78.7	257	1	VSP7_TRIMU	Q9dg94 trimeresu
37	37	78.7	257	1	VSPC_TRIGA	Q13062 trimeresu
38	37	78.7	257	2	Q9PT13_AKCHB	Q9pt13 agkistrodon
39	37	78.7	257	2	Q9YGJ9_AGRHP	Q9ygj9 agkistrodon
40	37	78.7	257	2	Q71QJ0_TRIST	Q71qj0 trimeresu
41	37	78.7	257	2	Q71QI7_TRIST	Q71qi7 trimeresu
42	37	78.7	257	2	Q71QI5_TRIST	Q71qi5 trimeresu
43	37	78.7	258	1	CTR2_ANOQA	Q17025 anopheles g
44	37	78.7	258	2	Q9XY53_CTEFE	Q9xy53 ctencoccephal
45	37	78.7	258	2	Q7SZE1_9SAUR	Q7szel gloydius sa

ALIGNMENTS

RESULT 1
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
RA Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum
RT chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

[2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC TISSUE=Keratinocyte;
RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
RA Diamandis E.P.;
RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
RT enzyme is a new member of the human kallikrein gene family - genomic
RT characterization, mapping, tissue expression and hormonal
RT regulation.";
RL Gene 254:119-128(2000).
RN [3]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepfer B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
RA Wallbrandt P., Egelrud T.;
RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
RT mice; a model for chronic itchy dermatitis.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
RP AND TISSUE SPECIFICITY.
RC TISSUE=Ovarian carcinoma;


```

RL DNA Res. 4:215-230(1997).
DR EMBL; AB005233; BAB1469.1; -; Genomic_DNA.
DR GO; GO:0006512; Pubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
SQ SEQUENCE 455 AA; 52305 MW; 763F5D5278D22F13 CRC64;

Query Match      85.1%; Score 40; DB 2; Length 455;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
Db      104 IINERWVL 111
      :|||||

RESULT 3
Q9MYV8_BOVIN PRELIMINARY;      PRT; 100 AA.
AC Q9MYV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Haptoglobin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oviduct;
RA Lavery K.S., Gabler C., Killian G.J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271156; CAC00531.1; -; mRNA.
DR HSP; P00751; 1DLR.
DR MEROPS; S01.972; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00889; Trypsin; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
FT NON_TER 1
FT NON_TER 100
FT NON_TER 100
SQ SEQUENCE 100 AA; 11239 MW; FFF6AE5AB43CED9 CRC64;

Query Match      83.0%; Score 39; DB 2; Length 100;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
Db      22 LINERWLL 29
      |:|||||:|

RESULT 4
Q4K9V0_PSEFS PRELIMINARY;      PRT; 235 AA.
AC Q4K9V0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Arginine-tRNA-protein transferase-related protein.
GN ORFNames=PF13883;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]_TaxID=220664;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;

RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY93147.1; -; Genomic_DNA.
KW Transferase.
SQ SEQUENCE 235 AA; 27624 MW; 75C5203A8254CCAF CRC64;

Query Match      83.0%; Score 39; DB 2; Length 235;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      225 LLVNQRWVI 233
      :|||||:

RESULT 5
Q8JFQ7_GADMO PRELIMINARY;      PRT; 249 AA.
AC Q8JFQ7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Trypsinogen Y precursor (Fragment).
GN Name=tryp1 gene;
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]_TaxID=8049;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pyloric caecum;
RA Gudmundsdottir A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ459311; CAD30563.1; -; mRNA.
DR HSP; P00746; 1FDP.
DR MEROPS; S01.124; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00889; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW SIGNAL.
FT SIGNAL 1 15 Potential.
FT CHAIN 23 >249 trypsinogen Y.
FT NON_TER 249
FT NON_TER 249
SQ SEQUENCE 249 AA; 27400 MW; 8FB98462CEDBEFC9 CRC64;

Query Match      83.0%; Score 39; DB 2; Length 249;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLVNERWVL 9
Db 50 VLVNDQWVL 58

RESULT 6
Q5M8G2_XENTR PRELIMINARY; PRT; 254 AA.
AC Q5M8G2;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE LOC496767 protein (Fragment).
GN Name=LOC496767;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]_TaxID=8364;
RP NUCLEOTIDE SEQUENCE.
RC TISSU=Whole body;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSU=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC088038; AAH88038.1; -; mRNA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001314; Peptidase_S1.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS050923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein.
SQ SEQUENCE 254 AA; 27526 MW; 642AFC41A467C38 CRC64;

Query Match 83.0%; Score 39; DB 2; Length 254;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
Db 53 LVNDQWVL 60

RESULT 7
Q5F3N3_CHICK PRELIMINARY; PRT; 690 AA.
AC Q5F3N3;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.11h6;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSU=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851617; CAH65251.1; -; mRNA.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB_Ca.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sush1; 2.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS050923; SUSHI; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein.
SQ SEQUENCE 690 AA; 77326 MW; E85A9C65A1D97E7B CRC64;

Query Match 83.0%; Score 39; DB 2; Length 690;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 465 VLVSRWVM 473

RESULT 8
Q9XY58_CTEFE PRELIMINARY; PRT; 223 AA.
AC Q9XY58;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Chymotrypsin-like serine protease (Fragment).
GN Name=SP-4;
OS Ctenocephalides felis (Cat flea).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Siphonaptera; Pulicidae; Pulicinae;
OC Ctenocephalides.
OX NCBI_TaxID=7515;
RN [1]
```

RP NUCLEOTIDE SEQUENCE.
 RA Gaines P.J., Sampson C.M., Rushlow K.E., Stiegler G.L.;
 RT "Cloning of a family of serine protease genes from the cat flea
 RL Ctenocephalides felis.";
 DR EMBL; AF053916; AAD21836.1; -, mRNA.
 DR HSSP; P00761; IEP.
 DR MEROPS; S01.166; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1_S6.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Protease.
 FT NON TER 1 1
 SQ SEQUENCE 223 AA; 24844 MW; C34BBE9455DD7DE9 CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 223;
 Best Local Similarity 75.0%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LVNERWVL 9
 DB 35 ILNERWVL 42
 RESULT 9
 QTSZ2 AGKCA
 ID QTSZ2 AGKCA PRELIMINARY; PRT; 234 AA.
 AC QTSZ2;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Thrombin-like enzyme defibrase (Fragment).
 OS Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=35671;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Snake venom gland;
 RA Sun D.-J., Yang T.-S.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY204242; AAP20637.1; -, mRNA.
 DR HSSP; Q91516; IBQY.
 DR SMR; Q7SZE2; 1-234.
 DR MEROPS; S01.347; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 FT NON TER 1 1
 SQ SEQUENCE 234 AA; 25351 MW; 0124C1485525F560 CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 234;

Best Local Similarity 87.5%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LVNERWVL 9
 DB 30 LVNEEWVL 37
 RESULT 10
 Q66PG8 FUGRU
 ID Q66PG8 FUGRU PRELIMINARY; PRT; 235 AA.
 AC Q66PG8;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Trypsinogen (Fragment).
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontoidea; Tetraodontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Roach J.C.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY661446; AAU06121.1; -, Genomic DNA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 FT NON TER 1 1
 SQ SEQUENCE 235 AA; 26025 MW; 489D3617C943CC5A CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 235;
 Best Local Similarity 66.7%; Pred. No. 72;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLNERWVL 9
 DB 36 VLINKQWVL 44
 RESULT 11
 KLK_PIG
 ID KLK_PIG STANDARD; PRT; 246 AA.
 AC P00752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Glandular kallikrein precursor (EC 3.4.21.35) (Tissue kallikrein).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP PROTEIN SEQUENCE OF 1-15 AND 95-102.
 RA MEDLINE=89230643; PubMed=3246048;
 RX Kamada M., Aoki K., Ikekita M., Kizuki K., Moriya H., Kamo M.,
 RA Tsugita A.;
 RT "Generation of alpha- and beta-kallikreins from porcine pancreatic
 RT prokallikrein by the action of trypsin."
 RL Chem. Pharm. Bull. 36:4891-4899 (1988).
 RN [2]

RP PROTEIN SEQUENCE OF 8-87 AND 95-246.
RC TISSUE=Pancreas;
RA Tschesche H., Mair G., Godes G., Fiedler P., Ehret W., Hirschauer C.,
RA Lemon M., Fritz H., Schmidt-Kastner G., Kutzbach C.;
RT "Primary structure of porcine glandular kallikreins.";
RL Adv. Exp. Med. Biol. 120:245-260(1979).
RN [3]
RP PROTEIN SEQUENCE OF 8-87; 95-127 AND 176-246.
RC TISSUE=Pancreas;
RA Ehret W.;
RT "The primary structure of the kallikrein from porcine pancreas.";
RL Thesis (1976), University of Munich, Germany.
RN [4]
RP PROTEIN SEQUENCE OF 84-98.
RX MEDLINE=90336040; PubMed=2379280;
RA kamada M., Ikeita M., Kurahashi T., Aoki K., Kizuki K., Moriya H.,
RA Sweeley C.C., Kamo M., Taugita A.;
RT "Generation of a different type of beta-kallikrein from porcine
RT pancreatic alpha-kallikrein by the action of chymotrypsin --
RT observation of proteolytic processing occurring around 'kallikrein
RT autolysis loop' region.";
RL Chem. Pharm. Bull. 38:1053-1057(1990).
RN [5]
RP PROTEIN SEQUENCE OF 128-175.
RC TISSUE=Pancreas;
RA Ehret W.;
RT "Investigation of the sequence of amino acid residues 127 to 174 of
RT the kallikrein from porcine pancreas.";
RL Thesis (1978), University of Munich, Germany.
RN [6]
RP REVIEW.
RX MEDLINE=82194877; PubMed=7043199;
RA Fiedler P., Fink E., Tschesche H., Fritz H.;
RA "Porcine glandular kallikreins.";
RL Meth. Enzymol. 80:493-533(1981).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS), AND SEQUENCE REVISION.
RX MEDLINE=83189107; PubMed=6581452;
RA Bode W., Chen Z., Bartels K., Kutzbach C., Schmidt-Kastner G.,
RA Bartunik H.;
RT "Refined 2-A X-ray crystal structure of porcine pancreatic kallikrein
RT A, a specific trypsin-like serine proteinase. Crystallization,
RT structure determination, crystallographic refinement, structure and
RT its comparison with bovine trypsin.";
RL J. Mol. Biol. 164:237-282(1983).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH BOVINE
RP PANCREATIC TRYPSIN INHIBITOR.
RX MEDLINE=83189108; PubMed=6188842;
RA Chen Z., Bode W.;
RT "Refined 2.5 A X-ray crystal structure of the complex formed by
RT porcine kallikrein A and the bovine pancreatic trypsin inhibitor.
RT Crystallization, Patterson search, structure determination,
RT refinement, structure and comparison with its components and with the
RT bovine trypsin-pancreatic trypsin inhibitor complex.";
RL J. Mol. Biol. 164:283-311(1983).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH HIRUSTASIN.
RX MEDLINE=97184690; PubMed=9032072; DOI=10.1016/S0969-2126(97)00183-4;
RA Mittl P.R.E., di Marco S., Fendrich G., Pohlig G., Heim J.,
RA Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.;
RT "A new structural class of serine protease inhibitors revealed by the
RT structure of the hirustasin-kallikrein complex.";
RL Structure 5:253-264(1997).
RN [10]
RP ERRATUM.
RA Mittl P.R.E., di Marco S., Fendrich G., Pohlig G., Heim J.,
RA Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.;
RL Structure 5:585-585(1997).
RN [11]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=89062455; PubMed=3196708;
RA Tomiya N., Yamaguchi T., Awaya J., Kurono M., Endo S., Arata Y.,

RA Takahashi N., Ishihara H., Mori M., Tejima S.;
RT "Structural analyses of asparagine-linked oligosaccharides of porcine
RT pancreatic kallikrein.";
RL Biochemistry 27:7146-7154(1988).
CC -!- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in
CC in kininogen to release Lys-bradykinin.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
CC Met-|-Xaa or Ieu-|-Xaa.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC -!- CAUTION: Native porcine kallikrein is a monomer. Chains of the
CC pancreatic beta-kallikrein are heterogeneous artifacts of
CC proteolytic degradation during isolation.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PDB; 1HIA; X-ray; A/X=8-87, B/Y=95-246.
CC PDB; 2KAI; X-ray; A=8-87, B=95-246.
CC PDB; 2PKA; X-ray; A/X=8-87, B/Y=95-246.
CC SMR; P00752; 8-245.
CC MEROPS; S01.160; -.
CC InterPro; IPR001254; Peptidase_S1_S6.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
CC Pancreas; Protease; Serine protease; Zymogen.
CC PROPEP 1 7
FT CHAIN 8 246 Glandular kallikrein.
FT DOMAIN 8 243 Peptidase S1.
FT REGION 85 104 Kallikrein (autolysis) loop.
FT ACT_SITE 48 48 Charge relay system.
FT ACT_SITE 103 103 Charge relay system.
FT ACT_SITE 198 198 Charge relay system.
FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
FT DISULFID 239 239 N-linked (GlcNAc...) (Potential).
FT DISULFID 14 158
FT DISULFID 33 49
FT DISULFID 135 204
FT DISULFID 169 183
FT DISULFID 194 219
FT STRAND 9 9
FT STRAND 12 13
FT TURN 16 17
FT TURN 20 21
FT TURN 22 27
FT STRAND 28 29
FT TURN 28 27
FT STRAND 30 39
FT TURN 40 41
FT STRAND 42 45
FT HELIX 47 49
FT STRAND 55 58
FT STRAND 62 62
FT TURN 63 64
FT TURN 71 80
FT STRAND 82 86
FT TURN 101 102
FT STRAND 105 109
FT STRAND 116 116
FT TURN 117 118
FT STRAND 119 119

FT TURN 131 132
 FT STRAND 134 139
 FT STRAND 155 155
 FT STRAND 157 164
 FT TURN 166 166
 FT HELIX 167 170
 FT TURN 171 172
 FT TURN 179 180
 FT STRAND 181 185
 FT TURN 187 188
 FT STRAND 192 192
 FT TURN 195 196
 FT TURN 198 199
 FT STRAND 201 204
 FT TURN 205 206
 FT STRAND 207 214
 FT TURN 219 220
 FT TURN 222 223
 FT STRAND 226 230
 FT HELIX 231 234
 FT HELIX 235 244
 SQ SEQUENCE 246 AA; 27172 MW; 5991CEDE406A19A1 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 246;

Best Local Similarity 77.8%; Pred. No. 76; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
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 DB 36 VLVNPKWVL 44

RESULT 12

Q5M908 XENTR Q5M908 XENTR PRELIMINARY; PRT; 252 AA.
 AC Q5M908; 29, Created
 DT 01-FEB-2005 (TREMELREL. 29, Last sequence update)
 DT 01-FEB-2005 (TREMELREL. 29, Last annotation update)
 DE LOC496635 protein (Fragment).
 GN Name=LOC496635;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Silurana.
 OX NCBI_TaxID=8364;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzywicki M.I., Skalska U., Smallos D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;

RA Klein S., Gerhard D.S.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC087753; AAH87753.1; -, mRNA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0030195; P:negative regulation of blood coagulation; IEA.
 DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 FT NON TER 1
 SQ SEQUENCE 252 AA; 27288 MW; DD68633914557564 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 252;

Best Local Similarity 77.8%; Pred. No. 78; Mismatches 7; Conservative 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
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 DB 48 VLVNEWWVL 56

RESULT 13

NRPN_MOUSE NRPN_MOUSE STANDARD; PRT; 260 AA.
 AC Q61955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Neuropeptide precursor (EC 3.4.21.-) (NP (kallikrein 8)).
 GN Name=Klk8; Synonyms=Nrpn, Press19;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c; TISSUE=Hippocampus;
 RX MEDLINE=95348817; PubMed=7623137;
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
 RA Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
 RT "Expression and activity-dependent changes of a novel limbic-serine
 protease gene in the hippocampus.";
 RL J. Neurosci. 15:5088-5097(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
 RT "Cloning and assignment of mouse neuropeptide gene, Press19 to chromosome
 7B4.";
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=Czech II; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan M., Rodriguez S., Sanchez A.,

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fischer; TISSUE=Brain;
RX MEDLINE=98399725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;
RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Latche R.;
RT "Serine proteases in rodent hippocampus";
RL J. Biol. Chem. 273:23004-23011(1998).
CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin (By similarity).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Restricted to hippocampus.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AJ005641; CAA06643.1; -; mRNA.
DR HSSP: Q61955; INPM.
DR SMR: O88780; 33-256.
DR MEROPS: S01.244; -.
DR Ensembl: ENSRNOG0000018580; Rattus norvegicus.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Protease; Serine protease; Signal; Zymogen.
FT SIGNAL 1 28 Potential.
FT PROPEP 29 32 By similarity.
FT CHAIN 33 260 Neuropsin.
FT DOMAIN 33 257 Peptidase S1.
FT ACT_SITE 73 73 Charge relay system (By similarity).
FT ACT_SITE 120 120 Charge relay system (By similarity).
FT ACT_SITE 212 212 Charge relay system (By similarity).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
FT DISULFID 39 173 By similarity.
FT DISULFID 58 74 By similarity.
FT DISULFID 145 246 By similarity.
FT DISULFID 152 218 By similarity.
FT DISULFID 184 198 By similarity.
FT DISULFID 208 233 By similarity.
SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 260;
Best Local Similarity 77.8%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
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DB 61 VLVGDRWVL 69

RESULT 15
Q720G5_9D1PT
ID Q720G5_9D1PT PRELIMINARY; PRT; 262 AA.
AC Q720G5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chymotrypsin.

GN Name=chym1;
OS Phlebotomus papatasi.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
OC Psychodidae; Phlebotomus; Phlebotomus.
OX NCBI_TaxID=29031;
RN [1]_TaxID=29031;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Midgut;
RA Ramalho-Ortigao M., Kamhawi S., Rowton E., Sacks D.L., Ribeiro J.M.,
RA Valenzuela J.G.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY128106; AAM96938.1; -; mRNA.
DR HSSP: PI8291; IF18.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:trypsin activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS02040; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 262 AA; 28863 MW; 31F11012206A65D4 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 262;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
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DB 57 ILNERWVL 64

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Job time : 98.3333 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	2 US-09-502-600-34	Sequence 34, Appl
2	47	100.0	9	2 US-09-918-243-34	Sequence 34, Appl
3	47	100.0	154	2 US-09-261-416-7	Sequence 7, Appl
4	47	100.0	224	2 US-08-944-483-33	Sequence 33, Appl
5	47	100.0	225	1 US-08-557-146-12	Sequence 12, Appl
6	47	100.0	225	1 US-09-027-337-4	Sequence 4, Appl
7	47	100.0	225	1 US-09-154-344-12	Sequence 12, Appl
8	47	100.0	225	2 US-09-644-600-4	Sequence 4, Appl
9	47	100.0	225	2 US-09-654-600A-4	Sequence 4, Appl
10	47	100.0	253	1 US-08-557-146-2	Sequence 2, Appl
11	47	100.0	253	1 US-08-824-874-3	Sequence 3, Appl
12	47	100.0	253	1 US-09-154-344-2	Sequence 2, Appl
13	47	100.0	253	2 US-08-930-188-2	Sequence 2, Appl
14	47	100.0	253	2 US-09-210-084-3	Sequence 3, Appl
15	47	100.0	253	2 US-09-764-762-3	Sequence 3, Appl
16	47	100.0	253	4 PCT-US96-04294-2	Sequence 2, Appl
17	47	100.0	265	2 US-09-949-016-7716	Sequence 7716, Ap
18	43	91.5	9	2 US-09-502-600-40	Sequence 40, Appl
19	43	91.5	9	2 US-09-502-600-50	Sequence 50, Appl
20	43	91.5	9	2 US-09-918-243-40	Sequence 40, Appl
21	43	91.5	9	2 US-09-918-243-50	Sequence 50, Appl
22	39	83.0	228	2 US-08-944-483-44	Sequence 44, Appl
23	39	83.0	228	2 US-10-202-676-6	Sequence 6, Appl
24	39	83.0	253	6 5223425-8	Patent No. 5223425
25	38	80.9	64	1 US-08-485-455D-75	Sequence 75, Appl
26	38	80.9	64	1 US-08-482-130C-75	Sequence 75, Appl
27	38	80.9	64	1 US-08-484-211C-75	Sequence 75, Appl

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28 38 80.9 64 2 US-08-906-769-75 Sequence 75, Appl
29 38 80.9 64 2 US-08-906-616-75 Sequence 75, Appl
30 38 80.9 64 2 US-08-817-795-75 Sequence 75, Appl
31 38 80.9 64 2 US-08-485-443B-75 Sequence 75, Appl
32 38 80.9 64 2 US-08-639-075A-75 Sequence 75, Appl
33 38 80.9 64 2 US-09-012-431-75 Sequence 75, Appl
34 38 80.9 64 2 US-09-012-692-75 Sequence 75, Appl
35 38 80.9 64 2 US-08-906-613-75 Sequence 75, Appl
36 38 80.9 64 4 PCT-US95-14442A-75 Sequence 75, Appl
37 38 80.9 223 1 US-08-485-455D-17 Sequence 17, Appl
38 38 80.9 223 1 US-08-482-130C-17 Sequence 17, Appl
39 38 80.9 223 1 US-08-484-211C-17 Sequence 17, Appl
40 38 80.9 223 2 US-08-817-795-17 Sequence 17, Appl
41 38 80.9 223 2 US-08-485-443B-17 Sequence 17, Appl
42 38 80.9 223 4 PCT-US95-14442A-17 Sequence 17, Appl
43 38 80.9 224 2 US-08-906-769-17 Sequence 17, Appl
44 38 80.9 224 2 US-08-906-616-17 Sequence 17, Appl
45 38 80.9 224 2 US-08-639-075A-17 Sequence 17, Appl

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ALIGNMENTS

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RESULT 1
US-09-502-600-34
; Sequence 34, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-502-600-34

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Query Match 100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLVNERWVL 9
   |||||
DB 1 VLVNERWVL 9

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RESULT 2
US-09-918-243-34
; Sequence 34, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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/
/
/ NAME/KEY: CHAIN
/
/ OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-918-243-34

Query Match      100.0%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 3
US-09-261-416-7
/ Sequence 7, Application US/09261416A
/ Patent No. 6291663
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Timothy J.
/ APPLICANT: Underwood, Lowell J.
/ TITLE OF INVENTION: TAGD-12: A No. 6291663el Transmembrane Serine Protease
/ FILE REFERENCE: D6192
/ CURRENT APPLICATION NUMBER: US/09/261,416A
/ CURRENT FILING DATE: 1999-03-03
/ NUMBER OF SEQ ID NOS: 14
/ SEQ ID NO 7
/ LENGTH: 154
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
/ OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar
/ OTHER INFORMATION: domain in TAGD-12
US-09-261-416-7

Query Match      100.0%; Score 47; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 4 VLVNERWVL 12

RESULT 4
US-09-944-483-33
/ Sequence 33, Application US/08944483
/ Patent No. 6232456
/ GENERAL INFORMATION:
/ APPLICANT: COHEN, MAURICE
/ APPLICANT: COLPITTS, TRACEY L.
/ APPLICANT: FRIEDMAN, PAULA N.
/ APPLICANT: GRANADOS, EDWARD N.
/ APPLICANT: KLASS, MICHAEL R.
/ APPLICANT: RUSSELL, JOHN C.
/ APPLICANT: STEWART, KENT D.
/ APPLICANT: STROUPE, STEVEN D.
/ TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
/ TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
/ TITLE OF INVENTION: OF THE PROSTATE
/ NUMBER OF SEQUENCES: 76
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Abbott Laboratories
/ STREET: 100 Abbott Park Road
/ CITY: Abbott Park
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible

/
/
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/944,483
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Becker, Cheryl L.
/ REGISTRATION NUMBER: 35,441
/ REFERENCE/DOCKET NUMBER: 6183.US.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 847/935-1729
/ TELEFAX: 847/938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 33:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 224 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match      100.0%; Score 47; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 29 VLVNERWVL 37

RESULT 5
US-08-557-146-12
/ Sequence 12, Application US/08557146
/ Patent No. 5834290
/ GENERAL INFORMATION:
/ APPLICANT: Egelrud, Torbjorn
/ APPLICANT: Hansson, Lennart
/ TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
/ TITLE OF INVENTION: Enzyme (SCCE)
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: White & Case, Patent Department
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2787
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/557,146
/ FILING DATE: 14-DEC-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sterner, Richard J.
/ REGISTRATION NUMBER: 35,372
/ REFERENCE/DOCKET NUMBER: 1103326-181
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 819-8783
/ TELEFAX: (212) 354-8113
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 amino acids
/ TYPE: amino acids
/ STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match      100.0%; Score 47; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 6
US-09-027-337-4
; Sequence 4, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
; OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Query Match      100.0%; Score 47; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 7
US-09-154-344-12
; Sequence 12, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
```

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-09-154-344-12

Query Match      100.0%; Score 47; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 8
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-644-600-4

Query Match      100.0%; Score 47; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 9
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
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; 09/027.337
; PRIOR FILING DATE: 1999-10-20
; 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4

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Query Match          100.0%; Score 47; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VLVNERWVL 9
Db      30 VLVNERWVL 38

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RESULT 10
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

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Query Match          100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66

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```

RESULT 11
US-08-824-874-3

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```

; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

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Query Match          100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66

```

```

RESULT 12
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 47; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 58 VLVNERWVL 66

RESULT 13
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 58 VLVNERWVL 66

RESULT 14
US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
DB 58 VLVNERWVL 66

RESULT 15
US-09-764-762-3

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; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match      100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66

Search completed: March 11, 2006, 01:24:25
Job time : 22.2222 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWVL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pgp:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pgp:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pgp:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pgp:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	3	US-09-918-243-34
2	47	100.0	9	3	US-09-905-083-34
3	47	100.0	9	4	US-10-372-521-34
4	47	100.0	9	5	US-10-831-075-34
5	47	100.0	97	4	US-10-262-511-100
6	47	100.0	136	5	US-10-450-763-53737
7	47	100.0	181	4	US-10-262-511-98
8	47	100.0	198	4	US-10-262-511-96
9	47	100.0	224	3	US-09-789-210-33
10	47	100.0	224	4	US-10-262-511-104
11	47	100.0	225	4	US-10-600-187-4
12	47	100.0	247	4	US-10-262-511-102
13	47	100.0	250	4	US-10-262-511-92
14	47	100.0	222	4	US-10-262-511-94
15	47	100.0	253	3	US-09-888-615-98
16	47	100.0	253	3	US-09-764-762-3
17	47	100.0	253	4	US-10-071-214-2
18	47	100.0	253	4	US-10-071-214-48
19	47	100.0	253	4	US-10-264-283-90
20	47	100.0	253	4	US-10-395-027-498
21	47	100.0	253	4	US-10-173-999-48
22	47	100.0	253	4	US-10-408-765A-639
23	47	100.0	253	5	US-10-643-795A-95
24	47	100.0	253	5	US-10-948-518-95
25	47	100.0	253	5	US-10-868-490A-1
26	47	100.0	257	4	US-10-344-394-38
27	43	91.5	9	3	US-09-918-243-40

28 43 91.5 9 3 US-09-918-243-50 Sequence 50, Appl
29 43 91.5 9 3 US-09-905-083-40 Sequence 40, Appl
30 43 91.5 9 3 US-09-905-083-50 Sequence 50, Appl
31 43 91.5 9 4 US-10-372-521-40 Sequence 40, Appl
32 43 91.5 9 4 US-10-372-521-50 Sequence 50, Appl
33 43 91.5 9 5 US-10-831-075-40 Sequence 40, Appl
34 43 91.5 9 5 US-10-831-075-50 Sequence 50, Appl
35 40 85.1 243 4 US-10-071-214-46 Sequence 46, Appl
36 40 85.1 249 4 US-10-071-214-47 Sequence 47, Appl
37 39 83.0 228 3 US-09-789-210-44 Sequence 44, Appl
38 39 83.0 228 5 US-10-202-676-6 Sequence 6, Appl
39 39 83.0 228 5 US-10-756-149-5803 Sequence 5803, Appl
40 38 80.9 81 4 US-10-045-367A-7 Sequence 7, Appl
41 38 80.9 81 4 US-10-170-789-57 Sequence 57, Appl
42 38 80.9 225 4 US-10-072-012-611 Sequence 611, Appl
43 38 80.9 259 4 US-10-072-012-222 Sequence 222, Appl
44 38 80.9 260 3 US-09-796-294-8 Sequence 8, Appl
45 38 80.9 260 4 US-10-461-787-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-918-243-34
; Sequence 34, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-918-243-34

Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|||||||
Db 1 VLVNERWVL 9

RESULT 2
US-09-905-083-34
; Sequence 34, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-905-083-34
Query Match          100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 3
US-10-372-521-34
; Sequence 34, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-10-372-521-34
Query Match          100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 4
US-10-831-075-34
; Sequence 34, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-10-831-075-34
Query Match          100.0%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 1 VLVNERWVL 9

RESULT 5
US-10-262-511-100
; Sequence 100, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 100
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-262-511-100

Query Match 100.0%; Score 47; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 39 VLVNERWVL 47

RESULT 6

US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61) .. (78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteases. domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36) .. (133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0

US-10-450-763-53737

Query Match 100.0%; Score 47; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 64 VLVNERWVL 72

RESULT 7

US-10-262-511-98
; Sequence 98, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana

; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michelle L.
; APPLICANT: Berghs, Constance

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-462C

; CURRENT APPLICATION NUMBER: US/10/262,511

; CURRENT FILING DATE: 2003-05-28

; PRIOR APPLICATION NUMBER: 60/326,483

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: 60/373,815

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 60/327,917

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/381,642

; PRIOR FILING DATE: 2002-05-17

; PRIOR APPLICATION NUMBER: 60/328,029

; PRIOR FILING DATE: 2002-10-09

; PRIOR APPLICATION NUMBER: 60/381,038

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/328,056

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/373,260

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: 60/373,826

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 60/327,435

; PRIOR FILING DATE: 2001-10-05

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 439

; SOFTWARE: CuraSeqlist version 0.1

; SEQ ID NO 98

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-262-511-98

Query Match 100.0%; Score 47; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 39 VLVNERWVL 47

RESULT 8

US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.

APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 96
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 47; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 58 VLVNERWVL 66
|||||

RESULT 9
US-09-789-210-33
Sequence 33, Application US/09789210
Publication No. US20040241646A1
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
COLPITS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWART, KENT D.

STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,210
FILING DATE: 20-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/944,483
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33

Query Match 100.0%; Score 47; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 29 VLVNERWVL 37
|||||

RESULT 10
US-10-262-511-104
Sequence 104, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei

APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 104
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-104

Query Match 100.0%; Score 47; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 44 VLVNERWVL 52

RESULT 11
US-10-600-187-4
Sequence 4, Application US/10600187
Publication No. US20040086910A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotsoshi
TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/10/600,187
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/654,600A
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/421,213
09/027,337
PRIOR FILING DATE: 1999-10-20
1998-02-20
NUMBER OF SEQ ID NOS: 98

SEQ ID NO 4
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: SCCE
US-10-600-187-4

Query Match 100.0%; Score 47; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.5; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVNERWVL 9
Db 30 VLVNERWVL 38

RESULT 12
US-10-262-511-102
Sequence 102, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19

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; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 102
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-102

Query Match      100.0%; Score 47; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 44 VLVNERWVL 52

RESULT 13
US-10-262-511-92
; Sequence 92, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
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; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 92
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-92

Query Match      100.0%; Score 47; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
Db 55 VLVNERWVL 63

RESULT 14
US-10-262-511-94
; Sequence 94, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
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; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 94
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-94

Query Match 100.0%; Score 47; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 7.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLVNERWVL 9
Db 57 VLVNERWVL 65

RESULT 15
US-09-888-615-98
; Sequence 98, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match 100.0%; Score 47; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLVNERWVL 9
Db 58 VLVNERWVL 66

Search completed: March 11, 2006, 01:37:23
Job time : 70.4444 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-34
Perfect score: 47
Sequence: 1 VLVNERWVL 9

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Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
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 - 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	48	6	US-10-412-748-21
2	47	100.0	253	6	US-10-412-748-11
3	47	100.0	253	6	US-10-412-748-14
4	47	100.0	253	6	US-10-412-748-17
5	47	100.0	253	7	US-11-037-243-98
6	38	80.9	81	7	US-11-151-601-39
7	37	78.7	359	7	US-11-037-243-114
8	36	76.6	345	7	US-11-174-816-44
9	36	76.6	345	7	US-11-174-816-59
10	36	76.6	345	7	US-11-174-819-13
11	36	76.6	345	7	US-11-174-819-78
12	36	76.6	1128	7	US-11-037-243-97
13	35	74.5	236	6	US-10-821-234-1274
14	35	74.5	239	7	US-11-043-788-140
15	35	74.5	307	7	US-11-043-788-141
16	35	74.5	347	7	US-11-043-788-133
17	35	74.5	347	7	US-11-043-788-137
18	35	74.5	348	7	US-11-177-506-40
19	35	74.5	365	7	US-11-096-568A-16466
20	35	74.5	366	7	US-11-043-788-139
21	35	74.5	403	7	US-11-096-568A-16465
22	35	74.5	406	7	US-11-043-788-131
23	35	74.5	406	7	US-11-043-788-132
24	35	74.5	406	7	US-11-189-120-6
25	35	74.5	406	7	US-11-177-506-39

26	35	74.5	445	7	US-11-096-568A-16464	Sequence 16464, A
27	35	74.5	688	6	US-10-821-234-1533	Sequence 1533, Ap
28	35	74.5	688	7	US-11-169-041-149	Sequence 149, App
29	34	72.3	38	7	US-11-129-861-11	Sequence 11, Appl
30	34	72.3	315	7	US-11-096-568A-23072	Sequence 23072, A
31	34	72.3	331	7	US-11-096-568A-23071	Sequence 23071, A
32	34	72.3	343	7	US-11-080-991-86	Sequence 86, Appl
33	34	72.3	343	7	US-11-019-711-130	Sequence 130, App
34	34	72.3	344	7	US-11-174-816-47	Sequence 47, Appl
35	34	72.3	344	7	US-11-174-816-62	Sequence 62, Appl
36	34	72.3	344	7	US-11-174-819-32	Sequence 32, Appl
37	34	72.3	344	7	US-11-174-819-81	Sequence 81, Appl
38	34	72.3	389	7	US-11-087-099-4063	Sequence 4063, Ap
39	34	72.3	393	6	US-10-821-234-1043	Sequence 1043, Ap
40	34	72.3	413	7	US-11-096-568A-23070	Sequence 23070, A
41	34	72.3	415	7	US-11-166-028-1	Sequence 1, Appli
42	34	72.3	462	7	US-11-183-205-10	Sequence 10, Appl
43	34	72.3	516	7	US-11-080-991-2	Sequence 2, Appli
44	34	72.3	687	7	US-11-074-176-260	Sequence 260, App
45	34	72.3	696	7	US-11-029-003-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-412-748-21
; Sequence 21, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-21

Query Match 100.0%; Score 47; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.024; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 VLVNERWVL 9
|||||||
Db 34 VLVNERWVL 42

RESULT 2
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 47; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66

RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 47; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66

RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 47; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66

RESULT 5
US-10-412-748-11
; Sequence 11, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARVDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 47; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
Db      58 VLVNERWVL 66

RESULT 6
US-11-151-601-39
; Sequence 39, Application US/11151601
; Publication No. US20060003413A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Welch, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; FILE REFERENCE: MPI00-054P1RCP10MNDIVM
; CURRENT APPLICATION NUMBER: US/11/151,601
; CURRENT FILING DATE: 2005-06-13
; PRIOR APPLICATION NUMBER: US 10/170,789
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-11-151-601-39

Query Match      80.9%; Score 38; DB 7; Length 81;
Best Local Similarity 75.0%; Pred. No. 1.8;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
      |:|:|:|
Db      5 LINEQWVL 12

RESULT 7
US-11-037-243-114
; Sequence 114, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-114

Query Match      78.7%; Score 37; DB 7; Length 359;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 LVNERWVL 9
      |||:|:|
Db      122 LVRERWVL 129

RESULT 8
US-11-174-816-44
; Sequence 44, Application US/11174816
; Publication No. US20060009441A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS
; FILE REFERENCE: 22645
; CURRENT APPLICATION NUMBER: US/11/174,816
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mTAAR6
US-11-174-819-13

Query Match      76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
      |:|:|:|
Db      192 VVVNQWVL 200

RESULT 9
US-11-174-816-59
; Sequence 59, Application US/11174816
; Publication No. US20060009441A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS
; FILE REFERENCE: 22645
; CURRENT APPLICATION NUMBER: US/11/174,816
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-174-816-59

Query Match      76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VLVNERWVL 9
      |:|:|:|
Db      192 VVVNQWVL 200

RESULT 10
US-11-174-819-13
; Sequence 13, Application US/11174819
; Publication No. US20060008880A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND
; FILE REFERENCE: 22646
; CURRENT APPLICATION NUMBER: US/11/174,819
; CURRENT FILING DATE: 2005-07-05
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mTAAR6
US-11-174-819-13

Query Match      76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 VLVNERWVL 9
|:|:|
Db 192 VVYNQWVL 200

RESULT 11
US-11-174-819-78
; Sequence 78, Application US/11174819
; Publication No. US20060008880A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTMAR
; TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 22646
; CURRENT APPLICATION NUMBER: US/11/174,819
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: EP 04103262.4
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 78
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-174-819-78

Query Match 76.6%; Score 36; DB 7; Length 345;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|
Db 192 VVYNQWVL 200

RESULT 12
US-11-037-243-97
; Sequence 97, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 1128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-97

Query Match 76.6%; Score 36; DB 7; Length 1128;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|
Db 925 VLVNERWVL 933

RESULT 13
US-10-821-234-1274
; Sequence 1274, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1274
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1274

Query Match 74.5%; Score 35; DB 6; Length 236;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLVNERWVL 9
|:|:|
Db 37 VLVNERWVL 45

RESULT 14
US-11-043-788-140
; Sequence 140, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 140
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-788-140

Query Match 74.5%; Score 35; DB 7; Length 299;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLVNERWVL 9
|:|:|
Db 84 LINEQWVL 91

RESULT 15
US-11-043-788-141
; Sequence 141, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 141
; LENGTH: 307

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-788-141

Query Match 74.5%; Score 35; DB 7; Length 307;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LVNERWVL 9
|:|:|:
Db 92 LINEQWLL 99

Search completed: March 11, 2006, 01:38:41
Job time : 9 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LPLQLILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	4	AAE08240 Human str
2	40	100.0	9	8	ADR68796 Human str
3	40	100.0	136	4	ABG23378 Novel hum
4	40	100.0	198	6	ADA05736 Human NOV
5	40	100.0	198	8	ADN62900 Human NOV
6	40	100.0	250	6	ADA05732 Human NOV
7	40	100.0	250	8	ADN62896 Human NOV
8	40	100.0	253	2	AAW05383 Human str
9	40	100.0	253	2	AAW05383 Human amy
10	40	100.0	253	5	ABB84421 Human SCC
11	40	100.0	253	5	ABB84406 Human SCC
12	40	100.0	253	5	AAU82740 Amino aci
13	40	100.0	253	6	ABU07440 Protein d
14	40	100.0	253	6	ABU07471 Protein d
15	40	100.0	253	6	ABR58471 Human str
16	40	100.0	253	7	ADB80484 Ovarian c
17	40	100.0	253	7	ADJ68833 Human hea
18	40	100.0	253	7	ADN39180 Cancer/tu
19	40	100.0	253	8	ADL06515 Human tan
20	40	100.0	253	8	ADN04182 Antipsori
21	40	100.0	253	8	ADR72880 Human ova
22	40	100.0	253	9	ADY67588 Human kal
23	40	100.0	253	9	AEC00353 Human kal
24	40	100.0	257	3	AAB21326 Human HSC

25	38	95.0	142	4	AAE08240	Human gas
26	38	95.0	156	4	AAE08240	Human gas
27	38	95.0	159	4	AAE08240	Human gas
28	36	90.0	9	4	AAE08238	Human str
29	36	90.0	9	8	ADR68794	Human str
30	36	90.0	845	6	ABU23951	Protein e
31	36	90.0	868	8	ADS21222	Bacterial
32	35	87.5	23	4	ABG43858	Peptide #
33	35	87.5	23	4	AAW37771	Peptide #
34	35	87.5	23	4	AAW64837	Human bra
35	35	87.5	23	4	ABG59233	Human liv
36	35	87.5	23	5	ABG46617	Human pep
37	35	87.5	480	2	AAW98431	H. pylori
38	35	87.5	637	8	ADY22422	Plant ful
39	34	85.0	70	2	AAV36291	Human sec
40	34	85.0	70	6	ADA11692	Human nov
41	34	85.0	73	2	AAW89030	Polypepti
42	34	85.0	73	4	ABB51130	Human sec
43	34	85.0	73	6	ABO45387	Novel hum
44	34	85.0	73	7	ABO26867	Protein a
45	34	85.0	86	4	AAO08397	Human pol

ALIGNMENTS

RESULT 1
AAE08240
ID AAE08240 standard; peptide; 9 AA.
XX
AC AAE08240;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #5 (residues 6-14).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperglasia.
XX
OS Homo sapiens.
XX
PN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
(UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ;
XX
DR WPI; 2001-514676/56.
XX
Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
Claim 25; Page 103; 127pp; English.
XX
The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX
Sequence 9 AA;
SQ

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
| | | | |
Db 1 LPLQLILL 9

RESULT 2
ADR68796
ID ADR68796 standard; peptide; 9 AA.
AC ADR68796;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:35.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
XX
DR WPI; 2004-653294/63.
XX
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX
PS Claim 5; SEQ ID NO 35; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
| | | | |
Db 1 LPLQLILL 9

ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS87565.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG0377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 136 AA;

Query Match 100.0%; Score 40; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
| | | | |
Db 12 LPLQLILL 20

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX

ADA05736;
06-NOV-2003 (first entry)
Human NOV18c protein SEQ ID NO:96.
human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
Homo sapiens.
WO2003029424-A2.
10-APR-2003.
02-OCT-2002; 2002WO-US031373.
02-OCT-2001; 2001US-0326483P.
05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327917P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328056P.
12-OCT-2001; 2001US-0328849P.
15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0330142P.
18-OCT-2001; 2001US-0330309P.
22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
17-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373884P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
01-OCT-2002; 2002US-00262511.
(CURA-) CURAGEN CORP.
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerkow BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
WPI; 2003-381626/36.
N-PSDB; ADA05735.
New NOVX polypeptides and nucleic acids, useful for diagnosing,
preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
cancer or dyslipidemia, and in chromosome mapping, tissue typing or
pharmacogenomics.
Claim 1; Page 170; 586pp; English.
The present invention describes NOVX proteins, where X can be 1 to 55
(e.g. NOV1). Also described: (1) a composition comprising a polypeptide

described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide described above; (13) methods of treating
or preventing a pathology associated with the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide. NOVX
sequences have antidiabetic, anorectic, antibacterial, virucide,
immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
and antilipemic activities, and can be used in gene therapy. The
polypeptide is useful in manufacturing a medicament for treating a
syndrome associated with a human disease. The polypeptide or the nucleic
acid molecule may be used to diagnose, treat or prevent metabolic
disorders such as diabetes or obesity, infections, cachexia, cancer,
neurodegenerative disorders such as Alzheimer's disease or Parkinson's
disease, immune disorders, haematopoietic disorders and various
dyslipidaemias. The nucleic acids can also be used as hybridisation
probes, in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. The present sequence represents a human NOVX from the
present invention.
XX Sequence 198 AA;
SQ
Query Match 100.0%; Score 40; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQLLLL 9
Db 6 LLPLQLLLL 14
RESULT 5
ADN62900
ID ADN62900 standard; protein; 198 AA.
AC ADN62900;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18c.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KERU/) KERUDA R.
 PA (JUGJ/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATY/) PATURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWV/) JI W.
 PA (MILL/) MILLER C E.
 PA (RST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIP/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malvankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2004-213931/20.
 DR N-PSDB; ADN62899.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 40; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 Db 6 LLPLQLLLL 14
 RESULT 6
 ADA05732
 ID ADA05732 standard; protein; 250 AA.
 XX
 AC ADA05732;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18a protein SEQ ID NO:92.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 OS Homo sapiens.
 XX
 XX WO2003029424-A2.
 PN
 XX 10-APR-2003.
 PD
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
XX
XX (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ott T, Gorman L, Zerkhuken BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Raetelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI: 2003-381626/36.
DR N-PSDB; ADA05731.
XX
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX
PS Claim 1; Page 169-170; 586pp; English.
XX
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to a
CC disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide. NOVX
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 40; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPQLILL 9
Db 3 LLPQLILL 11

RESULT 7
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX
AC ADN62896;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18a.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.

PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWV/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
DR WPI; 2004-213931/20.
DR N-PSDB; ADN62895.
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 92; 395pp; English.
XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 40; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQILL 9
Db 3 LLPLQILL 11
RESULT 8
AAR67888
ID AAR67888 standard; protein; 253 AA.
XX
AC AAR67888;
XX
DT 25-MAR-2003 (revised)
DT 09-AUG-1995 (first entry)
XX
DE Human stratum corneum chymotrophic recombinant enzyme (SCCE) .
XX
KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
KW callosities; keratosis pilaris; ichthyoses; eczema.
XX
OS Homo sapiens.
XX
PN WO9500651-A1.
XX
PD 05-JAN-1995.
XX
PF 20-JUN-1994; 94WO-IB000166.
XX
PR 18-JUN-1993; 93DK-00000725.
XX
PA (SYMB-) SYMBICOM AB.
XX
PI Egelrud T, Hansson L;
XX
DR WPI; 1995-052088/07.
DR N-PSDB; AAQ81203.
XX
PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
PT related vectors, transformed cells and polypeptides, useful for treating
PT skin disorders, e.g. acne or psoriasis, and for identification of
PT specific inhibitors.
XX
PS Disclosure; Page 97; 137pp; English.
XX
CC The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
CC and skin care products, especially to treat and prevent acne, xeroderma,
CC or other hyperkeratotic conditions (e.g. callosities or keratosis
CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
CC recombinantly following mammal, insect, plant, or microorganism
CC transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQILL 9
Db 6 LLPLQILL 14
RESULT 9

```

AAW05383
ID AAW05383 standard; protein; 253 AA.
XX
AC AAW05383;
XX
DT 31-DEC-1996 (first entry)
XX
DE Human amyloid precursor protein protease.
XX
KW Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN W09631122-A1.
XX
PD 10-OCT-1996.
XX
PF 02-APR-1996; 96WO-US004294.
XX
PR 04-APR-1995; 95US-00416257.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Dixon EP, Johnstone BM, Little SP;
XX
DR WPI; 1996-464694/46.
XX
DR N-PSDB; AAT39783.
XX
PT New isolated human amyloid precursor protein protease - used to develop
PT prod. for the treatment or diagnosis of associated conditions, esp.
PT Alzheimer's disease.
XX
PS Claim 1; Page 44-45; 55pp; English.
XX
CC Human amyloid precursor protein protease (AAW05383) is involved in the
CC processing or clearance of amyloid precursor protein to form beta-amyloid
CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
CC obtd. from a human lung library. Recombinant protease can be produced in
CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
CC (partic. AV-120 host cells. It is used to develop products for the design
CC and testing of cpds. useful for treating or preventing conditions
CC associated with beta-amyloid peptide, esp. Alzheimer's disease
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQLLLL 9
Db 6 LLPLQLLLL 14
RESULT 10
ID ABB84421
XX ABB84421 standard; peptide; 253 AA.
XX
AC ABB84421;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human SCCE protein N-terminal fragment SEQ ID 48.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.
XX
PN W0200262135-A2.

15-AUG-2002.
08-FEB-2002; 2002WO-IB001300.
09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
Egelrud T, Hansson L;
WPI; 2002-643380/69.
Transgenic mammal or its embryo useful as model for human disease, has
heterologous nucleotide sequence coding for stratum corneum chymotryptic
enzyme operably linked to promoter that drives its expression in skin.
Example 6; Page 37; 74pp; English.
This invention describes a novel non-human transgenic mammal or mammalian
embryo having integrated within its genome, a heterologous nucleotide
sequence comprising at least a significant part of a nucleotide sequence
coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
operably linked to a promoter that drives expression of heterologous scce
or its variant in skin. The product of the invention is useful as a model
for the study of disease with the aim of improving treatment, to relieve
or ameliorate a pathogenic condition, for development or testing of a
cosmetic or a pharmaceutical formulation, and for the development of a
diagnostic method. It can also be used as a model for a skin disease or
skin cancer. The invention is also useful for screening or identifying a
compound or composition effective for the prevention or treatment of an
abnormal or unwanted phenotype, and for screening or identifying a
compound or composition effective for the prevention or treatment of
inflammatory skin diseases selected from diseases consisting of epidermal
hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
with epidermal hyperkeratosis. The mammal of the invention is also useful
as a model for further studies of itch mechanisms and the testing of
potential compounds and compositions for relieve of various skin diseases
where itch is a component. This sequence represents the N-terminal
fragment of the human stratum corneum chymotryptic enzyme, SCCE
synonymous with human kallikrein 7 (KLK7), used in the development of the
transgenic mammals described in the invention
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLPLQLLLL 9
Db 6 LLPLQLLLL 14
RESULT 11
ID ABB84406
XX ABB84406 standard; protein; 253 AA.
XX
AC ABB84406;
XX
DT 08-NOV-2002 (first entry)
XX
DE Human SCCE protein.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.

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KW WO200262135-A2.
 PN 15-AUG-2002.
 PD 08-FEB-2002; 2002WO-IB001300.
 XX 09-FEB-2001; 2001CA-02332655.
 PR 09-FEB-2001; 2001DK-00000218.
 XX (EGBL/) EGBLRUD T.
 PA (HANS/) HANSSON L.
 PI Egelrud T, Hansson L;
 XX WPI; 2002-643380/69.
 DR N-PSDB; ABQ76226.
 XX Transgenic mammal or its embryo useful as model for human disease, has
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT enzyme operably linked to promoter that drives its expression in skin.
 PS Claim 10; Page 58-59; 74pp; English.
 XX This invention describes a novel non-human transgenic mammal or mammalian
 CC embryo having integrated within its genome, a heterologous nucleotide
 CC sequence comprising at least a significant part of a nucleotide sequence
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
 CC operably linked to a promoter that drives expression of heterologous scce
 CC or its variant in skin. The product of the invention is useful as a model
 CC for the study of disease with the aim of improving treatment, to relieve
 CC or ameliorate a pathological condition, for development or testing of a
 CC cosmetic or a pharmaceutical formulation, and for the development of a
 CC diagnostic method. It can also be used as a model for a skin disease or
 CC skin cancer. The invention is also useful for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC abnormal or unwanted phenotype, and for screening or identifying a
 CC compound or composition effective for the prevention or treatment of
 CC inflammatory skin diseases selected from diseases consisting of epidermal
 CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
 CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
 CC with epidermal hyperkeratosis. The mammal of the invention is also useful
 CC as a model for further studies of itch mechanisms and the testing of
 CC potential compounds and compositions for relieve of various skin diseases
 CC where itch is a component. This sequence represents the human stratum
 CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
 CC with human kallikrein 7 (KLK7) and is used in the development of the
 CC transgenic mammals described in the invention
 XX Sequence 253 AA;
 SQ Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 Db 6 LLPLQLLLL 14
 RESULT 12
 AAU82740
 ID AAU82740 standard; protein; 253 AA.
 XX AAU82740;
 XX 23-APR-2002 (first entry)
 DT Amino acid sequence of novel human protease #39.
 DE Human; protease; cancer; immune-related disorder; cardiovascular disease;
 XX neuronal-associated disease; metabolic disorder; inflammatory disorder;
 KW nervous system disorder; sexual dysfunction; pain; mood disorder;
 XX

KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
 KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
 KW ocular disease; cytostatic; enzyme.
 XX Homo sapiens.
 OS WO200200860-A2.
 PN 03-JAN-2002.
 PD 26-JUN-2001; 2001WO-US020171.
 XX 26-JUN-2000; 2000US-0214047P.
 PR (SUGE-) SUGEN INC.
 PA Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
 XX Charyczak G;
 PI WPI; 2002-139913/18.
 DR N-PSDB; ABK31782.
 XX Nucleic acids encoding novel human proteases, useful for useful for
 PT treating diseases and disorders such as cancers, immune-related diseases
 PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
 PT disorders.
 PS Claim 6; Fig 2N; 313pp; English.
 XX The present invention relates to the isolation of novel human proteases,
 CC and the nucleic acids encoding them. The sequences of the invention are
 CC useful for treating diseases and disorders such as cancers (e.g. breast,
 CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
 CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
 CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
 CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
 CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
 CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
 CC disorders, cognitive disorders, hypotension, hypertension, psychotic
 CC disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease) and dyskinesias. The nucleic acids and polypeptides are also
 CC useful for treating viral infections caused by human immunodeficiency
 CC virus (HIV), and non-viral infections such as ocular disease (e.g.
 CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
 CC human proteases of the invention
 XX Sequence 253 AA;
 SQ Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 Db 6 LLPLQLLLL 14
 RESULT 13
 ABU07440
 ID ABU07440 standard; protein; 253 AA.
 XX ABU07440;
 AC 28-JAN-2003 (first entry)
 DT Protein differentially regulated in prostate cancer #43.
 DE Prostate cancer; gene expression; differential regulation;
 XX molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX Homo sapiens.
 OS

PN WO200281638-A2.
 XX 17-OCT-2002.
 PD
 XX 08-APR-2002; 2002WO-US010824.
 XX
 PF
 XX 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 PR
 XX (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX
 XX Sun Z, Jay G;
 XX WPI; 2003-058520/05.
 XX N-PSDB; ABX10343.
 DR
 XX Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 PT
 XX Claim 1; Page 293-294; 416pp; English.
 PS
 XX The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLL 9
 Db 6 LLPLQLLL 14
 RESULT 14
 ABU07471
 ID ABU07471 standard; protein; 253 AA.
 XX
 AC ABU07471;

XX DT 28-JAN-2003 (first entry)
 XX
 DE Protein differentially regulated in prostate cancer #74.
 DE
 XX Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX
 OS Homo sapiens.
 XX
 XX WO200281638-A2.
 PN
 XX 17-OCT-2002.
 PD
 XX 08-APR-2002; 2002WO-US010824.
 PF
 XX 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 PR
 XX (ORIG-) ORIGENE TECHNOLOGIES INC.
 PA
 XX Sun Z, Jay G;
 PI
 XX WPI; 2003-058520/05.
 XX N-PSDB; ABX10375.
 DR
 XX Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 PT
 XX Claim 1; Page 351; 416pp; English.
 PS
 XX The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 15
ABR58471
ID ABR58471 standard; protein; 253 AA.
XX
XX
AC ABR58471;
XX
DT 07-JUL-2003 (first entry)
XX
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
XX
KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX
OS Homo sapiens.
XX
PN WO2003029468-A1.
XX
PD 10-APR-2003.
XX
XX 02-OCT-2002; 2002WO-US031467.
XX
PR 02-OCT-2001; 2001US-0327135P.
PR 30-MAY-2002; 2002US-0384531P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Algate PA, Mannion J;
XX
DR WPI; 2003-372001/35.
XX
PT New polynucleotide and polypeptide useful for diagnosing and/or treating
XX cancer, particularly ovarian cancer, and as a vaccine.
PS Claim 2; Page 157-158; 169pp; English.
XX
CC The invention relates to a novel isolated polynucleotide. The
CC polynucleotides of the invention have cytostatic activity, and may have a
CC use in gene therapy, and in a vaccine. The composition and methods are
CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
CC The composition may also be used as a vaccine to prevent cancer. The
CC present sequence is used in the exemplification of the invention
XX

SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred No. 27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
Db 6 LLPLQILL 14

Search completed: March 11, 2006, 00:24:14
Job time : 87.6667 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LLPLQLLLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: piri:*
2: piri2:*
3: piri3:*
4: piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	253	2 A53968	serine proteinase
2	36	90.0	845	2 D97163	cation transport p
3	35	87.5	493	2 A71875	hypothetical prote
4	35	87.5	496	2 B64838	conserved hypothet
5	34	85.0	266	2 JC7300	tax-responsive ele
6	34	85.0	267	2 JC4857	hepatocarcinogenes
7	34	85.0	369	2 S33603	surfactant protein
8	34	85.0	371	1 JN0450	conglutinin precur
9	34	85.0	371	2 I45878	conglutinin - bovi
10	34	85.0	429	2 T17215	hypothetical prote
11	34	85.0	539	2 H82994	probable permease
12	34	85.0	1092	2 T12520	hypothetical prote
13	34	85.0	1236	2 T50904	Mg protoporphyrin
14	33	82.5	146	2 H75201	hypothetical prote
15	33	82.5	277	2 H84314	cytochrome a3 con
16	33	82.5	282	2 E70890	hypothetical prote
17	33	82.5	294	2 A25970	transcription acti
18	33	82.5	294	2 E82257	cholera toxin tran
19	33	82.5	653	2 A46362	amyloid precursor-
20	32	80.0	245	2 E75440	hypothetical prote
21	32	80.0	253	2 AF1535	transport protein
22	32	80.0	286	2 JQ0708	lipopolysaccharide
23	32	80.0	394	1 B43750	chloramphenicol re
24	32	80.0	394	2 B85535	probable transport
25	32	80.0	394	2 F90684	probable transport
26	32	80.0	412	2 A57468	P-selectin glycopr
27	32	80.0	491	2 JC6197	stromelysin 3 (EC
28	32	80.0	492	2 A44399	stromelysin 3 (EC
29	32	80.0	543	2 A12088	Na+/H+-exchanging

30	32	80.0	1041	2 T29010	hypothetical prote
31	32	80.0	1306	1 A31759	peptidyl-di-peptida
32	32	80.0	1485	2 S23756	CfTR protein - Afr
33	31	77.5	157	2 A83214	probable transcrip
34	31	77.5	189	2 T43766	hypothetical prote
35	31	77.5	196	2 G65039	hypothetical prote
36	31	77.5	209	2 A54984	EUF-1 protein prec
37	31	77.5	213	2 JE0322	ephA2 - human
38	31	77.5	303	2 C84914	hypothetical prote
39	31	77.5	306	2 H86811	sugar ABC transpor
40	31	77.5	327	1 A41720	acid phosphatase (
41	31	77.5	328	1 A41927	insulin-like growt
42	31	77.5	370	2 AB3334	daunorubicin resis
43	31	77.5	372	2 A98157	probable permease
44	31	77.5	372	2 AH3130	ABC transporter, m
45	31	77.5	388	2 T26360	hypothetical prote

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hanson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:9521214; PIDN:1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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6	34	85.0	267	2 JC4857	hepatocarcinogenes
7	34	85.0	369	2 S33603	surfactant protein
8	34	85.0	371	1 JN0450	conglutinin precur
9	34	85.0	371	2 I45878	conglutinin - bovi
10	34	85.0	429	2 T17215	hypothetical prote
11	34	85.0	539	2 H82994	probable permease
12	34	85.0	1092	2 T12520	hypothetical prote
13	34	85.0	1236	2 T50904	Mg protoporphyrin
14	33	82.5	146	2 H75201	hypothetical prote
15	33	82.5	277	2 H84314	cytochrome a3 con
16	33	82.5	282	2 E70890	hypothetical prote
17	33	82.5	294	2 A25970	transcription acti
18	33	82.5	294	2 E82257	cholera toxin tran
19	33	82.5	653	2 A46362	amyloid precursor-
20	32	80.0	245	2 E75440	hypothetical prote
21	32	80.0	253	2 AF1535	transport protein
22	32	80.0	286	2 JQ0708	lipopolysaccharide
23	32	80.0	394	1 B43750	chloramphenicol re
24	32	80.0	394	2 B85535	probable transport
25	32	80.0	394	2 F90684	probable transport
26	32	80.0	412	2 A57468	P-selectin glycopr
27	32	80.0	491	2 JC6197	stromelysin 3 (EC
28	32	80.0	492	2 A44399	stromelysin 3 (EC
29	32	80.0	543	2 A12088	Na+/H+-exchanging

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLLLL 9
| | | | | | | | |
DB 6 LLPLQLLLL 14

RESULT 2

D97163
cation transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97163
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-845 <KUR>
A;Cross-references: UNIPROT:Q97H76; UNIPARC:UPI000000CA412; GB:AE001437; PIDN:AAK80095.1;

A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2137

```
Query Match      90.0%; Score 36; DB 2; Length 845;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 670 LLPLQIILL 678

RESULT 3
A71875
hypothetical protein jhp0880 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: A71875
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923382
A:Accession: A71875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <ARN>
A:Cross-references: UNIPROT:Q92K05; UNIPARC:UPI00000D7271; GB:AE001518; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0880

Query Match      87.5%; Score 35; DB 2; Length 493;
Best Local Similarity 88.9%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 254 LLPLSILL 262

RESULT 4
B64638
conserved hypothetical integral membrane protein HP0946 - Helicobacter pylori (strain 26
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: B64638
R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64638
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-496 <TOM>
A:Cross-references: UNIPROT:Q25600; UNIPARC:UPI00000D30BA; GB:AE000604; GB:AE000511; NID
C:Genetics:
A:Start codon: GTG

Query Match      87.5%; Score 35; DB 2; Length 496;
Best Local Similarity 88.9%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 254 LLPLSILL 262

RESULT 5
JC7300
tax-responsive element-binding protein 5 - mouse
C:Species: Mus musculus (house mouse)
```

```
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: JC7300
R:Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatau, K.
DNA Res. 7, 187-193, 2000
A:Title: Isolation and characterization of the gene encoding mouse tax-responsive element
A:Reference number: JC7300
A:Accession: JC7300
A:Molecule type: mRNA
A:Residues: 1-266 <MAS>
A:Cross-references: UNIPROT:Q9ESS3; UNIPARC:UPI00000E73B0; DDBJ:AB036745
C:Genetics:
A:Gene: treb5
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor

Query Match      85.0%; Score 34; DB 2; Length 266;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 187 LLPLQIILL 195

RESULT 6
JC4857
hepatocarcinogenesis-related transcription factor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4857
R:Kishimoto, T.; Kokura, K.; Kumaga, Y.; Makino, Y.; Tamura, T.
Biochem. Biophys. Res. Commun. 224, 746-751, 1996
A:Title: HTF: A b-zip transcription factor that is closely related to the human XBP/TREB1
A:Reference number: JC4857
A:Accession: JC4857
A:Molecule type: mRNA
A:Residues: 1-267 <KIS>
A:Cross-references: UNIPROT:Q9R1S4; UNIPARC:UPI00000E80AD
C:Comment: This is a basic-leucine zipper type transcription factor involved in hepatocel
C:Genetics:
A:Gene: htf
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor
F:58-98/Domain: fos/jun DNA-binding domain homology <FJD>
F:89-126/Region: leucine zipper motif

Query Match      85.0%; Score 34; DB 2; Length 267;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
   |||:||||:
Db 188 LLPLQIILL 196

RESULT 7
S33603
surfactant protein D - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C:Accession: S33603
R:Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A:Title: Structural similarity between bovine conglutinin and bovine lung surfactant prot
A:Reference number: S33603; MUID:93170856; PMID:8436402
A:Accession: S33603
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-369 <LIM>
A:Cross-references: UNIPARC:UPI0000177932
C:Superfamily: pulmonary surfactant protein D; C-type lectin homology
F:248-367/Domain: C-type lectin homology <LCH>
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Query Match 85.0%; Score 34; DB 2; Length 369;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 LLPLQILL 9
 |||| :|||
 Db 3 LLPLSVLL 11

RESULT 8
 JN0450
 conglutinin precursor - bovine
 N;Alternate names: C3b-binding protein
 N;Contains: Conglutinin-N
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C;Accession: JN0450; J02396; S33235; A23740; S36879; S35044; I46010; A29416; S34054
 R;Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
 Biochem. Biophys. Res. Commun. 191, 335-342, 1993
 A;Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
 A;Reference number: JN0450; MUID:93213261; PMID:8460993
 A;Accession: JN0450
 A;Molecule type: mRNA
 A;Residues: 1-371 <SUZ>
 A;Cross-references: UNIPROT:P23805; UNIPARC:UPI0000127EB3; DDBJ:D14085; NID:g285643; PID
 A;Experimental source: liver
 R;Kawasaki, N.; Itoh, N.; Kawasaki, T.
 Biochem. Biophys. Res. Commun. 198, 597-604, 1994
 A;Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamm
 A;Reference number: J02396; MUID:94128104; PMID:8297370
 A;Accession: J02396
 A;Molecule type: mRNA
 A;Residues: 1-371 <KA2>
 A;Cross-references: UNIPARC:UPI0000127EB3
 A;Note: The authors translated the codon GAT for residues 250 and 270 as Glu
 R;Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
 Biochem. J. 292, 157-162, 1993
 A;Title: The cDNA cloning of conglutinin and identification of liver as a primary site o
 A;Reference number: S33235; MUID:93277452; PMID:7684896
 A;Accession: S33235
 A;Molecule type: mRNA
 A;Residues: 1-172, 'H', 174-217, 'A', 219-271, 'V', 273-371 <LUJ>
 A;Cross-references: UNIPARC:UPI000016C2E3; EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PI
 A;Experimental source: liver
 R;Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarma, T.B.
 J. Biol. Chem. 266, 2715-2723, 1991
 A;Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin f
 A;Reference number: A23740; MUID:91131556; PMID:1993651
 A;Accession: A23740
 A;Molecule type: protein
 A;Residues: 21-209, 'S', 211-371 <LEE>
 A;Cross-references: UNIPARC:UPI000014DF2A
 R;Kawasaki, N.; Yokota, Y.; Kawasaki, T.
 Arch. Biochem. Biophys. 305, 533-540, 1993
 A;Title: Differentiation of conglutination activity and sugar-binding activity of conglu
 A;Reference number: S36879; MUID:93384312; PMID:8373191
 A;Accession: S36879
 A;Molecule type: protein
 A;Residues: 21-54; 75-86, 'X', 88-89, 'X', 91, 'X', 93-94; 208-209, 'X', 211-227 <KAW>
 A;Cross-references: UNIPARC:UPI00001741A3; UNIPARC:UPI00001741A4; UNIPARC:UPI00001741A5
 A;Experimental source: serum
 R;Lu, J.; Wiedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
 Eur. J. Biochem. 215, 793-799, 1993
 A;Title: Structural similarity between lung surfactant protein D and conglutinin. Two di
 A;Reference number: S35044; MUID:93358905; PMID:8354286
 A;Accession: S35044
 A;Molecule type: protein
 A;Residues: 75-86, 'X', 88-89, 'X', 91, 'I', <LUA>
 A;Cross-references: UNIPARC:UPI00001741A6
 A;Experimental source: lung
 R;Young, N.M.; Leon, M.A.
 Biochem. Biophys. Res. Commun. 143, 645-651, 1987
 A;Title: The carbohydrate specificity of conglutinin and its homology to proteins in the

A;Reference number: A29416; MUID:87184551; PMID:3566740
 A;Contents: annotation
 R;Malhotra, R.; Laursen, S.B.; Willis, A.C.; Sim, R.B.
 Biochem. J. 293, 15-19, 1993
 A;Title: Research Communication. Localization of the receptor-binding site in the collect
 A;Reference number: S34054; MUID:93319501; PMID:8328957
 A;Contents: annotation
 R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry,
 J. Immunol. 153, 173-180, 1994
 A;Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship to
 A;Reference number: I46010; MUID:94267222; PMID:8207234
 A;Accession: I46010
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-371 <LIO>
 A;Cross-references: UNIPARC:UPI0000127EB3; EMBL:U06860; NID:g507183; PIDN:AAB0624.1; PFI
 C;Comment: This protein mediates the agglutination of erythrocytes with antibody and com
 C;Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamin
 C;Genetics:
 A;Gene: CGN1
 A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
 C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 C;Keywords: calcium binding; glycoprotein; hydroxyllysine; hydroxyproline
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-371/Product: conglutinin #status predicted <MAT>
 F;46-214/Region: collagen-like
 F;75-371/Product: conglutinin-N #status predicted <MA2>
 F;248-369/Domain: C-type lectin homology <LCH>
 F;63,87,99,135,141,159,162,198,210/Binding site: carbohydrate (lys) (covalent) #status p
 F;63,87,99,135,141,159,162,198,210/Modified site: 5-hydroxyllysine (lys) #status experim
 F;78,96,108,111,129,132,147,153,171,195/Modified site: 4-hydroxyproline (pro) #status exp
 F;337/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 85.0%; Score 34; DB 1; Length 371;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
 |||| :|||
 Db 3 LLPLSVLL 11

RESULT 9
 I45878
 conglutinin - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
 C;Accession: I45878
 R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry,
 Gene 141, 277-281, 1994
 A;Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization of
 A;Reference number: I45878; MUID:94215917; PMID:8163202
 A;Accession: I45878
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-371 <LIO>
 A;Cross-references: UNIPROT:P23805; UNIPARC:UPI000016C2E0; GB:I18871; NID:g495012; PIDN:
 C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
 F;248-369/Domain: C-type lectin homology <LCH>

Query Match 85.0%; Score 34; DB 2; Length 371;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
 |||| :|||
 Db 3 LLPLSVLL 11

RESULT 10
 T17215
 hypothetical protein DKFP434H2235.1 - human
 C;Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17215
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18723
A:Accession: T17215
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-429 <POU>
A:Cross-references: UNIPARC:UPI000000D884; EMBL:AL117404
A:Experimental source: adult testis; clone DKFZp434H2235
C:Genetics:
A:Note: DKFZp434H2235.1

Query Match 85.0%; Score 34; DB 2; Length 429;

Best Local Similarity 87.5%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQIILL 9
|||:||||
DB 381 LPLQLLLL 388

RESULT 11

H82994
probable permease of ABC iron transporter PA5216 [imported] - Pseudomonas aeruginosa (st
C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: H82994
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H82994

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-539 <STO>

A:Cross-references: UNIPROT:Q9HTX4; UNIPARC:UPI000000CF5A; GB:AE004934; GB:AE004091; NID
A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA5216

C:Superfamily: sfuB protein

Query Match 85.0%; Score 34; DB 2; Length 539;

Best Local Similarity 77.8%; Pred. No. 64;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
|||:||||
DB 21 LLPLSVLLL 29

RESULT 12

T12520

hypothetical protein DKFZp434G173.1 - human

C:Species: Homo sapiens (man)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: T12520

R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z17524

A:Accession: T12520

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1092 <WAM>

A:Cross-references: UNIPARC:UPI00000711F2; EMBL:AL080133

A:Experimental source: adult testis; clone DKFZp434G173

C:Genetics:

A:Note: DKFZp434G173.1

Query Match 85.0%; Score 34; DB 2; Length 1092;

Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQIILL 9
|||:||||
DB 1044 LPLQLLLL 1051

RESULT 13

TS0904

Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus

C:Species: Rubrivivax gelatinosus

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C:Accession: T50904

R:Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

submitted to the EMBL Data Library, November 1999

A:Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt
A:Reference number: Z25270

A:Accession: T50904

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-1236 <NAG>

A:Cross-references: UNIPROT:Q9JPA4; UNIPARC:UPI00000B2528; EMBL:AB034704; PIDN:BA094057.1

A:Experimental source: strain IL144

C:Genetics:

A:Gene: bchH

C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match 85.0%; Score 34; DB 2; Length 1236;

Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
|||:||||
DB 946 LLPLQIKLL 954

RESULT 14

H75201

hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: H75201

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc

A:Reference number: A75001

A:Accession: H75201

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-146 <KAW>

A:Cross-references: UNIPROT:Q9V2D5; UNIPARC:UPI0000063243; GB:AJ248283; GB:AL096836; NID:

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB0088

C:Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

Query Match 82.5%; Score 33; DB 2; Length 146;

Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIILL 9
|||:||||
DB 68 LLPLQIIIV 76

RESULT 15

H84314

cytochrome aa3 controlling protein [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: H84314

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.

; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-277 <STO>
A:Cross-references: UNIPROT:Q9HPI3; UNIPARC:UPI0000063931; GB:AE004437; NID:gl0581096; E
C:Genetics:
A:Gene: ccp

Query Match 82.5%; Score 33; DB 2; Length 277;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLPLOILL 8
Db 98 LLPLOVIL 105

Search completed: March 11, 2006, 00:40:50
Job time : 15.1111 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LPLQLILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	100.0	66	2	Q6DTY1_HUMAN	Q6dtY1 homo sapien
2	40	100.0	253	1	KLK7_HUMAN	P49862 homo sapien
3	38	95.0	73	2	Q8VCA9_MOUSE	Q8vca9 mus musculus
4	38	95.0	104	2	Q8R5D6_MOUSE	Q8r5d6 mus musculus
5	38	95.0	138	2	Q6PKE2_MOUSE	Q6pke2 mus musculus
6	38	95.0	201	1	FKB11_MOUSE	Q6dlm7 mus musculus
7	38	95.0	381	1	INHA_TRITU	Q77755 trichosurus
8	37	92.5	552	2	Q75B55_ASHGO	Q75b55 ashbya goss
9	36	90.0	71	2	Q4XN42_PLACH	Q4xn42 plasmodium
10	36	90.0	79	2	Q8VB59_WSSV	Q8vb59 white spot
11	36	90.0	637	2	Q7R054_PLAYO	Q7rb54 plasmodium
12	36	90.0	845	2	Q97H76_CLOBAB	Q97h76 clostridium
13	36	90.0	887	2	Q5FMG7_LACAC	Q5fmg7 lactobacilli
14	35	87.5	181	2	Q6N996_RHOPA	Q6nb96 rhodospseudo
15	35	87.5	183	2	Q8MZZ0_HELAU	Q8mzz0 helicoverpa
16	35	87.5	208	2	Q21527_CLEGA	Q21527 clethrionom
17	35	87.5	233	2	Q8IMF1_DROME	Q8imf1 drosophila
18	35	87.5	433	2	Q9ZKQ5_HELPJ	Q9zkq5 helicobacte
19	35	87.5	496	2	Q25600_HELPJ	Q25600 helicobacte
20	35	87.5	545	2	Q5N0S0_SYNP6	Q5n0s0 synchococc
21	35	87.5	1620	2	Q622J8_ORYSA	Q622j8 oryza sativ
22	34	85.0	96	2	Q5XFW5_RAT	Q5xfw5 rattus norv
23	34	85.0	182	2	Q8MZV6_SPOLT	Q8mzv6 spodoptera
24	34	85.0	182	2	Q8MXZ7_PLOIN	Q8mxz7 plodia inte
25	34	85.0	182	2	Q8MZV6_NAMBR	Q8mzv6 mamestra br
26	34	85.0	182	2	Q8MZZ6_CYPDO	Q8mzz6 cydia pomon
27	34	85.0	205	2	Q653Z3_ORYSA	Q653z3 oryza sativ
28	34	85.0	242	2	Q7VHT6_HELPJ	Q7vht6 helicobacte
29	34	85.0	243	2	Q4QC15_LEIMA	Q4qci5 leishmania
30	34	85.0	245	2	Q50KZ3_CALJA	Q50kz3 callithrix
31	34	85.0	246	2	Q50KZ9_HUMAN	Q50kz9 homo sapien

32	34	85.0	246	2	Q585W6_TRYYP	Q585w6 trypanosoma
33	34	85.0	246	2	Q50KZ2_CEBAP	Q50kz2 cebus apell
34	34	85.0	246	2	Q50KZ4_MACWU	Q50kz4 macaca mula
35	34	85.0	246	2	Q50KZ5_HYLAG	Q50kz5 hylobates a
36	34	85.0	246	2	Q50KZ6_PONPY	Q50kz6 pongo pygma
37	34	85.0	262	2	Q8BMM1_MOUSE	Q8bmm1 mus musculus
38	34	85.0	267	1	XBPI_MOUSE	Q35426 mus musculus
39	34	85.0	267	1	XBPI_RAT	Q9rlr4 rattus norv
40	34	85.0	283	2	Q8KI47_MOUSE	Q8ki47 mus musculus
41	34	85.0	331	2	Q7XI51_ORYSA	Q7xi51 oryza sativ
42	34	85.0	338	2	Q6US81_SPOLI	Q6us81 spodoptera
43	34	85.0	369	1	SFTPD_BOVIN	P35246 bos taurus
44	34	85.0	369	2	Q863AI_BOVIN	Q863ai bos taurus
45	34	85.0	371	1	CL46_BOVIN	Q8mh29 bos taurus

ALIGNMENTS

RESULT 1
Q6DTY1_HUMAN
ID Q6DTY1_HUMAN PRELIMINARY; PRT; 66 AA.
AC Q6DTY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T., Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY646152; AN66047.1; -; mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 40; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 4,9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LPLQLILL	9
DB	6	LPLQLILL	14

RESULT 2
KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8NSN9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
RC TISSUE=keratinocyte; DOI=10.1016/S0378-1119(00)00280-8;
RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
RA Diamandis E.P.;
RT "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
RT enzyme is a new member of the human kallikrein gene family - genomic
RT characterization, mapping, tissue expression and hormonal
RT regulation.";
RL Gene 254:119-128(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepier B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J.,
RA Wallbrandt P., Egelrud T.;
RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
RT mice; a model for chronic itchy dermatitis.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
RC AND TISSUE SPECIFICITY.
RX TISSUE=Ovarian carcinoma;
RA MEDLINE=22623266; PubMed=12738725;
RD Dong Y., Kaushal A., Brattesand M., Nicklin J., Clements J.A.;
RT "Differential splicing of KLKS and KLK7 in epithelial ovarian cancer
RT produces novel variants with potential as cancer biomarkers.";
RL Clin. Cancer Res. 9:1710-1720(2003).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=95314630; PubMed=7794273;
RA Skytt A., Stromqvist M., Egelrud T.;
RT "Primary substrate specificity of recombinant human stratum corneum
RT chymotryptic enzyme.";
RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
CC -!- FUNCTION: May catalyze the degradation of intercellular cohesive
CC structures in the cornified layer of the skin in the continuous
CC shedding of cells from the skin surface. Specific for amino acid
CC residues with aromatic side chains in the P1 position. SCCE
CC cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-
CC Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the
CC activation of precursors to inflammatory cytokines.

CC -!- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
CC also observed at the apical membrane and in cytoplasm at the
CC invasive front.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=P49862-1; Sequences=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=P49862-2; Sequences=VSP_013581;
CC -!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
CC expressed by keratinocytes in the epidermis. Also expressed in the
CC brain, mammary gland, cerebellum, spinal cord and kidney. Lower
CC levels in salivary glands, uterus, thymus, thyroid, placenta,
CC trachea and testis. Up-regulated in ovarian carcinoma, especially
CC late-stage serous carcinoma, compared with normal ovaries and
CC benign adenomas (at the protein level).
CC -!- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
CC cell line.
CC -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 1 peptidase S1 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; L33404; AAC37551.1; -; mRNA.
DR EMBL; AF166330; AAD49718.1; -; Genomic DNA.
DR EMBL; AF243527; AAG33360.1; -; Genomic DNA.
DR EMBL; AF332583; AAK69624.1; -; Genomic DNA.
DR EMBL; AF411214; AAN03662.1; -; mRNA.
DR EMBL; AF411215; AAN03663.1; -; mRNA.
DR EMBL; BC032005; AAH32005.1; -; mRNA.
DR PIR; A53968; A53968.
DR HSP; P00760; 1EZX.
DR MEROPS; S01.300; -.
DR Ensembl; ENSG00000169035; Homo sapiens.
DR HGNC; HGNC:6368; KLK7.
DR H-InvDB; HIX0015373; -.
DR MIM; 604438; -.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR GO; GO:0008544; P:epidermis development; TAS.
DR InterPro; IPR001354; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Alternative splicing; Direct protein sequencing; Glycoprotein;
KW Hydroxylase; Peptidase; Serine protease; Signal; Zymogen.
FT SIGNAL 1 22
FT PROPEP 23 29 Activation peptide.
FT CHAIN 30 253 Kallikrein 7.
FT DOMAIN 30 250 Peptidase S1.
FT ACT_SITE 70 70 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 205 205 Charge relay system (By similarity).
FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 /FTId=VSP_013581.
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A68 CRC64; C -> W (in Ref. 6; AAH32005).


```
Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
DB 6 LLPLQILL 14

RESULT 3
ID Q8VCA9_MOUSE PRELIMINARY; PRT; 73 AA.
AC Q8VCA9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSSP; P18203; 1FKL.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PP1ASE.
DR Pfam; PF00254; FKBP_C; 1.
DR PROSITE; PS50059; FKBP_PP1ASE; 1.
SQ SEQUENCE 73 AA; 7819 MW; 938F5339BF3C11 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 73;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
DB 7 LLPLQILL 15

RESULT 4
ID Q8RSD6_MOUSE PRELIMINARY; PRT; 104 AA.
AC Q8RSD6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
```

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DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Casavant R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSSP; P18203; 1FKL.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PP1ASE.
DR Pfam; PF00254; FKBP_C; 1.
DR PROSITE; PS50059; FKBP_PP1ASE; 1.
SQ SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match 95.0%; Score 38; DB 2; Length 104;
Best Local Similarity 88.9%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
DB 7 LLPLQILL 15

RESULT 5
ID Q6PKE2_MOUSE PRELIMINARY; PRT; 138 AA.
AC Q6PKE2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.;
RA Strausberg R.J. to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002311; AAH02311.1; -; mRNA.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C1_PPIase.
DR PROSITE; PS5059; FKBP_PPIASE; 1.
SQ SEQUENCE 138 AA; 15105 MW; C138B8B0EFD59D CRC64;

Query Match 95.0%; Score 38; DB 2; Length 138;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLLLL 9
Db 7 LLPLQLLLL 15

RESULT 6
FKB11 MOUSE STANDARD; PRT; 201 AA.
AC Q9DIM7; O9CRE4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
DE trans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
DE (FKBP-19).
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

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DR PROSITE; PS00059; FKBP_PP1ASE; 1.
 KW isomerase; Rotamase; Signal. Potential.
 FT SIGNAL 1 27
 FT CHAIN 28 201 FK506 FKBP-type.
 FT DOMAIN 57 144
 FT CONFLICT 53 53 S -> F (in Ref. 1; BAB31559).
 FT CONFLICT 198 198 S -> R (in Ref. 1; BAB31559).
 SQ SEQUENCE 201 AA; 94D955C57264BD82 CRC64;
 Query Match 95.0%; Score 38; DB 1; Length 201;
 Best Local Similarity 88.9%; Pred. No. 36;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 DB 7 LLPLQLLLL 15
 RESULT 7
 INHA_TRIVU STANDARD; PRT; 361 AA.
 ID INHA_TRIVU
 AC 07755;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Inhibin alpha chain precursor.
 GN Name=INHA;
 OS Trichosurus vulpecula (Brush-tailed possum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 OX NCBI_TaxID=9337;
 RN [1]
 RP MEDLINE=99027340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
 RA Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tiedall D.J.,
 Greenwood P.J., McNatty K.;
 RT "cDNA sequence analysis, Gene expression and protein localisation of
 the inhibin alpha subunit of Australian brushtail possum (Trichosurus
 vulpecula).";
 RL J. Mol. Endocrinol. 21:141-152(1998).
 CC -!- FUNCTION: Inhibins and activins inhibit and activate,
 respectively, the secretion of follitropin by the pituitary gland.
 CC Inhibins/activins are involved in regulating a number of diverse
 CC functions such as hypothalamic and pituitary hormone secretion,
 CC gonadal hormone secretion, germ cell development and maturation,
 CC erythroid differentiation, insulin secretion, nerve cell survival,
 CC embryonic axial development or bone growth, depending on their
 CC subunit composition. Inhibins appear to oppose the functions of
 CC activins.
 CC -!- SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin A
 CC is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
 CC beta-B.
 CC -!- PTM: Proteolytic processing yields a number of bioactive forms,
 CC consisting either solely of the mature alpha chain, of the most N-
 CC terminal propeptide linked through a disulfide bond to the mature
 CC alpha chain, or of the entire proprotein.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF033340; AAC63945.1; -; mRNA.
 DR GO; GO:0005576; C:extracellular region; ISS.
 DR GO; GO:0017106; F:activin inhibitor activity; ISS.
 DR GO; GO:0005125; F:cytokine activity; ISS.
 DR GO; GO:0008083; F:growth factor activity; ISS.
 DR GO; GO:0005179; F:hormone activity; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0007050; P:cell cycle arrest; ISS.
 DR GO; GO:0030154; P:cell differentiation; ISS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . ; ISS.
 DR GO; GO:0007267; P:cell-cell signaling; ISS.
 DR GO; GO:0030218; P:erythrocyte differentiation; ISS.
 DR GO; GO:0042541; P:hemoglobin biosynthesis; ISS.
 DR GO; GO:0006917; P:induction of apoptosis; ISS.
 DR GO; GO:0045578; P:negative regulation of B cell differentiation; ISS.
 DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.
 DR GO; GO:0046882; P:negative regulation of follicle-stimulating. . ; ISS.
 DR GO; GO:0045077; P:negative regulation of interferon-gamma bio. . ; ISS.
 DR GO; GO:0045650; P:negative regulation of macrophage different. . ; ISS.
 DR GO; GO:0042326; P:negative regulation of phosphorylation; ISS.
 DR GO; GO:0007399; P:neurogenesis; ISS.
 DR GO; GO:0001541; P:ovarian follicle development; ISS.
 DR GO; GO:0046881; P:positive regulation of follicle-stimulating. . ; ISS.
 DR InterPro; IPR002405; Inhibin_alpha.
 DR InterPro; IPR001839; TGFB.
 DR Pfam; PF00019; TGF_beta; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR PRODOM; PD000357; TGFB; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein; Growth factor; Hormone; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 64
 FT PROPEP 65 230
 FT CHAIN 231 361
 FT SITE 64 65
 FT SITE 230 231
 FT CARBOHYD 48 48
 FT CARBOHYD 144 144
 FT CARBOHYD 266 266
 FT DISULFID 260 323
 FT DISULFID 289 358
 FT DISULFID 293 360
 FT DISULFID 322 360
 SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDAAB7D CRC64;
 Query Match 95.0%; Score 38; DB 1; Length 361;
 Best Local Similarity 88.9%; Pred. No. 63;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LLPLQLLLL 9
 DB 5 LLPLQLLLL 13
 RESULT 8
 Q75E55_ASHGO
 ID Q75E55_ASHGO PRELIMINARY; PRT; 552 AA.
 AC Q75E55;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ABL185CP.
 GN Name=ABL185C;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 Mohr C., Pöhlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
 Gaffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."; Science 304:304-307(2004).
 RL EMBL; AE016815; AAS50586.1; -; Genomic_DNA.
 DR AGD; ABL185C; -;
 DR InterPro; IPR005599; Alg9_trans.

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DR InterPro: IPR001202; WW_Rep5_WWP.
DR Pfam: PF03901; Glyco_transf_22; 1.
DR PROSITE: PS01159; WW_DOMAIN_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 552 AA; 62708 MW; 62A98842023DEEA04 CRC64;

Query Match          92.5%; Score 37; DB 2; Length 552;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
   |:|:|:|
Db 67 LMPQLVLL 75

RESULT 9
QAXN42 PLACH PRELIMINARY; PRT; 71 AA.
AC QAXN42.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
DE ORFNames=PC108599.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Christopher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01004512; CAH81670.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8015 MW; 5176BF698D94CAC2 CRC64;

Query Match          90.0%; Score 36; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQLILL 9
   |:|:|:|
Db 7 LPLQLILL 14

RESULT 10
Q8VB59 WSSV PRELIMINARY; PRT; 79 AA.
AC Q8VB59;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Wsv132 (WSSV187).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
OX NCBI_TaxID=92652;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21548311; PubMed=11689662;
RX DOI=10.1128/JVI.75.23.11811-11820.2001;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
virus.";
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RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332093; AAL33136.1; -; Genomic DNA.
DR EMBL; AF440570; AAL89055.1; -; Genomic DNA.
SQ SEQUENCE 79 AA; 9287 MW; 800910C7FFA0BC7E CRC64;

Query Match 90.0%; Score 36; DB 2; Length 79;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
Db 34 LPLQLILL 42

RESULT 11
Q7RQ54 PLAYO
ID Q7RQ54 PLAYO PRELIMINARY; PRT; 637 AA.
AC Q7RQ54;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE MCN3/saliva family, putative.
GN Name=PY01249;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22555706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluoia S.V., Suh B.B., Koolij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Fraiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000328; EAA20540.1; -; Genomic DNA.
DR GO; GO:0016020; C-membrane; IEA.
DR InterPro; IPR004316; Mtn3_slv.
DR PANTHER; PTHR10791; Mtn3_slv; 1.
DR Pfam; PF03083; Mtn3_slv; 2.
SQ SEQUENCE 637 AA; 70992 MW; BC506320B2AE1FE5 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQLILL 9
Db 7 LPLQLILL 14

RESULT 12
Q97H76 CLOAB
ID Q97H76 CLOAB PRELIMINARY; PRT; 845 AA.
AC Q97H76;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cation transport P-type ATPase.
GN OrderedLocusNames=CA2137;
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

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OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RX DOI=10.1128/JB.183.16.4823-4838.2001;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007714; AAK80095.1; -; Genomic DNA.
DR PIR; D97163; D97163.
DR HSP; P04191; 1SU4.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0015662; F-ATPase activity; coupled to transmembrane m. .; IEA.
DR GO; GO:0003824; F-catalytic activity; IEA.
DR GO; GO:0016820; F-hydrolase activity; IEA.
DR GO; GO:0006812; P-cation transport; IEA.
DR GO; GO:0008152; P-metabolism; IEA.
DR GO; GO:0015992; P-proton transport; IEA.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_Like_hydro.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR InterPro; IPR000695; H_ATPase_C.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00120; HATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 3.
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 845 AA; 93779 MW; 401293AA1PF9D757 CRC64;

Query Match 90.0%; Score 36; DB 2; Length 845;
Best Local Similarity 77.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLILL 9
Db 670 LPLQLILL 678

RESULT 13
Q5FMG7 LACAC
ID Q5FMG7 LACAC PRELIMINARY; PRT; 887 AA.
AC Q5FMG7;
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Cation transporter P-ATPase (EC 3.6.1.-).
GN OrderedLocusNames=LBA0212;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCFM;
RX PubMed=15671160; DOI=10.1073/pnas.0409188102;
RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAuliffe O., Southern N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
RT Lactobacillus acidophilus NCFM.";

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RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
DR EMBL; CP000033; RAV42107.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . .; IEA.
DR GO; GO:0015444; F:magnesium-importing ATPase activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0015693; P:magnesium ion transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR006415; ATPase-IIIB_Mg.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR InterPro; IPR000695; H_ATPase.
DR Pfam; PF00122; E1-E2_ATPase_N; 1.
DR Pfam; PF00702; HydroLase; 1.
DR PRINTS; PRO0119; HATPASE.
DR PRINTS; PRO0120; HATPASE.
DR TIGRFAMs; TIGR01524; ATPase-IIIB_Mg; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 1.
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
KW Complete proteome; HydroLase.
SQ SEQUENCE 887 AA; 99091 MW; 9071A032A09BE9CE CRC64;

Query Match 90.0%; Score 36; DB 2; Length 887;
Best Local Similarity 77.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||:|:
Db 708 LLPLQLLIL 716

RESULT 14
Q6NB96 RHOPA
ID Q6NB96 RHOPA PRELIMINARY; PRT; 181 AA.
AC Q6NB96;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RP0932;
OS Rhodopseudomonas palustris.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Rhodopseudomonas.
OX NCBI_TaxID=1076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CGA009 / ATCC BAA-98;
RX PubMed=14704707; DOI=10.1038/nbt923;
RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Maltatti S., Do L.,
RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Peres C.,
RA Gibson J.L., Hanson T.E., Robst C., Torres y Torres J.L., Peres C.,
RA Harrison F.H., Gibson J., Harwood C.S.;
RT "Complete genome sequence of the metabolically versatile
RT photosynthetic bacterium Rhodopseudomonas palustris.";
RL Nat. Biotechnol. 22:55-61(2004).
DR EMBL; BX572595; CAE26376.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 181 AA; 19632 MW; CDB44D8210E565D1 CRC64;

Query Match 87.5%; Score 35; DB 2; Length 181;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 8
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Db 24 LLPLQVLL 31

RESULT 15
Q8MZ20 HELAU
ID Q8MZ20 HELAU PRELIMINARY; PRT; 183 AA.
AC Q8MZ20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acyl-CoA desaturase HaasPPAE (Fragment).
OS Helicoverpa assulta (Oriental tobacco budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=52344;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22412134; PubMed=12524345;
RA Knipple D.C., Rosenfield C.L., Nielsen R., You K.M., Jeong S.E.;
RT "Evolution of the integral membrane desaturase gene family in moths
RT and flies";
RL Genetics 162:1737-1752(2002).
DR EMBL; AF482910; AAM28485.1; -; mRNA.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0036491; F:oxidoreductase activity; IEA.
DR GO; GO:0004768; F:stearyl-CoA 9-desaturase activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001522; Desaturase.
DR InterPro; IPR005804; Fa_desat.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00487; FA_desaturase; 1.
DR PRINTS; PR00075; FACDDSATRASE.
DR PRINTS; PR00024; HOMBOBOX.
KW Fatty acid biosynthesis; Iron; Lipid synthesis; Oxidoreductase;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 183
SQ SEQUENCE 183 AA; 21196 MW; 728DA94FAFCD14FA CRC64;
Query Match 87.5%; Score 35; DB 2; Length 183;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQILL 9
|||:|:
Db 14 LPLQVLL 21

Search completed: March 11, 2006, 00:38:48
Job time : 98.3333 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LLPLQILL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/6 COMB.pap.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pap.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pap.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	2	US-09-502-600-35
2	40	100.0	9	2	US-09-918-243-35
3	40	100.0	253	1	US-08-557-146-2
4	40	100.0	253	1	US-08-824-874-3
5	40	100.0	253	1	US-09-154-344-2
6	40	100.0	253	2	US-08-930-188-2
7	40	100.0	253	2	US-09-210-084-3
8	40	100.0	253	2	US-09-764-762-3
9	40	100.0	253	4	PCT-US96-04294-2
10	40	100.0	253	2	US-09-949-016-7716
11	36	90.0	9	2	US-09-502-600-33
12	36	90.0	9	2	US-09-918-243-33
13	34	85.0	73	2	US-09-205-258-1083
14	34	85.0	73	2	US-10-004-860-1083
15	34	85.0	302	2	US-09-393-634-37
16	34	85.0	424	2	US-09-205-258-1079
17	34	85.0	424	2	US-10-004-860-1079
18	34	85.0	569	2	US-09-252-991A-22870
19	34	85.0	812	2	US-09-489-039A-12075
20	33	82.5	180	2	US-09-270-767-42872
21	33	82.5	190	1	US-08-339-152A-19
22	33	82.5	190	1	US-08-007-999B-6
23	33	82.5	190	1	US-08-689-276A-6
24	33	82.5	201	2	US-09-919-039-311
25	33	82.5	201	2	US-09-591-181-99
26	33	82.5	201	2	US-09-929-769-5
27	33	82.5	201	2	US-09-990-444-99

28 33 82.5 201 2 US-09-997-333-99 Sequence 99, Appl
29 33 82.5 201 2 US-09-992-598-99 Sequence 99, Appl
30 33 82.5 232 1 US-08-956-047-36 Sequence 36, Appl
31 33 82.5 634 1 US-08-339-152A-17 Sequence 17, Appl
32 33 82.5 653 1 US-08-339-152A-16 Sequence 16, Appl
33 33 82.5 653 1 US-08-007-999B-3 Sequence 3, Appl
34 33 82.5 653 1 US-08-689-276A-3 Sequence 3, Appl
35 33 82.5 2787 2 US-09-245-041-15 Sequence 15, Appl
36 33 82.5 2787 2 US-09-358-055B-15 Sequence 15, Appl
37 33 82.5 2787 2 US-09-893-238-15 Sequence 36, Appl
38 32 80.0 9 2 US-09-502-600-36 Sequence 36, Appl
39 32 80.0 9 2 US-09-918-243-36 Sequence 28, Appl
40 32 80.0 12 2 US-09-502-600-28 Sequence 28, Appl
41 32 80.0 12 2 US-09-918-243-28 Sequence 28, Appl
42 32 80.0 91 2 US-09-605-703B-1574 Sequence 1574, A
43 32 80.0 135 2 US-09-270-767-37619 Sequence 37619, A
44 32 80.0 135 2 US-09-270-767-52836 Sequence 52836, A
45 32 80.0 142 2 US-09-248-796A-21399 Sequence 21399, A

ALIGNMENTS

RESULT 1
US-09-502-600-35
; Sequence 35, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-502-600-35

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||
Db 1 LLPLQILL 9

RESULT 2
US-09-918-243-35
; Sequence 35, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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;
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35

Query Match      100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
Db 1 LLPLQILL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
```

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sturner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 6 LLPLQLILL 14

RESULT 6

US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/930,188
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9219
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 6 LLPLQLILL 14

RESULT 7

US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLILL 9
DB 6 LLPLQLILL 14

RESULT 8

US-09-764-762-3
Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
;/ STREET: 3174 Porter Drive
;/ CITY: Palo Alto
;/ STATE: CA
;/ COUNTRY: USA
;/ ZIP: 94304
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: DOS
;/ SOFTWARE: FastSeq for Windows Version 2.0
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/764,762
;/ FILING DATE: 16-Jan-2001
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 09/210,084
;/ FILING DATE: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Billings, Lucy J.
;/ REGISTRATION NUMBER: 36,749
;/ REFERENCE/DOCKET NUMBER: PF-0252 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-855-0555
;/ TELEFAX: 415-845-4166
;/ INFORMATION FOR SEQ ID NO: 3:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 253 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ IMMEDIATE SOURCE:
;/ LIBRARY: GenBank
;/ CLONE: 532504
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 9
PCT-US96-04294-2
;/ Sequence 2, Application PC/TUS9604294
;/ GENERAL INFORMATION:
;/ APPLICANT: Dixon, Eric P.
;/ APPLICANT: Johnstone, Edward M.
;/ APPLICANT: Little, Sheila P.
;/ TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
;/ TITLE OF INVENTION: RELATED NUCLEIC ACIDS
;/ NUMBER OF SEQUENCES: 3
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Eli Lilly and Company
;/ STREET: Lilly Corporate Center
;/ CITY: Indianapolis
;/ STATE: Indiana
;/ COUNTRY: United States of America
;/ ZIP: 46285
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US96/04294
;/ FILING DATE:
;/ CLASSIFICATION:

;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/416,257
;/ FILING DATE: 04-APR-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Blalock, Donna K.
;/ REGISTRATION NUMBER: 38,082
;/ REFERENCE/DOCKET NUMBER: X9239
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 317-277-1090
;/ TELEFAX: 317-276-3861
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 253 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
PCT-US96-04294-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 10
US-09-949-016-7716
;/ Sequence 7716, Application US/09949016
;/ Patent No. 6812339
;/ GENERAL INFORMATION:
;/ APPLICANT: VENTER, J. Craig et al.
;/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;/ FILE REFERENCE: CL001307
;/ CURRENT APPLICATION NUMBER: US/09/949,016
;/ CURRENT FILING DATE: 2000-04-14
;/ PRIOR APPLICATION NUMBER: 60/241,755
;/ PRIOR FILING DATE: 2000-10-20
;/ PRIOR APPLICATION NUMBER: 60/237,768
;/ PRIOR FILING DATE: 2000-10-03
;/ PRIOR APPLICATION NUMBER: 60/231,498
;/ PRIOR FILING DATE: 2000-09-08
;/ NUMBER OF SEQ ID NOS: 207012
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 7716
;/ LENGTH: 265
;/ TYPE: PRT
;/ ORGANISM: Human
US-09-949-016-7716

Query Match 100.0%; Score 40; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
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Db 18 LLPLQILL 26

RESULT 11
US-09-502-600-33
;/ Sequence 33, Application US/09502600A
;/ Patent No. 6294344
;/ GENERAL INFORMATION:
;/ APPLICANT: O'Brien, Timothy J.
;/ TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
;/ TITLE OF INVENTION: Ovarian Cancer
;/ FILE REFERENCE: D6223CIP-C
;/ CURRENT FILING DATE: 2000-02-11
;/ CURRENT APPLICATION NUMBER: US/09/502,600A

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; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-502-600-33

Query Match          90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 8
Db 2 LLPLQILL 9

RESULT 12
US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match          90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 8
Db 2 LLPLQILL 9

RESULT 13
US-09-205-258-1083
; Sequence 1083, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
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; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1083
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; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1083

Query Match 85.0%; Score 34; DB 2; Length 73;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQLLLL 9
|||:|
DB 25 LPLQLLLL 32

RESULT 14
US-10-004-860-1083
; Sequence 1083, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1083
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-1083

Query Match 85.0%; Score 34; DB 2; Length 73;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPLQLLLL 9
|||:|
DB 25 LPLQLLLL 32

RESULT 15
US-09-393-634-37
; Sequence 37, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 302
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR02
; NAME/KEY: MOD_RES
; LOCATION: (143)
; OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-37

Query Match 85.0%; Score 34; DB 2; Length 302;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLQLLLL 9
|:|:|
DB 42 LMPIQLLL 50

Search completed: March 11, 2006, 01:24:26
Job time : 22.2222 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-35

Perfect score: 40

Sequence: 1 LLPLQLLLL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	40	100.0	9	3	US-09-918-243-35
2	40	100.0	9	3	US-09-905-083-35
3	40	100.0	9	4	US-10-372-521-35
4	40	100.0	9	5	US-10-831-075-35
5	40	100.0	136	5	US-10-450-763-53737
6	40	100.0	198	4	US-10-262-511-96
7	40	100.0	250	4	US-10-262-511-92
8	40	100.0	253	3	US-09-888-615-98
9	40	100.0	253	3	US-09-764-762-3
10	40	100.0	253	4	US-10-071-214-2
11	40	100.0	253	4	US-10-071-214-48
12	40	100.0	253	4	US-10-264-283-90
13	40	100.0	253	4	US-10-295-027-498
14	40	100.0	253	4	US-10-173-999-48
15	40	100.0	253	4	US-10-408-765A-639
16	40	100.0	253	5	US-10-643-795A-95
17	40	100.0	253	5	US-10-948-518-95
18	40	100.0	253	5	US-10-868-490A-1
19	40	100.0	257	4	US-10-344-394-38
20	38	95.0	229	4	US-10-425-115-227327
21	36	90.0	9	3	US-09-918-243-33
22	36	90.0	9	3	US-09-905-083-33
23	36	90.0	9	4	US-10-372-521-33
24	36	90.0	9	5	US-10-831-075-33
25	36	90.0	70	4	US-10-424-599-207950
26	36	90.0	637	5	US-10-732-923-928
27	36	90.0	845	4	US-10-282-122A-51875

28 36 90.0 868 4 US-10-369-493-10355 Sequence 10255, A
29 35 87.5 23 3 US-09-864-761-46097 Sequence 46097, A
30 35 87.5 58 4 US-10-424-599-234176 Sequence 234176, A
31 35 87.5 215 4 US-10-425-115-284316 Sequence 284316, A
32 35 87.5 305 4 US-10-335-977-6098 Sequence 6098, A
33 35 87.5 306 4 US-10-335-977-6097 Sequence 6097, A
34 35 87.5 329 4 US-10-335-977-6099 Sequence 6099, A
35 35 87.5 477 4 US-10-335-977-6100 Sequence 6100, A
36 35 87.5 477 4 US-10-335-977-6101 Sequence 6101, A
37 35 87.5 480 3 US-09-895-913A-92 Sequence 92, Appl
38 35 87.5 637 4 US-10-425-114-70206 Sequence 70206, A
39 35 87.5 637 4 US-10-425-115-294490 Sequence 294490, A
40 35 87.5 1498 4 US-10-437-963-121544 Sequence 121544, A
41 34 85.0 61 4 US-10-425-115-218429 Sequence 218429, A
42 34 85.0 70 4 US-10-097-065-220 Sequence 220, App
43 34 85.0 70 4 US-10-372-876-220 Sequence 220, App
44 34 85.0 73 3 US-09-933-767-1083 Sequence 1083, A
45 34 85.0 73 4 US-10-004-860-1083 Sequence 1083, A

ALIGNMENTS

RESULT 1

US-09-918-243-35

; Sequence 35, Application US/09918243

; Patent No. US20020142317A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 35

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 6-14 of the SCCE protein

US-09-918-243-35

Query Match 100.0%; Score 40; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLLLL 9

Db 1 LLPLQLLLL 9

RESULT 2

US-09-905-083-35

; Sequence 35, Application US/09905083

; Patent No. US20020146708A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP/C/Div

; CURRENT APPLICATION NUMBER: US/09/905,083

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 09/502,600

; PRIOR FILING DATE: 2000-02-11

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 35

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-905-083-35

Query Match 100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||
Db 1 LLPLQILL 9

RESULT 3
US-10-372-521-35
; Sequence 35, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-10-372-521-35

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||
Db 1 LLPLQILL 9

RESULT 4
US-10-831-075-35
; Sequence 35, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-10-831-075-35

Query Match 100.0%; Score 40; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||
Db 1 LLPLQILL 9

RESULT 5
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match 100.0%; Score 40; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
|||
Db 12 LLPLQILL 20

RESULT 6
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.

APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michelle L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 96
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 40; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 7
US-10-262-511-92
Sequence 92, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana

APPLICANT: Gorman, Linda
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michelle L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 92
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-92

Query Match 100.0%; Score 40; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILL 9
Db 3 LLPLQILL 11

RESULT 8
US-09-888-615-98
Sequence 98, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEL, SEAN
APPLICANT: CHARIDCZAK, GLEN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26

; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 9

US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 10

US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 11

US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
US-10-071-214-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14

RESULT 12

US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US2003014494A1

GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 13
US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 14
US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US2004000563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 6 LLPLQILLL 14

RESULT 15
US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US2004010187A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
|||
Db 6 LLPLQILL 14
|||

Search completed: March 11, 2006, 01:37:23
Job time : 69.4444 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-35
Perfect score: 40
Sequence: 1 LLPQLLLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	253	6	US-10-412-748-11
2	40	100.0	253	6	US-10-412-748-14
3	40	100.0	253	6	US-10-412-748-17
4	40	100.0	253	7	US-11-037-243-98
5	33	82.5	146	7	US-11-000-463-881
6	33	82.5	181	7	US-11-000-463-409
7	33	82.5	213	7	US-11-087-099-8768
8	32	80.0	71	7	US-11-096-568A-27354
9	32	80.0	71	7	US-11-096-568A-27391
10	32	80.0	85	7	US-11-096-568A-27353
11	32	80.0	85	7	US-11-096-568A-27390
12	32	80.0	1302	6	US-10-395-561-1024
13	31	77.5	93	7	US-11-230-180-12
14	31	77.5	140	6	US-10-821-234-1347
15	31	77.5	213	7	US-11-203-251A-93
16	31	77.5	278	6	US-10-131-826A-136
17	31	77.5	278	6	US-10-973-115B-136
18	31	77.5	328	6	US-10-501-035-268
19	31	77.5	328	7	US-11-169-041-227
20	31	77.5	328	7	US-11-072-175-232
21	31	77.5	461	6	US-10-878-556A-162
22	31	77.5	465	6	US-10-793-626-1676
23	31	77.5	469	6	US-10-821-234-1151
24	31	77.5	480	6	US-10-821-234-1465
25	31	77.5	498	7	US-11-051-720-1355

26	31	77.5	499	6	US-10-508-263-94	Sequence 94, Appl
27	31	77.5	505	7	US-11-051-720-1357	Sequence 1357, Ap
28	31	77.5	519	7	US-11-051-720-1350	Sequence 1350, Ap
29	31	77.5	541	7	US-11-051-720-1351	Sequence 1351, Ap
30	31	77.5	541	7	US-11-096-568A-20889	Sequence 20889, A
31	31	77.5	544	7	US-11-051-720-1352	Sequence 1352, Ap
32	31	77.5	588	7	US-11-051-720-1356	Sequence 1356, Ap
33	31	77.5	597	7	US-11-051-720-1354	Sequence 1354, Ap
34	31	77.5	619	7	US-11-051-720-1353	Sequence 1353, Ap
35	31	77.5	650	7	US-11-051-720-1439	Sequence 1439, Ap
36	30	75.0	256	7	US-11-072-512-3255	Sequence 3255, Ap
37	30	75.0	434	7	US-11-087-099-2216	Sequence 2216, Ap
38	30	75.0	478	7	US-11-092-353-4	Sequence 4, Appl
39	30	75.0	544	7	US-11-245-400-7	Sequence 7, Appl
40	30	75.0	558	7	US-11-096-568A-26217	Sequence 26217, A
41	29	72.5	125	7	US-11-096-568A-23862	Sequence 23862, A
42	29	72.5	184	7	US-11-096-568A-5642	Sequence 5642, Ap
43	29	72.5	239	7	US-11-096-568A-5641	Sequence 5641, Ap
44	29	72.5	264	7	US-11-096-568A-5640	Sequence 5640, Ap
45	29	72.5	349	7	US-11-096-568A-14701	Sequence 14701, A

ALIGNMENTS

RESULT 1
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LLPLQLLLL	9
Db	6	LLPLQLLLL	14

RESULT 2
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; TYPE: PRT

```
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 4
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LLPLQILL 9
Db 6 LLPLQILL 14

RESULT 5
US-11-000-463-881
; Sequence 881, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 78SCIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 881
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-881

Query Match      82.5%; Score 33; DB 7; Length 146;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLPLQILL 9
Db 7 LLPLHLLL 15

RESULT 6
US-11-000-463-409
; Sequence 409, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
```

FILE REFERENCE: 785CIP4CN
CURRENT APPLICATION NUMBER: US/11/000,463
PRIOR FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: PastSeq for Windows Version 3.0
SEQ ID NO 409
LENGTH: 181
TYPE: PRT
ORGANISM: Homo sapiens
US-11-000-463-409

Query Match 82.5%; Score 33; DB 7; Length 181;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQLLL 9
||| :|||
Db 7 LLPLHLLL 15

RESULT 7

US-11-087-099-8768
Sequence 8768, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 8768
LENGTH: 213
TYPE: PRT
ORGANISM: Zea mays
US-11-087-099-8768

Query Match 82.5%; Score 33; DB 7; Length 213;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQLLL 9
||| :|||
Db 39 LLPLSLLL 47

RESULT 8

US-11-096-568A-27354
Sequence 27354, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27354

LENGTH: 71
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(71)
OTHER INFORMATION: Ceres Seq. ID no. 5677704
US-11-096-568A-27354

Query Match 80.0%; Score 32; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLL 7
||| :|||
Db 2 LLPLQLL 8

RESULT 9

US-11-096-568A-27391
Sequence 27391, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27391
LENGTH: 71
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(71)
OTHER INFORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391

Query Match 80.0%; Score 32; DB 7; Length 71;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQLL 7
||| :|||
Db 2 LLPLQLL 8

RESULT 10

US-11-096-568A-27353
Sequence 27353, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27353
LENGTH: 85
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(85)
OTHER INFORMATION: Ceres Seq. ID no. 5677703
US-11-096-568A-27353

Query Match 80.0%; Score 32; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 16;

```
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIL 7
Db 16 LLPLQIL 22

RESULT 11
US-11-096-568A-27390
; Sequence 27390, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27390
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)-(85)
; OTHER INFORMATION: Ceres Seq. ID no. 13500183
US-11-096-568A-27390

Query Match 80.0%; Score 32; DB 7; Length 85;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLPLQIL 7
Db 16 LLPLQIL 22

RESULT 12
US-10-995-561-1024
; Sequence 1024, Application US/10995561
; Publication No. US2005072054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1024
; LENGTH: 1302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1024

Query Match 80.0%; Score 32; DB 6; Length 1302;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 13 LLPLPLLL 21

RESULT 13
US-11-230-180-12
; Sequence 12, Application US/11230180
; Publication No. US20060035263A1
; GENERAL INFORMATION:
; APPLICANT: Woolf, Clifford J.
```

```
; APPLICANT: Samad, Tarek A.
; TITLE OF INVENTION: DRG11-RESPONSIVE (DRAGON) GENE FAMILY
; FILE REFERENCE: 00786/419002
; CURRENT APPLICATION NUMBER: US/11/230,180
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: US/10/419,296
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/373,519
; PRIOR FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-230-180-12

Query Match 77.5%; Score 31; DB 7; Length 93;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 9 LLPLLLLL 17

RESULT 14
US-10-821-234-1347
; Sequence 1347, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pf Seq_genes Version 1.0
; SEQ ID NO 1347
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1347

Query Match 77.5%; Score 31; DB 6; Length 140;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLPLQILLL 9
Db 88 LLPPQLLL 96

RESULT 15
US-11-203-251A-93
; Sequence 93, Application US/11203251A
; Publication No. US20060039904A1
; GENERAL INFORMATION:
; APPLICANT: MedImmune Inc.
; TITLE OF INVENTION: EPH RECEPTOR FC VARIANTS WITH ENHANCED ANTIBODY DEPENDENT
; TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY
; FILE REFERENCE: AE702US
; CURRENT APPLICATION NUMBER: US/11/203,251A
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: 60/601,634
; PRIOR FILING DATE: 2004-08-16
```

```
; PRIOR APPLICATION NUMBER: 60/608,852
; PRIOR FILING DATE: 2004-09-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-203-251A-93
```

```
Query Match      77.5%; Score 31; DB 7; Length 213;
Best Local Similarity 77.8%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 LLPLQLILL 9
      ||| :|||
Db      8 LLPLLLLLL 16
```

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Job time : 8 secs
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	4 AAE08241	Aae08241 Human str
2	40	100.0	9	8 ADR68797	Adr68797 Human str
3	40	100.0	136	4 ABG23378	Abg23378 Novel hum
4	40	100.0	198	6 ADA05736	Ada05736 Human NOV
5	40	100.0	198	8 ADN62900	Adn62900 Human NOV
6	40	100.0	250	6 ADA05732	Ada05732 Human NOV
7	40	100.0	250	8 ADN62896	Adn62896 Human NOV
8	40	100.0	253	2 AAW05383	Aaw05383 Human str
9	40	100.0	253	2 AAW05383	Aaw05383 Human amy
10	40	100.0	253	5 ABB84421	Abb84421 Human SCC
11	40	100.0	253	5 ABB84406	Abb84406 Human SCC
12	40	100.0	253	5 AAU82740	Aau82740 Amino aci
13	40	100.0	253	6 ABU07440	Abu07440 Protein d
14	40	100.0	253	6 ABU07471	Abu07471 Protein d
15	40	100.0	253	6 ABR58471	Abr58471 Human str
16	40	100.0	253	7 ADB80484	Adb80484 Ovarian c
17	40	100.0	253	7 ADJ68833	Adj68833 Human hea
18	40	100.0	253	7 ADN39180	Adn39180 Cancer/an
19	40	100.0	253	8 ADL06515	Adl06515 Human tum
20	40	100.0	253	8 ADN04182	Adn04182 Antipsori
21	40	100.0	253	8 ADR72880	Adr72880 Human ova
22	40	100.0	253	9 ADY67588	Ady67588 Human kal
23	40	100.0	253	9 AEC00353	Aec00353 Human kal
24	40	100.0	257	3 AAB21326	Aab21326 Human HSC

25	36	90.0	9	4 AAE08238	Aae08238 Human str
26	36	90.0	9	8 ADR68794	Adr68794 Human str
27	35	87.5	138	8 ADX90484	Adx90484 Plant ful
28	35	87.5	868	8 ADS21222	Ads21222 Bacterial
29	34	85.0	61	4 AAO12472	Aao12472 Human pol
30	34	85.0	812	7 ABO65558	Abo65558 Klebsiell
31	33	82.5	394	6 ABUI7803	Abui7803 Protein e
32	33	82.5	397	7 ADJ71036	Adj71036 Human hea
33	33	82.5	804	6 ABP70828	Abp70828 Murine C1
34	32	80.0	9	4 AAE08240	Aae08240 Human str
35	32	80.0	9	4 AAE08320	Aae08320 Human str
36	32	80.0	9	8 ADR68877	Adr68877 Human str
37	32	80.0	9	8 ADR68796	Adr68796 Human str
38	32	80.0	71	4 AAM89706	Aam89706 Human imm
39	32	80.0	73	4 ABG19347	Abg19347 Novel hum
40	32	80.0	78	8 ADL81901	Adl81901 P. aerugi
41	32	80.0	139	7 ADB65713	Adb65713 Human pro
42	32	80.0	196	7 ADJ92327	Adj92327 Mouse hai
43	32	80.0	267	2 AAW22303	Aaw22303 Rat CRTI.
44	32	80.0	267	8 ADL27274	Adl27274 Amino aci
45	32	80.0	282	7 ADD30604	Add30604 Plant yie

ALIGNMENTS

RESULT 1

AAE08241
ID AAE08241 standard; peptide; 9 AA.
XX
XX AAE08241;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #6 (residues 4-12).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
PN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
PP (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ;
XX
DR WPI; 2001-514676/56.
XX
PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
PS Claim 25; Page 103; 127pp; English.
XX
CC The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 2
ADR68797
ID ADR68797 standard; peptide; 9 AA.
XX
AC ADR68797;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:36.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
XX (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
XX WPI; 2004-653294/63.
DR
XX
XX Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
XX
PS Claim 5; SEQ ID NO 36; 117pp; English.
XX
XX The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
XX Sequence 9 AA;

Query Match 100.0%; Score 40; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS87565.
DR
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 136 AA;

Query Match 100.0%; Score 40; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 8.9; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 10 SLLPLQL 18

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX

AC ADA05736;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 XX Human NOV18c protein SEQ ID NO:96.
 XX
 XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO2003029424-A2.
 XX
 XX 10-APR-2003.
 XX
 XX 02-OCT-2002; 2002WO-U8031373.
 XX
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327517P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 12-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Smithson G., Millet I., Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerkush BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2003-381626/36.
 DR N-PSDB; ADA05735.
 XX
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; Page 170; 586pp; English.
 XX
 XX The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 CC and antilipaeamic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 198 AA;

Query Match 100.0%; Score 40; DB 6; Length 198;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
 Db 4 SLLPLQL 12

RESULT 5

ADN62900
 ID ADN62900 standard; protein; 198 AA.

XX ADN62900;

XX 01-JUL-2004 (first entry)

XX Human NOV18c.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.

OS Homo sapiens.

XX US2004038223-A1.

XX 26-FEB-2004.

XX 01-OCT-2002; 2002US-00262511.

XX 02-OCT-2001; 2001US-0326483P.

XX 05-OCT-2001; 2001US-0327435P.

XX 05-OCT-2001; 2001US-0327449P.

XX 09-OCT-2001; 2001US-0327917P.

XX 09-OCT-2001; 2001US-0328029P.

09-OCT-2001; 2001US-0328044P.
 09-OCT-2001; 2001US-0328056P.
 12-OCT-2001; 2001US-0328849P.
 15-OCT-2001; 2001US-0329414P.
 17-OCT-2001; 2001US-0330142P.
 18-OCT-2001; 2001US-0330309P.
 22-OCT-2001; 2001US-0341058P.
 24-OCT-2001; 2001US-0339266P.
 29-OCT-2001; 2001US-0343629P.
 29-OCT-2001; 2001US-0349575P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381038P.
 16-MAY-2002; 2002US-0381042P.
 17-MAY-2002; 2002US-0381542P.
 28-MAY-2002; 2002US-0383656P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 (SMIT/) SMITHSON G.
 (MILL/) MILLET I.
 (PEYM/) PEYMAN J A.
 (KEKU/) KEKUDA R.
 (JUUJ/) JU J.
 (LILL/) LI L.
 (GUOX/) GUO X.
 (PATT/) PATTURAJAN M.
 (SPYT/) SPYTEK K A.
 (EDIN/) EDINGER S R.
 (ELLE/) ELLERMAN K.
 (MALY/) MALYANKAR U M.
 (ORTT/) ORT T.
 (GORM/) GORMAN L.
 (ZERH/) ZERHUSEN B D.
 (ANDE/) ANDERSON D W.
 (ZHON/) ZHONG M.
 (CATT/) CATTERTON E.
 (JIWW/) JI W.
 (MILL/) MILLER C E.
 (RAST/) RASTELLI L.
 (STON/) STONE D J.
 (PENA/) PENA C E A.
 (SHEN/) SHENOY S G.
 (SHIM/) SHIMKETS R A.
 (ROTH/) ROTHENBERG M E.
 (LEAC/) LEACH M D.
 (AGEE/) AGEE M L.
 (BERG/) BERGHS C.
 (DIPI/) DIPIPO V A.
 (EISE/) EISEN A.
 (GANG/) GANGOLLI E A.
 (RIEG/) RIEGER D K.
 (SPAD/) SPADERNA S K.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malvankar UM;
 Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S G;
 Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 WPI: 2004-213931/20.
 N-PSDB; ADN62899.
 Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 40; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 Db 4 SLLPLQL 12
 RESULT 6
 ADA05732
 ID ADA05732 standard; protein; 250 AA.
 XX
 AC ADA05732;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18a protein SEQ ID NO:92.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.

PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ot T, Gorman L, Zerkushen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shimkete RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2003-381626/36.
 DR N-PSDB; ADA05731.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; Page 169-170; 586pp; English.
 XX
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
 CC and antilipemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's

CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 40; DB 6; Length 250;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SLLPLQIL 9
 Db 1 SLLPLQIL 9
 RESULT 7
 ADN62896
 ID ADN62896 standard; protein; 250 AA.
 XX
 AC ADN62896;
 XX
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV18a.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 01-OCT-2002; 2002US-00262511.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.

(PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPPIO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62895.
XX
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
XX Claim 1; SEQ ID NO 92; 395pp; English.
XX
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and

CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 40; DB 8; Length 250;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
DB 1 SLLPLQL 9
RESULT 8
AAR67888
ID AAR67888 standard; protein; 253 AA.
XX
AC AAR67888;
XX
XX 25-MAR-2003 (revised)
DT 09-AUG-1995 (first entry)
XX
XX Human stratum corneum chymotrophic recombinant enzyme (SCCE).
XX
XX Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
KW callosities; keratosis pilaris; ichthyoses; eczema.
XX
XX Homo sapiens.
XX
XX WO9500651-A1.
XX
XX 05-JAN-1995.
XX
XX 20-JUN-1994; 94WO-IB000166.
XX
XX 18-JUN-1993; 93DK-00000725.
XX
XX (SYMB-) SYMBICOM AB.
XX
XX Egelrud T, Hansson L;
XX
XX WPI; 1995-052088/07.
DR N-PSDB; AAQ81203.
XX
XX Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
PT related vectors, transformed cells and polypeptides, useful for treating
PT skin disorders, e.g. acne or psoriasis, and for identification of
PT specific inhibitors.
XX
XX Disclosure; Page 97; 137pp; English.
XX
XX The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
CC and skin care products, especially to treat and prevent acne, xeroderma,
CC or other hyperkeratotic conditions (e.g. callosities or keratosis
CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
CC recombinantly following mammal, insect, plant, or microorganism
CC transformation with plasmid pBS07. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX Sequence 253 AA;
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
DB 4 SLLPLQL 12
RESULT 9

```

AAW05383
ID AAW05383 standard; protein; 253 AA.
XX
XX AAW05383;
XX AC
XX 31-DEC-1996 (first entry)
XX DT
XX DE Human amyloid precursor protein protease.
XX
XX Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
XX KW therapy.
XX KW
XX OS Homo sapiens.
XX
XX WO9631122-A1.
XX PN
XX
XX 10-OCT-1996.
XX PD
XX 02-APR-1996; 96WO-US004294.
XX PF
XX 04-APR-1995; 95US-00416257.
XX PR
XX (ELIL ) LILLY & CO ELI.
XX PA
XX Dixon EP, Johnstone EM, Little SP;
XX PI
XX WPI; 1996-464694/46.
XX DR
XX N-PSDB; AAT39783.
XX DR
XX New isolated human amyloid precursor protein protease - used to develop
XX PT prods. for the treatment or diagnosis of associated conditions, esp.
XX PT Alzheimer's disease.
XX
XX Claim 1; Page 44-45; 55pp; English.
XX PS
XX
XX Human amyloid precursor protein protease (AAW05383) is involved in the
XX CC processing or clearance of amyloid precursor protein to form beta-amyloid
XX CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
XX CC obtd. from a human lung library. Recombinant protease can be produced in
XX CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
XX CC (partic. AV-120 host cells. It is used to develop products for the design
XX CC and testing of cpds. useful for treating or preventing conditions
XX CC associated with beta-amyloid peptide, esp. Alzheimer's disease
XX
XX Sequence 253 AA;
SQ
Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
Db 4 SLLPLQL 12
RESULT 10
ABB84421
ID ABB84421 standard; peptide; 253 AA.
XX
XX ABB84421;
XX AC
XX
XX 08-NOV-2002 (first entry)
XX DT
XX Human SCCE protein N-terminal fragment SEQ ID 48.
XX DE
XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
XX KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
XX KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
XX KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
XX Homo sapiens.
XX OS
XX WO200262135-A2.
XX PN
15-AUG-2002.
08-FEB-2002; 2002WO-IB001300.
09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
(EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
XX Egelrud T, Hansson L;
XX
XX WPI; 2002-643380/69.
XX
Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
XX Example 6; Page 37; 74pp; English.
XX
This invention describes a novel non-human transgenic mammal or mammalian
XX embryo having integrated within its genome, a heterologous nucleotide
XX sequence comprising at least a significant part of a nucleotide sequence
XX coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
XX operably linked to a promoter that drives expression of heterologous scce
XX or its variant in skin. The product of the invention is useful as a model
XX for the study of disease with the aim of improving treatment, to relieve
XX or ameliorate a pathogenic condition, for development or testing of a
XX cosmetic or a pharmaceutical formulation, and for the development of a
XX diagnostic method. It can also be used as a model for a skin disease or
XX skin cancer. The invention is also useful for screening or identifying a
XX compound or composition effective for the prevention or treatment of an
XX abnormal or unwanted phenotype, and for screening or identifying a
XX compound or composition effective for the prevention or treatment of
XX inflammatory skin diseases selected from diseases consisting of epidermal
XX hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
XX pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
XX with epidermal hyperkeratosis. The mammal of the invention is also useful
XX as a model for further studies of itch mechanisms and the testing of
XX potential compounds and compositions for relieve of various skin diseases
XX where itch is a component. This sequence represents the N-terminal
XX fragment of the human stratum corneum chymotryptic enzyme, SCCE
XX synonymous with human kallikrein 7 (KLK7), used in the development of the
XX transgenic mammals described in the invention
XX
XX Sequence 253 AA;
SQ
Query Match 100.0%; Score 40; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SLLPLQL 9
Db 4 SLLPLQL 12
RESULT 11
ABB84406
ID ABB84406 standard; protein; 253 AA.
XX
XX ABB84406;
XX AC
XX
XX 08-NOV-2002 (first entry)
XX DT
XX Human SCCE protein.
XX DE
XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
XX KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
XX KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
XX KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
XX Homo sapiens.
XX OS

```

XX WO200262135-A2.
 PN 15-AUG-2002.
 XX 08-FEB-2002; 2002WO-IB001300.
 XX 09-FEB-2001; 2001CA-02332655.
 PR 09-FEB-2001; 2001DK-00000218.
 XX (EGEL/) EGELRUD T.
 PA (HANS/) HANSSON L.
 XX Egelrud T, Hansson L;
 PI WPI; 2002-643380/69.
 DR N-PSDB; ABQ76226.
 XX Transgenic mammal or its embryo useful as model for human disease, has
 PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
 PT enzyme operably linked to promoter that drives its expression in skin.
 XX Claim 10; Page 58-59; 74pp; English.
 XX This invention describes a novel non-human transgenic mammal or mammalian
 CC embryo having integrated within its genome, a heterologous nucleotide
 CC sequence comprising at least a significant part of a nucleotide sequence
 CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
 CC operably linked to a promoter that drives expression of heterologous scce
 CC or its variant in skin. The product of the invention is useful as a model
 CC for the study of disease with the aim of improving treatment, to relieve
 CC or ameliorate a pathogenic condition, for development or testing of a
 CC cosmetic or a pharmaceutical formulation, and for the development of a
 CC diagnostic method. It can also be used as a model for a skin disease or
 CC skin cancer. The invention is also useful for screening or identifying a
 CC compound or composition effective for the prevention or treatment of an
 CC abnormal or unwanted phenotype, and for screening or identifying a
 CC compound or composition effective for the prevention or treatment of
 CC inflammatory skin diseases selected from diseases consisting of epidermal
 CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
 CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
 CC with epidermal hyperkeratosis. The mammal of the invention is also useful
 CC as a model for further studies of itch mechanisms and the testing of
 CC potential compounds and compositions for relieve of various skin diseases
 CC where itch is a component. This sequence represents the human stratum
 CC corneum chymotryptic enzyme, SCCE which is a serine protease synonymous
 CC with human kallikrein 7 (KLK7) and is used in the development of the
 CC transgenic mammals described in the invention
 XX Sequence 253 AA;
 SQ Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 Db |||||
 4 SLLPLQL 12
 RESULT 12
 AAU82740
 ID AAU82740 standard; protein; 253 AA.
 XX AAU82740;
 AC AAU82740;
 XX 23-APR-2002 (first entry)
 DT Amino acid sequence of novel human protease #39.
 DE Human; protease; cancer; immune-related disorder; cardiovascular disease;
 XX neuronal-associated disease; metabolic disorder; inflammatory disorder;
 KW nervous system disorder; sexual dysfunction; pain; mood disorder;
 XX

KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
 KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
 XX ocular disease; cytostatic; enzyme.
 OS Homo sapiens.
 XX WO200200860-A2.
 PN 03-JAN-2002.
 PD 26-JUN-2001; 2001WO-US020171.
 PF 26-JUN-2000; 2000US-0214047P.
 PR (SUGE-) SUGEN INC.
 XX Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
 XX Charyczak G;
 PI WPI; 2002-139913/18.
 DR N-PSDB; ABK31782.
 XX Nucleic acids encoding novel human proteases, useful for useful for
 PT treating diseases and disorders such as cancers, immune-related diseases
 PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
 PT disorders.
 XX Claim 6; Fig 2N; 313pp; English.
 XX The present invention relates to the isolation of novel human proteases,
 CC and the nucleic acids encoding them. The sequences of the invention are
 CC useful for treating diseases and disorders such as cancers (e.g. breast,
 CC colon, lung), immune-related diseases and disorders (e.g. inflammatory
 CC diseases and asthma), cardiovascular diseases (e.g. restenosis and
 CC coronary thrombosis), brain or neuronal-associated diseases, metabolic
 CC disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
 CC rheumatoid arthritis and psoriasis), central or peripheral nervous system
 CC diseases, migraines, pain, sexual dysfunction, mood disorders, attention
 CC disorders, cognitive disorders, hypotension, hypertension, psychotic
 CC disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease) and dyskinesias. The nucleic acids and polypeptides are also
 CC useful for treating viral infections caused by human immunodeficiency
 CC virus (HIV), and non-viral infections such as ocular disease (e.g.
 CC glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
 CC human proteases of the invention
 XX Sequence 253 AA;
 SQ Query Match 100.0%; Score 40; DB 5; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 Db |||||
 4 SLLPLQL 12
 RESULT 13
 ABU07440
 ID ABU07440 standard; protein; 253 AA.
 XX ABU07440;
 AC ABU07440;
 XX 28-JAN-2003 (first entry)
 DT Protein differentially regulated in prostate cancer #43.
 DE Prostate cancer; gene expression; differential regulation;
 XX molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX Homo sapiens.
 OS

PN WO200281638-A2.
 PD 17-OCT-2002.
 PP
 PF 08-APR-2002; 2002WO-US010824.
 PR 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 XX
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 PI Sun Z, Jay G;
 XX WPI; 2003-058520/05.
 DR N-PSDB; ABX10343.
 XX
 PT Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX
 PS Claim 1; Page 293-294; 416pp; English.
 XX
 CC The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 Db 4 SLLPLQL 12
 |||||
 |||||
 RESULT 14
 ABU07471
 ID ABU07471 standard; protein; 253 AA.
 XX
 AC ABU07471;

XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Protein differentially regulated in prostate cancer #74.
 XX
 KW Prostate cancer; gene expression; differential regulation;
 KW molecular marker; drug target; cancer detection; cancer diagnosis;
 KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
 XX
 OS Homo sapiens.
 XX
 PN WO200281638-A2.
 XX
 PD 17-OCT-2002.
 XX
 PP 08-APR-2002; 2002WO-US010824.
 XX
 PR 06-APR-2001; 2001US-0281731P.
 PR 06-APR-2001; 2001US-0281732P.
 XX
 PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX
 PI Sun Z, Jay G;
 XX WPI; 2003-058520/05.
 DR N-PSDB; ABX10375.
 XX
 PT Novel genes which are differentially regulated in prostate cancer, useful
 PT for diagnosing prostate cancer in prostate tissue sample and assessing
 PT therapeutic or preventive intervention in prostate cancer patients.
 XX
 PS Claim 1; Page 351; 416pp; English.
 XX
 CC The invention describes genes (I) which are differentially regulated in
 CC prostate cancer. (I) is useful for diagnosing a prostate cancer in a
 CC sample comprising prostate tissue, which involves determining the number
 CC of target genes which are differentially-regulated in the sample, where
 CC the number is indicative of the probability that the sample comprises
 CC prostate cancer. (I) is useful for assessing a therapeutic or preventive
 CC intervention in a subject having a prostate cancer, which involves
 CC determining the expression levels in a sample comprising prostate tissue
 CC of target genes which are differentially-regulated in prostate cancer.
 CC Preferably, the expression levels of at least 10 genes are determined.
 CC (I) is also useful for identifying agents that modulate a biological
 CC activity of a polypeptide differentially-regulated in prostate cancer
 CC cells, which involves contacting a polypeptide differentially-regulated
 CC in prostate cancer cells with a test agent under conditions effective for
 CC the test agent to modulate a biological activity of the polypeptide, and
 CC determining whether the test agent modulates the biological activity. (I)
 CC is useful as molecular markers, as drug targets, and for detecting,
 CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
 CC preventing or treating, determining predisposition to diseases and
 CC conditions especially relating to prostate cancer. (I) and its expression
 CC products are used in the diagnostic test to assay for presence of cancer
 CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
 CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
 CC of cancer, its stage of development, the nature of genetic defect, etc.
 CC The polypeptide encoded by (I) can be used as target for therapy or drug
 CC discovery. (I) can also be used for expressing the polypeptide and thus
 CC for searching specific binding partners of the polypeptide. (I) is useful
 CC in therapeutic applications to treat prostate cancer. The identification
 CC of specific genes, and groups of genes, expressed in pathways
 CC physiologically relevant to prostate cancer permits the definition of
 CC functional and disease pathways and the delineation of targets in these
 CC pathways which are useful in diagnostic, therapeutic, and clinical
 CC applications. This is the amino acid sequence of a protein differentially
 CC regulated in prostate cancer
 XX
 SQ Sequence 253 AA;
 Query Match 100.0%; Score 40; DB 6; Length 253;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

RESULT 15
ABR58471
ID ABR58471 standard; protein; 253 AA.
XX
AC ABR58471;
XX
DT 07-JUL-2003 (first entry)
XX
DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
XX
KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
XX
OS Homo sapiens.
XX
PN WO2003029468-A1.
XX
PD 10-APR-2003.
XX
PF 02-OCT-2002; 2002WO-US031467.
XX
PR 02-OCT-2001; 2001US-032713SP.
PR 30-MAY-2002; 2002US-0384531P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Mannion J;
XX
DR WPI; 2003-372001/35.
XX
PT New polynucleotide and polypeptide useful for diagnosing and/or treating
XX cancer, particularly ovarian cancer, and as a vaccine.
PS Claim 2; Page 157-158; 169pp; English.
XX
CC The invention relates to a novel isolated polynucleotide. The
CC polynucleotides of the invention have cytostatic activity, and may have a
CC use in gene therapy, and in a vaccine. The composition and methods are
CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
CC The composition may also be used as a vaccine to prevent cancer. The
CC present sequence is used in the exemplification of the invention
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

Search completed: March 11, 2006, 00:24:16
Job time : 88.6667 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	253	2 A53968	serine proteinase
2	38	95.0	146	2 H75201	hypothetical prote
3	33	82.5	370	2 AB3334	daunorubicin resis
4	32	80.0	218	2 T02912	probable transcrip
5	32	80.0	264	2 C97402	probable acyltrans
6	32	80.0	266	2 AC2620	1-acyl-sn-glycerol
7	32	80.0	266	2 JC7300	tax-responsive ele
8	32	80.0	267	2 JC4857	hepatocarcinogenes
9	32	80.0	282	2 B85327	probable transcrip
10	32	80.0	494	2 C43349	probable succinogl
11	32	80.0	494	2 B95976	probable transport
12	32	80.0	582	2 S40176	Exor protein - Rhi
13	32	80.0	622	2 S61692	probable membrane
14	31	77.5	196	2 G65039	hypothetical prote
15	31	77.5	303	2 C84914	hypothetical prote
16	31	77.5	354	2 T48649	glycerol-3-phospha
17	31	77.5	372	2 A98157	probable permease
18	31	77.5	372	2 AB3130	ABC transporter, m
19	31	77.5	392	2 D83934	hypothetical prote
20	31	77.5	395	2 D69779	antibiotic resista
21	31	77.5	398	2 C91063	hypothetical prote
22	31	77.5	401	2 B90120	SNF1-related prote
23	31	77.5	413	2 AC0834	probable membrane
24	31	77.5	470	2 A90083	hypothetical prote
25	31	77.5	475	1 A69149	O-antigen transpor
26	31	77.5	754	2 AE0614	probable competenc
27	31	77.5	783	2 A46136	myosin-heavy-chain
28	31	77.5	913	2 AC2445	hypothetical prote
29	30	75.0	155	2 I45913	interleukin-2 prec

30	75.0	155	2 S38662	interleukin-2 - go
31	75.0	155	2 S11488	interleukin-2 prec
32	75.0	168	2 E96979	probable membrane
33	75.0	189	2 T43766	hypothetical prote
34	75.0	190	2 T39622	probable phosphate
35	75.0	208	2 T17092	NADH2 dehydrogenas
36	75.0	214	1 G69798	hypothetical prote
37	75.0	223	2 F83598	cell division prote
38	75.0	277	2 H84314	cytochrome a3 con
39	75.0	289	2 T43663	probable high affi
40	75.0	333	1 HLHUCB	T-cell surface gly
41	75.0	349	2 E82656	conserved hypotet
42	75.0	369	2 S33603	surfactant protein
43	75.0	371	1 JN0450	conglutinin precu
44	75.0	371	2 I45878	conglutinin - bovi
45	75.0	375	2 S47704	hypothetical 41.1K

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N:Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A53968
R:Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A:Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A:Reference number: A53968; MUID:94308225; PMID:8034709
A:Accession: A53968
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <HAN>
A:Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:GS21214; PIDN:?
C:Genetics:
A:Gene: GDB:PRSS6; SCCE
A:Cross-references: GDB:377730
A:Map position: 7q35-7q35
C:Superfamily: trypsin; trypsin homology
F:30-245/Domain: trypsin homology <TRY>

RESULT 2

H75201
hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H75201
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: H75201
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <KAW>
A:Cross-references: UNIPROT:Q9V2D5; UNIPARC:UPI0000063243; GB:AJ248283; GB:AL096836; NID:
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0088
C:Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

Query Match 95.0%; Score 38; DB 2; Length 146;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLLPLQL 9
Db 66 LLLPLQL 74

RESULT 3
AB3334
daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain 1
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3334
R:DelVecchio, V.G.; Kapratlal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <KUR>
A:Cross-references: UNIPROT:Q8YHY9; UNIPROT:Q8FZX1; UNIPARC:UPI0000057D7A; GB:AE008917;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0656
A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 370;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
Db 293 LLLPLQL 300

RESULT 4
T02912
probable transcription factor MYB41 [similarity] - Arabidopsis thaliana (fragment)
N:Alternate names: protein T1J38.220
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Oct-2004
C:Accession: T02912; T51654
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuel
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z14766
A:Accession: T02912
A:Molecule type: DNA
A:Residues: 1-218 <BEV>
A:Cross-references: UNIPROT:Q9ZTE3; UNIPARC:UPI00000A46AC; EMBL:AL035524
A:Experimental source: cultivar Columbia; BAC clone T13J8
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
Paz-Ares, J.; Weissbach, B.
Plant J. 16, 263-276, 1998
A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
A:Reference number: Z14349; MUID:9839469; PMID:9839469
A:Accession: T51654
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-218 <KRA>
A:Cross-references: UNIPARC:UPI00000A46AC; EMBL:AF062882; PIDN:AAC83604.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB41
A:Map position: 4
A:Note: T13J8.220
A:Note: intron positions not resolved
C:Keywords: transcription factor
F:1-48/Domain: myb DNA-binding repeat homology (fragment) <MYB>

Query Match 80.0%; Score 32; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
Db 104 SLLPLQ 110

RESULT 5
C97402
probable acyltransferase (AF232919) [imported] - Agrobacterium tumefaciens (strain C58,
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004
C:Accession: C97402
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: C97402
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <KUR>
A:Cross-references: UNIPROT:Q8UIE2; UNIPARC:UPI00000D17A6; GB:AE007869; PIDN:AAK86172.1;
C:Genetics:
A:Gene: AGR_C 621
A:Map position: circular chromosome
C:Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase

Query Match 80.0%; Score 32; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
Db 19 LLLPLQL 26

RESULT 6
AC2620
1-acyl-sn-glycerol-3-phosphate acyltransferase p1sc [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
C:Accession: AC2620
R:Wood, D.W.; Scubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC2620
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <KUR>
A:Cross-references: UNIPROT:Q8UIE2; UNIPARC:UPI00000D17A6; GB:AE008688; PIDN:AAL41377.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: p1sc
A:Map position: circular chromosome
C:Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase

Query Match 80.0%; Score 32; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
Db 19 LLLPLQL 26

RESULT 7
JC7300
tax-responsive element-binding protein 5 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: JCY7300
R:Masaki, T.; Noguichi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
DNA Res. 7, 187-193, 2000
A:Title: Isolation and characterization of the gene encoding mouse tax-responsive element
A:Reference number: JC7300
A:Accession: JCY7300
A:Molecule type: mRNA
A:Residues: 1-266 <MAS>
A:Cross-references: UNIPROT:Q9ES53; UNIPARC:UPI00000E73B0; DDBJ:AB036745
C:Genetics:
A:Gene: trebs
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor

Query Match 80.0%; Score 32; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLPLQL 9
|||
Db 187 LLPLQL 193

RESULT 8
JC4857
hepatocarcinogenesis-related transcription factor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4857
R:Kishimoto, T.; Kikura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
Biochem. Biophys. Res. Commun. 224, 746-751, 1996
A:Title: HTF: A b-zip transcription factor that is closely related to the human XBP/TREB
A:Reference number: JC4857
A:Accession: JC4857
A:Molecule type: mRNA
A:Residues: 1-267 <KIS>
A:Cross-references: UNIPROT:Q9R1S4; UNIPARC:UPI00000E80AD
C:Comment: This is a basic-leucine zipper type transcription factor involved in hepatocarcinogenesis
C:Genetics:
A:Gene: htf
C:Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C:Keywords: leucine zipper; transcription factor
F:58-98/Domain: fos/jun DNA-binding domain homology <FJD>
F:89-126/Region: leucine zipper motif

Query Match 80.0%; Score 32; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLPLQL 9
|||
Db 188 LLPLQL 194

RESULT 9
B85327
probable transcription factor MYB41 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C:Accession: B85327
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: B85327
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <STO>

A:Cross-references: UNIPROT:Q9M0J5; UNIPARC:UPI00000BD4E; GB:NC_001268; NID:G7269665; P1
C:Genetics:
A:Gene: AT4g28110
A:Map position: 4
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 80.0%; Score 32; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
|||
Db 168 SLLPLQ 174

RESULT 10
C49349
probable succinoglycan transport protein ExoT - Rhizobium meliloti
C:Species: Rhizobium meliloti
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: C49349
R:Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.
J. Bacteriol. 175, 7045-7055, 1993
A:Title: Genes needed for the modification, polymerization, export, and processing of suc
A:Reference number: A49349; MUID:94042870; PMID:8226646
A:Accession: C49349
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <GLU>
A:Cross-references: UNIPROT:P33699; UNIPARC:UPI000012A381; GB:L20758; NID:G393240; PIDN:1
C:Superfamily: hypothetical protein b2046
C:Keywords: transmembrane protein

Query Match 80.0%; Score 32; DB 2; Length 494;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 8
|||
Db 122 SLLPLQ 129

RESULT 11
B95976
probable transport protein, similar to Wzx exoT [imported] - Sinorhizobium meliloti (str
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95976
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: B95976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <KUR>
A:Cross-references: UNIPROT:P33699; UNIPARC:UPI000012A381; GB:AL591985; PIDN:CAC49474.1;
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, L.; Hyma
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: exoT; SMD20950
A:Genome: plasmid
C:Superfamily: hypothetical protein b2046

Query Match 80.0%; Score 32; DB 2; Length 494;

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Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQI 8
   |||:|:|
Db 122 SLLPLQL 129

RESULT 12
S40176
Exot protein - Rhizobium melliloti
C:Species: Rhizobium melliloti
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
C:Accession: S40176
R:Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A.
submitted to the EMBL Data Library, April 1993
A:Description: Analysis of the Rhizobium melliloti genes exoU, exoV, exoW, exoT and exoI
see.
A:Reference number: S40173
A:Accession: S40176
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-582 <BEC>
A:Cross-references: UNIPARC:UPI00001787F9; EMBL:Z22646
C:Superfamily: hypothetical protein b2046

Query Match 80.0%; Score 32; DB 2; Length 582;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQI 8
   |||:|:|
Db 122 SLLPLQL 129

RESULT 13
S61692
probable membrane protein YOR137c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O3329; hypothetical protein YOR3329c
C:Species: Saccharomyces cerevisiae
C>Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: S61692; S67022
R:Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banreivi, A.; Sander, C.; Valencia
submitted to the EMBL Data Library, December 1995
A:Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome
A:Reference number: S61643
A:Accession: S61692
A:Molecule type: DNA
A:Residues: 1-622 <BEN>
A:Cross-references: UNIPROT:Q12212; UNIPARC:UPI000006BB6F; EMBL:X94335; NID:g1262139; PI
R:Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansorge, W.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66965
A:Accession: S67022
A:Molecule type: DNA
A:Residues: 1-622 <VOS>
A:Cross-references: UNIPARC:UPI000006BB6F; EMBL:Z75045; NID:g1420348; PID:e252028; PID:9
A:Experimental source: strain S288C
C:Genetics:
A:Cross-references: SGD:S0005663
A:Map position: 15R
C:Keywords: transmembrane protein
F:11-27/Domain: transmembrane #status predicted <TMM>

Query Match 80.0%; Score 32; DB 2; Length 622;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
   |||:|:|
Db 141 SALIPLQL 149
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RESULT 14
G65039
hypothetical protein b2612 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: G65039
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G65039
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <BLAT>
A:Cross-references: UNIPARC:UPI000016ED74; GB:AE000347; GB:U00096; NID:g2367142; PIDN:AA
A:Experimental source: strain K-12, substrain MG1655

Query Match 77.5%; Score 31; DB 2; Length 196;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
   |||:|:|
Db 123 LLAPLQIL 130

RESULT 15
C84914
hypothetical protein At2g47360 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84914
R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; A
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84914
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <STO>
A:Cross-references: UNIPROT:O22910; UNIPARC:UPI00000A2116; GB:AE002093; NID:g2275214; PI
C:Genetics:
A:Gene: At2g47360
A:Map position: 2

Query Match 77.5%; Score 31; DB 2; Length 303;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
   |||:|:|
Db 29 SLLPLSFL 37

Search completed: March 11, 2006, 00:40:51
Job time : 15.1111 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	100.0	66	2	Q6DTY1_HUMAN
2	40	100.0	253	1	KLK7_HUMAN
3	38	95.0	146	2	Q9V2D5_PYRAB
4	37	92.5	208	2	O21527_CLEGA
5	36	90.0	4183	2	Q4Q1C5_LEIMA
6	35	87.5	545	2	Q5N0S0_SYNP6
7	34	85.0	73	2	Q8VCA9_MOUSE
8	34	85.0	104	2	Q8R5D6_MOUSE
9	34	85.0	138	2	Q6PKE2_MOUSE
10	34	85.0	201	1	FKB11_MOUSE
11	34	85.0	246	2	Q585W6_9TRYP
12	34	85.0	361	1	INHA_TRIVU
13	34	85.0	373	2	Q4R9Q7_GROSL
14	34	85.0	745	2	Q4RXR8_TETNG
15	33	82.5	148	2	Q6N500_RHOPA
16	33	82.5	302	2	Q6GNT6_XENLA
17	33	82.5	370	2	Q8F2X1_BRUSU
18	33	82.5	370	2	Q8YHY9_BRUME
19	33	82.5	374	2	Q57CF5_BRUAB
20	33	82.5	379	2	Q7U9J6_SYNPX
21	33	82.5	381	2	Q7V4U4_PROMM
22	33	82.5	392	2	Q732B9_BACCL
23	33	82.5	392	2	Q819M8_BACCR
24	33	82.5	393	2	Q6HBL6_EACHK
25	33	82.5	393	2	Q5NY82_AZOSE
26	33	82.5	393	2	Q635X8_BACCC
27	33	82.5	394	2	Q6HU78_BACAN
28	33	82.5	494	2	Q4LIC3_9BURK
29	33	82.5	1017	1	EMILL1_MOUSE
30	32	80.0	68	2	Q6KG65_9CAUD
31	32	80.0	72	2	Q8VBB6_WSSV

32	32	80.0	78	2	Q7WXY8_PSEAE
33	32	80.0	102	2	Q8BRV0_MOUSE
34	32	80.0	161	2	Q4KJH4_PSEFS
35	32	80.0	171	2	Q7U5R4_SYNPX
36	32	80.0	196	2	Q9D226_MOUSE
37	32	80.0	205	2	Q653Z3_ORYSA
38	32	80.0	218	2	Q9ZTE3_ARATH
39	32	80.0	226	2	Q5AXD4_EMENI
40	32	80.0	230	2	Q876R3_EMENI
41	32	80.0	258	2	Q4HS88_CAMUP
42	32	80.0	264	2	Q8UIE2_AGR75
43	32	80.0	267	1	XBPI_MOUSE
44	32	80.0	267	1	XBPI_RAT
45	32	80.0	282	2	Q9M0J5_ARATH

ALIGNMENTS

RESULT 1

Q6DTY1_HUMAN
ID Q6DTY1_HUMAN PRELIMINARY; PRT; 66 AA.
AC Q6DTY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T., Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646152; AAT66047.1; -; mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 40; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
DB 4 SLLPLQL 12

RESULT 2

KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8N5N9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

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Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 3
Q9V2D5 PYRAB
ID Q9V2D5 PYRAB PRELIMINARY; PRT; 146 AA.
AC Q9V2D5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=PYRAB01390; ORFNames=PAB0088;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
DOI=10.1046/j.1365-2958.2003.03381.x;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
DR EMBL; AJ248283; CAB49063.1; -; Genomic_DNA.
DR PIR; H75201; H75201.
DR InterPro; IPR008537; DUF819.
DR Pfam; PF05684; DUF819; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 146 AA; 16092 MW; 7182941371258C1F CRC64;

Query Match      95.0%; Score 38; DB 2; Length 146;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 66 SLLPLQL 74

RESULT 4
O21527 CLEGA
ID O21527 CLEGA PRELIMINARY; PRT; 208 AA.
AC O21527;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN Name=ND4;
OS Clethrionomys gapperi (Southern red-backed vole).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Arvicolinae; Clethrionomys.
OX NCBI_TaxID=56223;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98152303; PubMed=9491603;
RA Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
RT "Molecular systematics and paleobiogeography of the South American
RT sigmodontine rodents.";
RL Mol. Biol. Evol. 15:35-49(1998).
DR EMBL; U83808; AAB87188.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.

Query Match      90.0%; Score 36; DB 2; Length 4183;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 2801 SLLPLQL 2809

RESULT 6
Q5N0S0 SYN6
ID Q5N0S0 SYN6 PRELIMINARY; PRT; 545 AA.
AC Q5N0S0;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Probable Na+/H+-exchanging protein.
GN OrderedLocNames=syc1910.c;
OS Synchococcus sp. (strain_PCC_6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxID=269084;
RN [1]

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DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0018491; F:oxidoreductase activity; IEA.
DR GO; GO:0042773; P:ATP synthase coupled electron transport; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR003918; NADH_oxred4.
DR InterPro; IPR000260; Oxidored_g5_N.
DR Pfam; PF01059; Oxidored_g5_N; 1.
DR PRINTS; PR01437; NUOXDRDTASE4.
KW Mitochondrion.
FT NON_TER 208
SQ SEQUENCE 208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;

Query Match      92.5%; Score 37; DB 2; Length 208;
Best Local Similarity 88.9%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 97 SLLPLQL 105

RESULT 5
Q4Q1C5 LEIMA
ID Q4Q1C5 LEIMA PRELIMINARY; PRT; 4183 AA.
AC Q4Q1C5;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF36.2940;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neill S.,
RA Saunders D., Seeger K., Warren T., Rajadream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT005272; CAJ09256.1; -; Genomic_DNA.
DR InterPro; IPR001547; Glyco_hydro_5.
DR InterPro; IPR000403; PI3_4_kinase_cat.
DR Pfam; PF00454; PI3_Pi4_kinase; 1.
DR SMART; SM00146; PI3Kc; 1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW Hypothetical protein; Nucleotide-binding.
SQ SEQUENCE 4183 AA; 452241 MW; 3F6FB63A80F3EB02 CRC64;

Query Match      90.0%; Score 36; DB 2; Length 4183;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 2801 SLLPLQL 2809

RESULT 6
Q5N0S0 SYN6
ID Q5N0S0 SYN6 PRELIMINARY; PRT; 545 AA.
AC Q5N0S0;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Probable Na+/H+-exchanging protein.
GN OrderedLocNames=syc1910.c;
OS Synchococcus sp. (strain_PCC_6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxID=269084;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCC6301;
RA Sugita M.;
RT "Complete genome structure of the unicellular cyanobacterium Anacystis
RL nidulans 6301 (Synecococcus sp. PCC6301).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008231; BAD80100.1; -; Genomic DNA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR006153; Na_H_porter.
DR InterPro; IPR006015; Usp.
DR InterPro; IPR006016; UspA.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR Pfam; PF00582; Usp; 1.
DR PRINTS; PR01438; UNVRSLSTRESS.
KW Complete proteome.
SQ SEQUENCE 545 AA; 58143 MW; 2DB84E920CD7DEDC CRC64;

Query Match 87.5%; Score 35; DB 2; Length 545;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
DB 193 LLLPLQVL 200

RESULT 7
Q8VCA9_MOUSE PRELIMINARY; PRT; 73 AA.
AC Q8VCA9;
DT 01-WAR-2002 (TrEMBLrel. 20, Created)
DT 01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshuyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZEC II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSP; P18203; 1FKL.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; Fkbp_PPase.
DR Pfam; PF00254; Fkbp_C; 1.
DR PROSITE; PS50059; Fkbp_PPase; 1.
SQ SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 104;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
DB 6 LLLPLQLL 13

RESULT 8
Q8R5D6_MOUSE PRELIMINARY; PRT; 104 AA.
AC Q8R5D6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fkbp11 protein.
GN Name=Fkbp11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZEC II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshuyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZEC II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022900; AAH22900.1; -; mRNA.
DR HSP; P18203; 1FKL.
DR MGI; MGI:1913370; Fkbp11.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001179; Fkbp_PPase.
DR Pfam; PF00254; Fkbp_C; 1.
DR PROSITE; PS50059; Fkbp_PPase; 1.
SQ SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 104;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
DB 6 LLLPLQLL 13
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RESULT 9
 Q6PK22 MOUSE PRELIMINARY; PRT; 138 AA.
 AC Q6PK22
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DE Fkbp11 protein.
 GN Name=Fkbp11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.;
 RA Strausberg R.;
 RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002311; AAH02311.1; -; mRNA.
 DR MGI; MGI:1913370; Fkbp11.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0014021; C:integral to membrane; TAS.
 DR InterPro; IPR001195; Fkbp_PPIase.
 DR Pfam; PF00254; Fkbp_C; 1.
 DR PROSITE; P850059; Fkbp_PPIase; 1.
 SQ SEQUENCE 138 AA; 15105 MW; C130B8B0EFD59D CRC64;
 Query Match 85.0%; Score 34; DB 2; Length 138;
 Best Local Similarity 87.5%; Pred. No. 96;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLLPLQL 9
 Db 6 LLLPLQLL 13
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 RESULT 10
 FKB11_MOUSE
 ID FKB11_MOUSE STANDARD; PRT; 201 AA.
 AC Q9D1M7; Q9CRE4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)
 FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis-
 trans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
 (FKBP-19).
 GN Name=Fkbp11;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziera R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sullana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RT Nature 420:563-573 (2002).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulyk S.J.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N;
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
 RC virgin mouse. Taken by biopsy.;
 RA Strausberg R.;
 RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002311; AAH02311.1; -; mRNA.
 DR MGI; MGI:1913370; Fkbp11.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0014021; C:integral to membrane; TAS.
 DR InterPro; IPR001195; Fkbp_PPIase.
 DR Pfam; PF00254; Fkbp_C; 1.
 DR PROSITE; P850059; Fkbp_PPIase; 1.
 SQ SEQUENCE 138 AA; 15105 MW; C130B8B0EFD59D CRC64;

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EMBL; AK003331; BAB22719.1; -; mRNA.
EMBL; AK019132; BAB31559.1; -; mRNA.
EMBL; BC037596; AAH37596.1; -; mRNA.
HSSP; P20071; LTCO.
Ensembl; ENSMUSG00000003355; Mus musculus.
MGI; MGI:1913370; Fkbp11.

GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP_C; 1.
PROSITE; PS0059; FKBP_PPIASE; 1.
Kw Isomerase; Rotamase; Signal.

FT SIGNAL 1 27 Potential.
FT CHAIN 28 201 FK506 binding protein 11.
FT DOMAIN 57 144 PPIase FKBP-type.
FT CONFLICT 53 53 S -> F (in Ref. 1; BAB31559).
FT CONFLICT 198 198 S -> R (in Ref. 1; BAB31559).
SQ SEQUENCE 201 AA; 22137 MW; 94D955C57264BD82 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 201;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
DB 6 LLLPLQLL 13

RESULT 11
Q585W6 9TRYP PRELIMINARY; PRT; 246 AA.
AC Q585W6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFName=TB927.6.3680;
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Shedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L., Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J., Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J., Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S., Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.; Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA El-Sayed N.M., Khalak H., Adams M.D.; Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Haas B., Blandin G., El-Sayed N.; Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC009259; AAX80785.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 246 AA; 27875 MW; 70DDB38AB6B46AB CRC64;

Query Match 85.0%; Score 34; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
DB 163 LMLPLQLL 170

RESULT 12
INHA TRIVU STANDARD; PRT; 361 AA.
AC O77755;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Inhibin alpha chain precursor.

GN Name=INHA;
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99027340; PubMed=9801457; DOI=10.1677/jme.0.0210141;
RA Vamontfort D., Fielder A.B., Heath D.A., Lawrence S.B., Tisdall D.J., Greenwood P.J., McNatty K.;
RT "cDNA sequence analysis, gene expression and protein localisation of the inhibin alpha subunit of Australian brushtail possum (Trichosurus vulpecula)";
RT J. Mol. Endocrinol. 21:141-152(1998).

CC -!- FUNCTION: Inhibins and activins inhibit and activate, respectively, the secretion of follitropin by the pituitary gland. Inhibins/activins are involved in regulating a number of diverse functions such as hypothalamic and pituitary hormone secretion, gonadal hormone secretion, germ cell development and maturation, erythroid differentiation, insulin secretion, nerve cell survival, embryonic axial development or bone growth, depending on their subunit composition. Inhibins appear to oppose the functions of activins.
CC -!- SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin A is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and beta-B.
CC -!- PTM: Proteolytic processing yields a number of bioactive forms, consisting either solely of the mature alpha chain, of the most N-terminal propeptide linked through a disulfide bond to the mature alpha chain, or of the entire proprotein.

CC -!- SIMILARITY: Belongs to the TGF-beta family.

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EMBL; AF033340; AAC63945.1; -; mRNA.
GO; GO:0005576; C:extracellular region; ISS.
GO; GO:0017106; F:activin inhibitor activity; ISS.
GO; GO:0005125; F:cytokine activity; ISS.
GO; GO:0008083; F:growth factor activity; ISS.
GO; GO:0005179; F:hormone activity; ISS.
GO; GO:0005515; F:protein binding; ISS.
GO; GO:0007050; P:cell cycle arrest; ISS.
GO; GO:0030154; P:cell differentiation; ISS.
GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.

GO; GO:0007267; P:cell-cell signaling; ISS.
GO; GO:0030218; P:erythrocyte differentiation; ISS.
GO; GO:0042541; P:hemoglobin biosynthesis; ISS.
GO; GO:0006917; P:induction of apoptosis; ISS.
GO; GO:0045578; P:negative regulation of B cell differentiation; ISS.
GO; GO:0045786; P:negative regulation of cell cycle; ISS.
GO; GO:0046882; P:negative regulation of follicle-stimulating .; ISS.
GO; GO:0045077; P:negative regulation of interferon-gamma bio. .; ISS.
GO; GO:0045650; P:negative regulation of macrophage different. .; ISS.
GO; GO:0042326; P:negative regulation of phosphorylation; ISS.
GO; GO:0007399; P:neurogenesis; ISS.

DR GO: GO:0001541; P:ovarian follicle development; ISS.
 DR GO: GO:0046881; P:positive regulation of follicle-stimulating. . .; ISS.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR Pfam: PF0001839; TGFb.
 DR Pfam: PF00019; TGF_beta; 1.
 DR PRINTS: PR00669; INHIBINA.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Glycoprotein; Growth factor; Hormone; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 64
 FT PROPEP 65 230
 FT CHAIN 231 361
 FT SITE 64 65
 FT SITE 230 231
 FT CARBOHYD 48 48
 FT CARBOHYD 144 144
 FT CARBOHYD 266 266
 FT DISULFID 260 323
 FT DISULFID 289 358
 FT DISULFID 293 360
 FT DISULFID 322 322
 SQ SEQUENCE 361 AA; 38945 MW; D661CDF93CDAA87D CRC64;
 Query Match 85.0%; Score 34; DB 1; Length 361;
 Best Local Similarity 87.5%; Pred. No. 2.5e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLLPLQL 9
 DB 4 LLLPLQL 11
 RESULT 13
 Q749Q7_GEOSL
 ID Q749Q7_GEOSL PRELIMINARY; PRT; 373 AA.
 AC Q749Q7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=GSU2685;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.B., Beanan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolony J.F., Sullivan J.F., Haft D.H., Selengut J.,
 RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments";
 RL Science 302:1967-1969 (2003).
 DR EMBL; AE017180; AAR36057.1; -; Genomic_DNA.
 DR TIGR; GSU2685; -;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR000412; ABC 2.
 DR Pfam: PF01061; ABC2 membrane; 1.
 DR PROSITE: PSS1012; ABC_TM2; 1.
 KW Complete proteome.
 SQ SEQUENCE 373 AA; 40412 MW; 94B9D6AFF570D4A2 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 373;
 Best Local Similarity 87.5%; Pred. No. 2.6e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLLPLQL 9
 DB 293 LLLPLQL 300
 RESULT 14
 Q4RKR8_TETNG
 ID Q4RKR8_TETNG PRELIMINARY; PRT; 745 AA.
 AC Q4RKR8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 5 SCAP15026, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00032814001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coataz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype";
 RL Nature 431:946-957 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; CAAE01015026; CAG11014.1; -; Genomic_DNA.
 FT NON_TER 1 1
 SQ SEQUENCE 745 AA; 83291 MW; 697BD870E5019DF1 CRC64;
 Query Match 85.0%; Score 34; DB 2; Length 745;
 Best Local Similarity 77.8%; Pred. No. 5.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 DB 692 SLLPLQL 700
 RESULT 15
 Q6N500_RHOPA
 ID Q6N500_RHOPA PRELIMINARY; PRT; 148 AA.
 AC Q6N500;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein precursor.
 GN OrderedLocusNames=RPA183;
 OS Rhodospseudomonas palustris.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Peres C.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,
 RA Harrison P.H., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; EX572603; CAE28624.1; -; Genomic_DNA.
 DR InterPro; IPR000975; Interleukin_1.
 DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN 1.
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL 1 22 Potential.
 SQ SEQUENCE 148 AA; 16860 MW; 9501B7C6C2808F45 CRC64;
 Query Match 82.5%; Score 33; DB 2; Length 148;
 Best Local Similarity 77.8%; Pred. NO. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SLLPLQL 9
 Db 7 SLLPLMLL 15

Search completed: March 11, 2006, 00:38:50
 Job time : 97.3333 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-36
Perfect score: 40
Sequence: 1 SLLPLQL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	9	2	US-09-502-600-36
2	40	100.0	9	2	US-09-918-243-36
3	40	100.0	253	1	US-08-557-146-2
4	40	100.0	253	1	US-08-824-874-3
5	40	100.0	253	1	US-09-154-344-2
6	40	100.0	253	2	US-08-930-188-2
7	40	100.0	253	2	US-09-210-084-3
8	40	100.0	253	2	US-09-764-762-3
9	40	100.0	253	4	PCT-US96-04294-2
10	40	100.0	265	2	US-09-949-016-7716
11	36	90.0	9	2	US-09-502-600-33
12	36	90.0	9	2	US-09-918-243-33
13	34	85.0	812	2	US-09-489-039A-12075
14	32	80.0	9	2	US-09-502-600-35
15	32	80.0	9	2	US-09-502-600-116
16	32	80.0	9	2	US-09-918-243-35
17	32	80.0	9	2	US-09-918-243-116
18	32	80.0	139	2	US-10-104-047-3867
19	32	80.0	285	2	US-09-270-767-39889
20	32	80.0	295	2	US-09-270-767-55106
21	32	80.0	557	2	US-09-489-039A-10804
22	31	77.5	181	2	US-09-543-681A-5937
23	31	77.5	246	2	US-10-012-231A-338
24	31	77.5	246	2	US-10-015-389A-338
25	31	77.5	246	2	US-10-006-768A-338
26	31	77.5	246	2	US-10-015-671A-338
27	31	77.5	246	2	US-10-015-393A-338

28	31	77.5	246	2	US-10-011-833A-338	Sequence 338, App
29	31	77.5	246	2	US-10-006-041A-338	Sequence 338, App
30	31	77.5	246	2	US-10-012-064A-338	Sequence 338, App
31	31	77.5	307	2	US-09-177-249-13	Sequence 13, Appl
32	31	77.5	307	2	US-09-812-283-13	Sequence 13, Appl
33	31	77.5	461	2	US-09-605-703B-436	Sequence 436, App
34	31	77.5	472	2	US-09-543-681A-5049	Sequence 5049, Ap
35	31	77.5	893	2	US-09-605-703B-434	Sequence 434, App
36	31	77.5	1279	2	US-09-170-496D-293	Sequence 58, Appl
37	31	77.5	1279	2	US-09-364-425B-58	Sequence 58, Appl
38	30	75.0	41	2	US-10-317-252B-95	Sequence 95, Appl
39	30	75.0	135	1	US-08-383-621-5	Sequence 5, Appli
40	30	75.0	135	2	US-08-459-906-5	Sequence 5, Appli
41	30	75.0	169	2	US-09-328-352-7861	Sequence 7861, Ap
42	30	75.0	231	2	US-09-252-991A-22663	Sequence 22663, A
43	30	75.0	308	2	US-09-252-991A-27921	Sequence 27921, A
44	30	75.0	333	2	US-09-949-016-6128	Sequence 6128, Ap
45	30	75.0	340	2	US-09-949-016-10615	Sequence 10615, A

ALIGNMENTS

RESULT 1
US-09-502-600-36
; Sequence 36, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-502-600-36

Query Match 100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
|||
Db 1 SLLPLQL 9

RESULT 2
US-09-918-243-36
; Sequence 36, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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;
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36

Query Match      100.0%; Score 40; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; REFERENCE/DOCKET NUMBER: PF-0252 US
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: U.S.A.
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; REFERENCE/DOCKET NUMBER: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
   |||||
Db 4 SLLPLQL 12

RESULT 6
US-08-930-188-2
; Sequence 2, Application US/08930188
; Patent No. 6093397
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; ADDRESSEE: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; STREET: Lilly Lilly and Company
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,188
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-188-2

; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
   |||||
Db 4 SLLPLQL 12

RESULT 7
US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; ADDRESSEE: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
   |||||
Db 4 SLLPLQL 12

RESULT 8
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; ADDRESSEE: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
```

; CORRESPONDENCE ADDRESS:
; ADDRESSES: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 9
PCT-US96-04294-2
; Sequence 2. Application PC/TUS9604294
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; APPLICANT: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/04294
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-04294-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 4 SLLPLQL 12

RESULT 10
US-09-949-016-7716
; Sequence 7716, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7716
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7716

Query Match 100.0%; Score 40; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 16 SLLPLQL 24

RESULT 11
US-09-502-600-33
; Sequence 33, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223C1P-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A

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; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-502-600-33

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
Db 1 LLLPLQL 8

RESULT 12
US-09-918-243-33
; Sequence 33, Application US/0918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CLIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33

Query Match      90.0%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
Db 1 LLLPLQL 8

RESULT 13
US-09-489-039A-12075
; Sequence 12075, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12075
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12075
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Query Match      85.0%; Score 34; DB 2; Length 812;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQL 9
Db 429 LLLPLQL 436

RESULT 14
US-09-502-600-35
; Sequence 35, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-502-600-35

Query Match      80.0%; Score 32; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLLPLQL 9
Db 1 LLLPLQL 7

RESULT 15
US-09-502-600-116
; Sequence 116, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-502-600-116

Query Match      80.0%; Score 32; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
Db 3 SLLPLQ 9

Search completed: March 11, 2006, 01:24:27
Job time : 22.2222 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-36

Perfect score: 40

Sequence: 1 SLLPLQL 9

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	9	3	US-09-918-243-36
2	40	100.0	9	3	US-09-905-083-36
3	40	100.0	9	4	US-10-372-521-36
4	40	100.0	9	5	US-10-831-075-36
5	40	100.0	136	5	US-10-450-763-53737
6	40	100.0	198	4	US-10-262-511-96
7	40	100.0	250	4	US-10-262-511-92
8	40	100.0	253	3	US-09-888-615-98
9	40	100.0	253	3	US-09-764-762-3
10	40	100.0	253	4	US-10-071-214-2
11	40	100.0	253	4	US-10-071-214-48
12	40	100.0	253	4	US-10-264-283-90
13	40	100.0	253	4	US-10-295-027-498
14	40	100.0	253	4	US-10-173-999-48
15	40	100.0	253	4	US-10-408-765A-639
16	40	100.0	253	5	US-10-643-795A-95
17	40	100.0	253	5	US-10-948-518-95
18	40	100.0	253	5	US-10-868-490A-1
19	40	100.0	257	4	US-10-344-394-38
20	36	90.0	9	3	US-09-918-243-33
21	36	90.0	9	3	US-09-905-083-33
22	36	90.0	9	4	US-10-372-521-33
23	36	90.0	9	5	US-10-831-075-33
24	35	87.5	138	4	US-10-425-114-53148
25	35	87.5	868	4	US-10-369-493-10255
26	34	85.0	56	4	US-10-424-599-164977
27	34	85.0	70	4	US-10-424-599-207950

28 34 85.0 379 4 US-10-437-963-111334 Sequence 111334,
29 33 82.5 46 4 US-10-424-599-265948 Sequence 265948,
30 33 82.5 86 4 US-10-424-599-199921 Sequence 199921,
31 33 82.5 137 4 US-10-425-115-264649 Sequence 264649,
32 33 82.5 394 4 US-10-282-122A-45727 Sequence 45727, A
33 33 82.5 397 4 US-10-408-765A-2842 Sequence 2842, Ap
34 33 82.5 804 4 US-10-236-055A-28 Sequence 28, Appl
35 32 80.0 9 3 US-09-918-243-35 Sequence 35, Appl
36 32 80.0 9 3 US-09-918-243-116 Sequence 116, App
37 32 80.0 9 3 US-09-905-083-35 Sequence 35, Appl
38 32 80.0 9 3 US-09-905-083-116 Sequence 116, App
39 32 80.0 9 4 US-10-372-521-35 Sequence 35, Appl
40 32 80.0 9 4 US-10-372-521-116 Sequence 116, App
41 32 80.0 9 5 US-10-831-075-35 Sequence 35, Appl
42 32 80.0 9 5 US-10-831-075-116 Sequence 116, App
43 32 80.0 54 4 US-10-425-115-368614 Sequence 368614,
44 32 80.0 73 5 US-10-450-763-49706 Sequence 49706, A
45 32 80.0 74 4 US-10-424-599-252879 Sequence 252879,

ALIGNMENTS

RESULT 1

US-09-918-243-36
; Sequence 36, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36

Query Match 100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
|||
Db 1 SLLPLQL 9

RESULT 2

US-09-905-083-36
; Sequence 36, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-905-083-36

Query Match      100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 3
US-10-372-521-36
; Sequence 36, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-10-372-521-36

Query Match      100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 4
US-10-831-075-36
; Sequence 36, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-10-831-075-36

Query Match      100.0%; Score 40; DB 5; Length 9;
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 1 SLLPLQL 9

RESULT 5
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match      100.0%; Score 40; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
Db 10 SLLPLQL 18

RESULT 6
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
```

; APPLICANT: Zhong, Mei
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Rothenberg, Mark E.
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Agee, Michele L.
 ; APPLICANT: Berghs, Constance
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-462C
 ; CURRENT APPLICATION NUMBER: US/10/262,511
 ; CURRENT FILING DATE: 2003-05-28
 ; PRIOR APPLICATION NUMBER: 60/326,483
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: 60/373,815
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,917
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/328,029
 ; PRIOR FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/381,038
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 60/328,056
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/373,260
 ; PRIOR FILING DATE: 2002-04-17
 ; PRIOR APPLICATION NUMBER: 60/373,826
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,435
 ; PRIOR FILING DATE: 2001-10-05
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 439
 ; SOFTWARE: CuraseqList version 0.1
 ; SEQ ID NO 96
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-262-511-96

Query Match 100.0%; Score 40; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
 |||||
 Db 4 SLLPLQL 12

RESULT 7
 US-10-262-511-92
 ; Sequence 92, Application US/10262511
 ; Publication No. US20040038223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Ju, Jingfang
 ; APPLICANT: Li, Li
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Elleman, Karen
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Ort, Tatiana

; APPLICANT: Gorman, Linda
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Pena, Carol E. A.
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Rothenberg, Mark E.
 ; APPLICANT: Leach, Martin D.
 ; APPLICANT: Agee, Michele L.
 ; APPLICANT: Berghs, Constance
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-462C
 ; CURRENT APPLICATION NUMBER: US/10/262,511
 ; CURRENT FILING DATE: 2003-05-28
 ; PRIOR APPLICATION NUMBER: 60/326,483
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: 60/373,815
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,917
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/381,642
 ; PRIOR FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/328,029
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: 60/381,038
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 60/328,056
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/373,260
 ; PRIOR FILING DATE: 2002-04-17
 ; PRIOR APPLICATION NUMBER: 60/373,826
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/327,435
 ; PRIOR FILING DATE: 2001-10-05
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 439
 ; SOFTWARE: CuraseqList version 0.1
 ; SEQ ID NO 92
 ; LENGTH: 250
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-262-511-92

Query Match 100.0%; Score 40; DB 4; Length 250;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQL 9
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 Db 1 SLLPLQL 9

RESULT 8
 US-09-888-615-98
 ; Sequence 98, Application US/09888615
 ; Patent No. US20020064856A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOWMAN, GREGORY
 ; APPLICANT: WHYTE, DAVID
 ; APPLICANT: CAENEPEEL, SEAN
 ; APPLICANT: CHARYDCZAK, GLEN
 ; APPLICANT: MANNING, GERARD
 ; APPLICANT: SUDARSANAM, SUCHA
 ; TITLE OF INVENTION: NOVEL PROTEASES
 ; FILE REFERENCE: 038602/1214
 ; CURRENT APPLICATION NUMBER: US/09/888,615
 ; CURRENT FILING DATE: 2001-06-26

; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
| | | | |
Db 4 SLLPLQL 12

RESULT 9

US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match 100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
| | | | |
Db 4 SLLPLQL 12

RESULT 10

US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON-3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
| | | | |
Db 4 SLLPLQL 12

RESULT 11

US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON-3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
| | | | |
Db 4 SLLPLQL 12

RESULT 12

US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US2003014494A1

; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

RESULT 13

US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

RESULT 14

US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Ros Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
Db 4 SLLPLQIL 12

RESULT 15

US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLLPLQL 9
|||
Db 4 SLLPLQL 12
|||

Search completed: March 11, 2006, 01:37:24
Job time : 70.444 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-36

Perfect score: 40

Sequence: 1 SLLPLQIL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.New.*
1: /cgn2_6/prodata/2/pubpa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	253	6	US-10-412-748-11
2	40	100.0	253	6	US-10-412-748-14
3	40	100.0	253	6	US-10-412-748-17
4	40	100.0	253	7	US-11-037-243-98
5	34	85.0	71	7	US-11-096-568A-27354
6	34	85.0	71	7	US-11-096-568A-27391
7	34	85.0	85	7	US-11-096-568A-27353
8	34	85.0	85	7	US-11-096-568A-27390
9	32	80.0	139	7	US-11-072-512-3867
10	31	77.5	401	7	US-11-087-099-6642
11	30	75.0	41	7	US-11-121-612-95
12	30	75.0	202	7	US-11-098-686-10163
13	30	75.0	333	7	US-11-181-234-5
14	30	75.0	333	7	US-11-181-234-7
15	29	72.5	68	7	US-11-096-568A-6331
16	29	72.5	79	7	US-11-096-568A-6330
17	29	72.5	125	7	US-11-096-568A-23862
18	29	72.5	326	7	US-11-096-568A-20656
19	29	72.5	336	7	US-11-096-568A-30761
20	29	72.5	376	7	US-11-096-568A-30760
21	29	72.5	419	7	US-11-067-884-8
22	29	72.5	498	7	US-11-096-568A-30759
23	28	70.0	40	7	US-11-121-612-80
24	28	70.0	40	7	US-11-121-612-144
25	28	70.0	40	7	US-11-121-612-176

26	28	70.0	40	7	US-11-121-612-246	Sequence 246, App
27	28	70.0	40	7	US-11-121-612-247	Sequence 247, App
28	28	70.0	40	7	US-11-121-612-248	Sequence 248, App
29	28	70.0	40	7	US-11-121-612-249	Sequence 249, App
30	28	70.0	40	7	US-11-121-612-320	Sequence 320, App
31	28	70.0	40	7	US-11-121-612-342	Sequence 342, App
32	28	70.0	40	7	US-11-121-612-349	Sequence 349, App
33	28	70.0	41	7	US-11-121-612-100	Sequence 100, App
34	28	70.0	41	7	US-11-121-612-270	Sequence 270, App
35	28	70.0	72	6	US-10-895-064-631	Sequence 631, App
36	28	70.0	72	7	US-11-129-741-631	Sequence 631, App
37	28	70.0	98	6	US-10-467-657-3826	Sequence 3826, App
38	28	70.0	102	7	US-11-072-512-2266	Sequence 2266, App
39	28	70.0	109	6	US-10-821-234-1175	Sequence 1175, App
40	28	70.0	145	7	US-11-205-225-8	Sequence 8, Appli
41	28	70.0	299	7	US-11-096-568A-12300	Sequence 12300, A
42	28	70.0	317	7	US-11-205-225-2	Sequence 2, Appli
43	28	70.0	334	7	US-11-096-568A-18598	Sequence 18598, A
44	28	70.0	354	7	US-11-096-568A-18597	Sequence 18597, A
45	28	70.0	359	7	US-11-089-425A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

Query Match 100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9

DB 4 SLLPLQIL 12

RESULT 2

US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT

```
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLPLQL 9
        |||||
Db      4 SLLPLQL 12

RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 40; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLLPLQL 9
        |||||
Db      4 SLLPLQL 12

RESULT 4
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 40; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 SLLPLQL 9
        |||||
Db      4 SLLPLQL 12

RESULT 5
US-11-096-568A-27354
; Sequence 27354, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27354
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 5677704
US-11-096-568A-27354

Query Match      85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLLPLQL 9
        :|||
Db      1 LLLPLQL 8

RESULT 6
US-11-096-568A-27391
; Sequence 27391, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27391
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71)
; OTHER INFORMATION: Ceres Seq. ID no. 13500184
US-11-096-568A-27391

Query Match      85.0%; Score 34; DB 7; Length 71;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LLLPLQL 9
        :|||
Db      1 LLLPLQL 8

RESULT 7
US-11-096-568A-27353
; Sequence 27353, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
```

```
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27353
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(85)
; OTHER INFORMATION: Ceres Seq. ID no. 5677703
US-11-096-568A-27353

Query Match      85.0%; Score 34; DB 7; Length 85;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
   :|||||
Db 15 MLLPLQIL 22

RESULT 8
US-11-096-568A-27390
; Sequence 27390, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27390
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(85)
; OTHER INFORMATION: Ceres Seq. ID no. 13500183
US-11-096-568A-27390

Query Match      85.0%; Score 34; DB 7; Length 85;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLLPLQIL 9
   :|||||
Db 15 MLLPLQIL 22

RESULT 9
US-11-072-512-3867
; Sequence 3867, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
```

```
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3867
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3867

Query Match      80.0%; Score 32; DB 7; Length 139;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
   :|||||
Db 33 SLLPLQ 39

RESULT 10
US-11-087-099-6642
; Sequence 6642, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6642
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Guillardia theta
US-11-087-099-6642

Query Match      77.5%; Score 31; DB 7; Length 401;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLLPLQIL 9
   :|||||
Db 304 SFLPLQLV 312

RESULT 11
US-11-121-612-95
; Sequence 95, Application US/11121612
; Publication No. US20060025339A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847MD
; CURRENT APPLICATION NUMBER: US/11/121,612
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
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; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/317,252
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (41)..(41)
; OTHER INFORMATION: AMIDATION
US-11-121-612-95
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Query Match 75.0%; Score 30; DB 7; Length 41;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 0;
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```
QY 1 SLLPLQL 9
||| | | | | |
Db 7 SLDLPQLL 15
```

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RESULT 12
US-11-098-686-10163
; Sequence 10163, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10163
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10163
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```
Query Match 75.0%; Score 30; DB 7; Length 202;
Best Local Similarity 87.5%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
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```
QY 2 LLLPLQL 9
||| | | | | |
Db 146 LLLPLTIL 153
```

```
RESULT 13
US-11-181-234-5
; Sequence 5, Application US/11181234
; Publication No. US20060021075A1
; GENERAL INFORMATION:
; APPLICANT: WANG, CHYUNG-RU
; TITLE OF INVENTION: GROUP 1 CD1 TRANSGENIC MICE AND THEIR
; FILE REFERENCE: 21117.0001U2
; CURRENT APPLICATION NUMBER: US/11/181,234
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: 60/588,192
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```
; PRIOR FILING DATE: 2004-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-11-181-234-5
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```
Query Match 75.0%; Score 30; DB 7; Length 333;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 2 LLLPLQL 9
||| | | | | |
Db 2 LLLPPQLL 9
```

```
RESULT 14
US-11-181-234-7
; Sequence 7, Application US/11181234
; Publication No. US20060021075A1
; GENERAL INFORMATION:
; APPLICANT: WANG, CHYUNG-RU
; TITLE OF INVENTION: GROUP 1 CD1 TRANSGENIC MICE AND THEIR
; FILE REFERENCE: 21117.0001U2
; CURRENT APPLICATION NUMBER: US/11/181,234
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: 60/588,192
; PRIOR FILING DATE: 2004-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-11-181-234-7
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Query Match 75.0%; Score 30; DB 7; Length 333;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 2 LLLPLQL 9
||| | | | | |
Db 2 LLLPPQLL 9
```

```
RESULT 15
US-11-096-568A-6331
; Sequence 6331, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6331
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(68)
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; OTHER INFORMATION: Ceres Seq. ID no. 14314773
US-11-096-568A-6331

Query Match 72.5%; Score 29; DB 7; Length 68;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLPLQ 7
:|||||
Db 30 NULLPLQ 36

Search completed: March 11, 2006, 01:38:42
Job time : 9 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GFLVCRGTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	4 AAE08285	Aae08285 Human str
2	50	100.0	9	8 ADR68841	Adr68841 Human str
3	50	100.0	181	6 ADA05738	Ada05738 Human NOV
4	50	100.0	181	8 ADN62902	Adn62902 Human NOV
5	50	100.0	198	6 ADA05736	Ada05736 Human NOV
6	50	100.0	198	8 ADN62900	Adn62900 Human NOV
7	50	100.0	224	6 ADA05744	Ada05744 Human NOV
8	50	100.0	224	8 ADN62908	Adn62908 Human NOV
9	50	100.0	224	9 ADV21100	Adv21100 Human str
10	50	100.0	225	4 AAB98502	Aab98502 Human str
11	50	100.0	247	6 ADA05742	Ada05742 Human NOV
12	50	100.0	247	8 ADN62906	Adn62906 Human NOV
13	50	100.0	250	6 ADA05732	Ada05732 Human NOV
14	50	100.0	250	8 ADN62896	Adn62896 Human NOV
15	50	100.0	252	6 ADA05734	Ada05734 Human NOV
16	50	100.0	252	8 ADN62898	Adn62898 Human NOV
17	50	100.0	253	2 AAR67888	Aar67888 Human str
18	50	100.0	253	2 AAW05383	Aaw05383 Human str
19	50	100.0	253	5 ABB84421	Abb84421 Human SCC
20	50	100.0	253	5 ABB84406	Abb84406 Human SCC
21	50	100.0	253	5 AAU82740	Aau82740 Amino aci
22	50	100.0	253	6 ABU07440	Abu07440 Protein d
23	50	100.0	253	6 ABU07471	Abu07471 Protein d
24	50	100.0	253	6 ABR58471	Abr58471 Human str

ALIGNMENTS

RESULT 1

AAE08285
ID AAE08285 standard; peptide; 9 AA.
XX AAE08285;
AC AAE08285;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #50 (residues 207-215).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
FN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
(UYAR-) UNIV ARKANSAS.
XX
PI O'Brien TJ;
XX
WPI; 2001-514676/56.
XX
Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
Claim 25; Page 113; 127pp; English.
XX
The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
XX Sequence 9 AA;
SQ

Adb80484 Ovarian c
Adj68833 Human hea
Adn39180 Cancer/an
Adl06515 Human tum
Adn04182 Antipsori
Adr72880 Human ova
Ady67588 Human kal
Aec00353 Human kal
Abb21326 Human HSC
Abb84420 Porcine S
Aau86677 Novel hum
Aau23217 Novel hum
Aau23752 Novel hum
Aau17043 Human nov
Adb60011 Connectiv
Adb21298 Human KJK
Abp64969 Human pro
Abr55400 Amino aci
Adn05516 Antipsori
Ady53877 Human kal
Aau16971 Human nov

Query Match 100.0%; Score 50; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

RESULT 2

ADR68841
ID ADR68841 standard; peptide; 9 AA.

XX AC ADR68841;

XX DT 02-DEC-2004 (first entry)

XX DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:80.

XX KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
XX KW immune response; ovarian cancer; lung cancer; prostate cancer;
XX KW pancreatic cancer; colon cancer.

XX OS Homo sapiens.

XX PN WO2004075723-A2.

XX PD 10-SEP-2004.

XX PF 20-FEB-2004; 2004WO-US005134.

XX PR 21-FEB-2003; 2003US-00372521.

XX PA (UYAR-) UNIV ARKANSAS.

XX PI O'brien TJ, Cannon MJ, Santin A;

XX DR WPI; 2004-653294/63.

XX PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.

XX PS Claim 5; SEQ ID NO 80; 117pp; English.

XX CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

RESULT 3

ADA05738

ID ADA05738 standard; protein; 181 AA.

XX AC ADA05738;

XX DT 06-NOV-2003 (first entry)

XX DE Human NOV18d protein SEQ ID NO:98.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
XX KW immunomodulator; cytostatic; nootropic; neuroprotective;
XX KW antiparkinsonian; antilipaeic; gene therapy; human disease;
XX KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
XX KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 12-OCT-2001; 2001US-0328056P.

XX PR 15-OCT-2001; 2001US-0328849P.

XX PR 17-OCT-2001; 2001US-0329414P.

XX PR 18-OCT-2001; 2001US-0330142P.

XX PR 22-OCT-2001; 2001US-0330309P.

XX PR 24-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 22-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 16-MAY-2002; 2002US-0381042P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerkusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

XX DR N-PSDB; ADA05737.

XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing,

XX PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,

XX PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or

XX PT pharmacogenomics.

XX PS Claim 1; Page 171; 586pp; English.

CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 181 AA;

Query Match 100.0%; Score 50; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. NO. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 133 GPLVCRGTL 141
|||||

RESULT 4
ADN62902
ID ADN62902 standard; protein; 181 AA.
XX
AC ADN62902;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18d.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
XX 26-FEB-2004.
PD
XX
PF 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR
PR 05-OCT-2001; 2001US-0327435P.
PR
PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 12-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KERODA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Sheno S G;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI: 2004-213931/20.
DR N-PSDB; ADN62901.
XX
XX
PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,

diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
Claim 1; SEQ ID NO 98; 395pp; English.

The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polynucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.

Sequence 181 AA;

Query Match 100.0%; Score 50; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9

Db 133 GPLVCRGTL 141

RESULT 5

ID ADA05736 standard; protein; 198 AA.

AC ADA05736;

DT 06-NOV-2003 (first entry)

DE Human NOV18c protein SEQ ID NO:96.

KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; neurotropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX WO2003029424-A2.

PD 10-APR-2003.

XX 02-OCT-2002; 2002WO-US031373.

XX 02-OCT-2001; 2001US-0326483P.

PR 05-OCT-2001; 2001US-0327435P.

PR 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerkusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36.

N-PSDB; ADA05735.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian and antilipaeamic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic

CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.

XX Sequence 198 AA;

Query Match 100.0%; Score 50; DB 6; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9

Db 152 GPLVCRGTL 160

RESULT 6

ADN62900
 ID ADN62900 standard; protein; 198 AA.

XX AC ADN62900;

XX DT 01-JUL-2004 (first entry)

XX DE Human NOV18c.

XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.

XX OS Homo sapiens.

XX PN US2004038223-A1.

XX PD 26-FEB-2004.

XX PF 01-OCT-2002; 2002US-00262511.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 09-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373460P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 16-MAY-2002; 2002US-0381042P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX

PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERRHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C B.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIP/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerrhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2004-213931/20.

DR N-PSDB; ADN62899.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX Claim 1; SEQ ID NO 96; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,

CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents the amino acid sequence of a human NOVX protein.
XX
SQ Sequence 198 AA;

Query Match 100.0%; Score 50; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
|||
Db 152 GPLVCRGTL 160

RESULT 7
ADA05744
ID ADA05744 standard; protein; 224 AA.

XX AC ADA05744;

XX DT 06-NOV-2003 (first entry)

XX DE Human NOV18g protein SEQ ID NO:104.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW immunomodulator; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 05-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 12-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 24-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 16-MAY-2002; 2002US-0381042P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX PR 01-OCT-2002; 2002US-00262511.

(CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patcurajan M, Szytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerkusen BD, Anderson DW, Zhong M, Catterton B;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimketa RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05743.

XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.

XX PS Claim 1; Page 172; 586pp; English.

XX CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, neuroprotective, antiparkinsonian
CC and antilipaeamic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

XX SQ Sequence 224 AA;

Query Match 100.0%; Score 50; DB 6; Length 224;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9

|||
Db 193 GPLVCRGTL 201

RESULT 8

ADN62908

ID ADN62908 standard; protein; 224 AA.

XX AC ADN62908;

XX DT 01-JUL-2004 (first entry)

DE Human NOV18g.
 XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX Homo sapiens.
 OS US2004038223-A1.
 PN 26-FEB-2004.
 PD
 XX 01-OCT-2002; 2002US-00262511.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327439P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJJ/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATI/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON B.
 PA (JIW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHINKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.

PA (AGEB/) AGESE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPPIO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dippio VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX WPI; 2004-213931/20.
 DR N-PSDB; ADN62907.
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX Claim 1; SEQ ID NO 104; 395pp; English.
 XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX Sequence 224 AA;
 SQ
 Query Match 100.0%; Score 50; DB 8; Length 224;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPLVCRGTL 9
 Db 193 GPLVCRGTL 201
 |||||
 RESULT 9
 ADV21100
 ID ADV21100 standard; protein; 224 AA.
 XX
 AC ADV21100;
 DT
 XX 24-FEB-2005 (first entry)
 XX Human stratum corneum chymotrypsin protein.
 DE
 XX

KW Protein purification; PS133 protein; serine protease; prostate disease;
 KW andrology; genitourinary disease; prostatic cancer; cytostatic;
 KW protein therapy; chymotrypsin; enzyme.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 26..42
 FT /note = Catalytically functional motif
 FT Domain 83..187
 FT /note = Catalytically functional motif
 FT Domain 174..179
 FT /note = Catalytically functional motif
 XX
 XX US2004241646-A1.
 XX
 XX 02-DEC-2004.
 XX
 XX 20-FEB-2001; 2001US-00789210.
 XX
 XX 06-OCT-1997; 97US-00944483.
 XX
 XX (COHE/) COHEN M.
 PA (COLP/) COLPITTS T L.
 PA (FRIE/) FRIEDMAN P N.
 PA (GRAN/) GRANADOS E.
 PA (KLAS/) KLAS M R.
 PA (RUS/) RUSSELL J C.
 PA (STEW/) STEWART K D.
 PA (STRO/) STROUPE S D.
 XX
 XX Cohen M, Colpitts TL, Friedman PM, Granados E, Kلاس MR;
 PI Russell JC, Stewart KD, Stroupe SD;
 XX
 XX WPI; 2005-011614/01.
 DR GENBANK; L33404.
 XX
 XX New isolated polypeptides, useful for detecting, diagnosing, staging,
 PT monitoring, prognosticating, preventing or treating, or determining
 PT predisposition to diseases or conditions of the prostate such as prostate
 PT cancer.
 XX
 XX Example 1; SEQ ID NO 33; 96pp; English.
 PS
 XX The invention relates to PS133 protein, a member of the human serine
 CC protease family and its corresponding nucleic acid sequence. PS133
 CC polypeptide is useful for detecting, diagnosing, staging, monitoring,
 CC prognosticating, preventing or treating or determining predisposition to
 CC diseases or conditions of the prostate such as prostatic cancer. The
 CC present sequence is the human stratum corneum chymotrypsin protein. This
 CC sequence is used to align with PS133 consensus protein.
 XX
 XX Sequence 224 AA;
 SQ
 Query Match 100.0%; Score 50; DB 9; Length 224;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GPLVCRGTL 9
 Db 178 GPLVCRGTL 186
 RESULT 10
 ID AAB98502 standard; protein; 225 AA.
 XX
 AC AAB98502;
 XX
 DT 03-AUG-2001 (first entry)
 DE Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
 XX

KW Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
 KW tumour antigen-derived gene 15; serine protease;
 KW Stratum Corneum Chymotryptic Enzyme; SCCE.
 XX
 OS Homo sapiens.
 XX
 PN WO200129056-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000WO-US029095.
 XX
 PR 20-OCT-1999; 99US-00421213.
 XX
 XX (UYAR-) UNIV ARKANSAS.
 PA
 XX O'brien TJ, Tanimoto H;
 PI
 XX WPI; 2001-381031/40.
 DR
 XX Novel extracellular serine protease, termed tumor antigen-derived gene 15
 PT protein overexpressed in carcinomas and DNA encoding it, for diagnosis,
 PT treatment, prevention of cancer, particularly breast, ovarian cancer.
 PT
 XX Example 10; Fig 1; 130pp; English.
 PS
 XX The present invention relates to human tumour antigen-derived gene 15
 CC (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-
 CC 15 is an extracellular serine protease. It was found that TADG-15 is over
 CC -expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20
 CC residues that lack TADG-15 protease activity are useful for vaccinating
 CC an individual against TADG-15, having, suspected of having or at risk of
 CC getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic
 CC or therapeutic target in cancer. The present sequence was used in a
 CC sequence homology alignment with the catalytic domain of TADG-15
 XX
 XX Sequence 225 AA;
 SQ
 Query Match 100.0%; Score 50; DB 4; Length 225;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GPLVCRGTL 9
 Db 179 GPLVCRGTL 187
 RESULT 11
 ADA05742
 ID ADA05742 standard; protein; 247 AA.
 XX
 AC ADA05742;
 XX
 DT 06-NOV-2003 (first entry)
 DE Human NOV18f protein SEQ ID NO:102.
 XX
 XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 XX

PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381042P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
PR (CURA-) CURAGEN CORP.
PR
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ji T, Gorwan L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Or W, Miller CE, Raetzelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05741.
DR
XX
PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 1; Page 172; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
CC and antilipaemic activities, and can be used in gene therapy. The

CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 50; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
Db 193 GPLVCRGTL 201
RESULT 12
ADN62906
ID ADN62906 standard; protein; 247 AA.
XX
AC ADN62906;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18f.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.

PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J. A.
 PA (KERU/) KERUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PAT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K. A.
 PA (EDIN/) EDINGER S. R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U. M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B. D.
 PA (ANDE/) ANDERSON D. W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIWW/) JI W.
 PA (MILL/) MILLER C. E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D. J.
 PA (PENA/) PENA C. E. A.
 PA (SHEN/) SHENOY S. G.
 PA (SHIM/) SHIMKETS R. A.
 PA (ROTH/) ROTHENBERG M. E.
 PA (LEAC/) LEACH M. D.
 PA (AGRE/) AGEE M. L.
 PA (BERG/) BERGHS C.
 PA (DIP/) DIPPO V. A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E. A.
 PA (RIEG/) RIEGER D. K.
 PA (SPAD/) SPADERNA S. K.
 XX
 PI Smithson G., Millet I., Peyman JA, Kekuda R., Ju J., Li L., Guo X;
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2004-213931/20.
 DR N-PSDB; ADN62905.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO 102; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,

CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 247 AA;

Query Match 100.0%; Score 50; DB 8; Length 247;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPLVCRGTL 9
 Db 193 GPLVCRGTL 201
 |||||

RESULT 13
 ADA05732
 ID ADA05732 standard; protein; 250 AA.

XX
 AC ADA05732;

XX
 DT 06-NOV-2003 (first entry)

XX
 DE Human NOV18a protein SEQ ID NO:92.

XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.

OS Homo sapiens.

XX
 PN WO2003029424-A2.

XX
 PD 10-APR-2003.

XX
 PF 02-OCT-2002; 2002WO-US031373.

XX
 PR 02-OCT-2001; 2001US-0326483P.

PR
 PR 05-OCT-2001; 2001US-0327435P.

PR
 PR 05-OCT-2001; 2001US-0327449P.

PR
 PR 09-OCT-2001; 2001US-0327917P.

PR
 PR 09-OCT-2001; 2001US-0328029P.

PR
 PR 09-OCT-2001; 2001US-0328044P.

PR
 PR 09-OCT-2001; 2001US-0328056P.

PR
 PR 12-OCT-2001; 2001US-0328849P.

PR
 PR 15-OCT-2001; 2001US-0329414P.

PR
 PR 17-OCT-2001; 2001US-0330142P.

PR
 PR 18-OCT-2001; 2001US-0330309P.

PR
 PR 22-OCT-2001; 2001US-0341058P.

PR
 PR 24-OCT-2001; 2001US-0339266P.

PR
 PR 24-OCT-2001; 2001US-0343629P.

PR
 PR 29-OCT-2001; 2001US-0349575P.

PR
 PR 01-NOV-2001; 2001US-0346357P.

PR
 PR 17-APR-2002; 2002US-0373260P.

PR
 PR 19-APR-2002; 2002US-0373815P.

PR
 PR 19-APR-2002; 2002US-0373826P.

PR
 PR 19-APR-2002; 2002US-0373884P.

PR
 PR 22-APR-2002; 2002US-0374977P.

PR
 PR 16-MAY-2002; 2002US-0381037P.

PR
 PR 16-MAY-2002; 2002US-0381038P.

PR
 PR 16-MAY-2002; 2002US-0381042P.

PR
 PR 17-MAY-2002; 2002US-0381642P.

PR
 PR 28-MAY-2002; 2002US-0383656P.

PR
 PR 29-MAY-2002; 2002US-0383831P.

PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytka KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05731.
XX
XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 169-170; 586pp; English.
PS
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
CC and antipaleptic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
XX present invention.
XX
XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 50; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
|||
Db 204 GPLVCRGTL 212
RESULT 14
ADN62896
ID ADN62896 standard; protein; 250 AA.
XX
XX AC ADN62896;

XX
DT 01-JUL-2004 (first entry)
XX
XX Human NOV18a.
XX
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX Homo sapiens.
XX
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 16-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
XX (SMIT/) SMITHSON G.
PA (MIL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.

PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M B.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 XX WPI; 2004-213931/20.
 DR N-PSDB; ADN62895.
 DR
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 XX Claim 1; SEQ ID NO 92; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 XX Sequence 250 AA;
 SQ
 Query Match 100.0%; Score 50; DB 8; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPLVCRGTL 9
 Db 204 GPLVCRGTL 212
 RESULT 15
 ADA05734
 ID ADA05734 standard; protein; 252 AA.
 XX
 AC ADA05734;
 XX
 DT 06-NOV-2003 (first entry)

XX Human NOV18b protein SEQ ID NO:94.
 DE
 XX human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO2003029424-A2.
 PN
 XX 10-APR-2003.
 PD
 XX
 XX 02-OCT-2002; 2002WO-US031373.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383833P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX (CURA-) CURAGEN CORP.
 XX
 XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 XX WPI; 2003-381626/36.
 DR N-PSDB; ADA05733.
 DR
 XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 XX Claim 1; Page 170; 586pp; English.
 XX
 CC The present invention describes NOVX proteins, where X can be 1 to 55
 CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOVX protein of the invention; (4) a vector

CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOVX
 CC sequences have antidiabetic, anorectic, antibacterial, virucide,
 CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
 CC and antilipase activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders, such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidaemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence represents a human NOVX from the
 CC present invention.
 XX
 SQ Sequence 252 AA;

Query Match 100.0%; Score 50; DB 6; Length 252;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPLVCRGTL 9
 Db 206 GPLVCRGTL 214
 |||||

Search completed: March 11, 2006, 00:24:16
 Job time : 86.6667 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GPLVCRGTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	253	2 A53968	serine proteinase
2	40	80.0	261	1 A32297	semenogelase (EC 3
3	40	80.0	261	2 A29586	tissue kallikrein
4	40	80.0	262	2 T35999	probable aminoglyc
5	39	78.0	155	2 G72548	hypothetical prote
6	39	78.0	265	1 KQRTP	tissue kallikrein
7	38	76.0	246	1 DBHU	complement factor
8	38	76.0	261	1 S35711	semenogelase (EC 3
9	37	74.0	46	2 I49416	glandular kallikre
10	37	74.0	96	2 A05308	tissue kallikrein
11	37	74.0	104	2 S15395	tissue kallikrein
12	37	74.0	156	2 B23863	tissue kallikrein
13	37	74.0	188	2 B32340	tissue kallikrein
14	37	74.0	225	2 S45356	probable serine pr
15	37	74.0	239	2 A27207	tissue kallikrein
16	37	74.0	240	2 S39047	trypsin (EC 3.4.21
17	37	74.0	241	2 S39048	trypsin (EC 3.4.21
18	37	74.0	244	2 A44284	tissue kallikrein
19	37	74.0	250	2 S15685	kallikrein, glandu
20	37	74.0	254	2 S35585	chymotrypsin-like
21	37	74.0	258	2 I56220	trypsin 2 - rat
22	37	74.0	259	1 KQRTIN	tonin (EC 3.4.21.-
23	37	74.0	259	2 A29746	tissue kallikrein
24	37	74.0	259	2 D23863	tissue kallikrein
25	37	74.0	260	2 I56559	neutropsin - mouse
26	37	74.0	261	1 KQMS1	tissue kallikrein
27	37	74.0	261	1 NGMSG	7S nerve growth fa
28	37	74.0	261	1 TRMSM5	tissue kallikrein
29	37	74.0	261	2 S45303	tissue kallikrein

30	37	74.0	261	2 A28062	gamma-renin (EC 3.
31	37	74.0	261	2 A25606	tissue kallikrein
32	37	74.0	261	2 S01971	tissue kallikrein
33	37	74.0	261	2 A29745	tissue kallikrein
34	37	74.0	261	2 A34079	tissue kallikrein
35	37	74.0	263	2 S15686	tissue kallikrein
36	37	74.0	264	2 S65663	granzyme 3 (EC 3.4
37	37	74.0	599	2 T12994	riboflavin biosynt
38	36	72.0	66	2 I52972	kallikrein - mouse
39	36	72.0	73	2 S44462	elastase (EC 3.4.2
40	36	72.0	149	1 KQMSM	tissue kallikrein
41	36	72.0	226	2 S69370	duodenase - bovine
42	36	72.0	229	1 TRDPS	trypsin (EC 3.4.21
43	36	72.0	231	1 TRPOTR	trypsin (EC 3.4.21
44	36	72.0	231	2 S31778	trypsin (EC 3.4.21
45	36	72.0	236	1 A32121	snake venom factor

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:9521214; PIDN:7
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||
DB 207 GPLVCRGTL 215

RESULT 2

A32297
semenogelase (EC 3.4.21.77) precursor [validated] - human
N;Alternate names: gamma-geminoprotein; P-30 antigen; prostate-specific antigen; prostate
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A32297; A32423; S03604; S05468; S05467; A32546; S02239; A26757; C31567; A315
R;Riegman, P.H.J.; Vlietstra, R.J.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
Biochem. Biophys. Res. Commun. 159, 95-102, 1989
A;Title: Characterization of the prostate-specific antigen gene: a novel human kallikrein
A;Reference number: A32297; MUID:89165891; PMID:2466464
A;Accession: A32297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-261 <RIE>
A;Cross-references: UNIPROT:P07288; UNIPARC:UPI0000001C9E; GB:M24543
R;Lundwall, A.
Biochem. Biophys. Res. Commun. 161, 1151-1159, 1989
A;Title: Characterization of the gene for prostate-specific antigen, a human glandular ka
A;Reference number: A32423; MUID:89302090; PMID:2472789

A:Accession: A32423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-261 <LUN>
A:Cross-references: UNIPARC:UPI0000001C98; GB:M27274; NID:g190552; PIDN:AAA60192.1; PID: R; Digby, M.; Zhang, X.Y.; Richards, R.I.
Nucleic Acids Res. 17, 2137, 1989
A:Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallikrein gene
A:Reference number: S03604; MUID:89183632; PMID:2467258
A:Accession: S03604
A:Molecule type: DNA
A:Residues: 1-261 <DTG>
A:Cross-references: UNIPARC:UPI0000001C98; EMBL:X13940
R; Klobbeck, H.G.; Combratio, G.; Schulz, P.; Arbush, V.; Fittler, F.
submitted to the EMBL Data Library, May 1989
A:Reference number: S05468
A:Accession: S05468
A:Molecule type: DNA
A:Residues: 1-261 <KL1>
A:Cross-references: UNIPARC:UPI0000001C98; EMBL:X14810; NID:g35732; PIDN:CAA32915.1; PID: R; Klobbeck, H.G.; Combratio, G.; Schulz, P.; Arbush, V.; Fittler, F.
Nucleic Acids Res. 17, 3981, 1989
A:Title: Genomic sequence of human prostate specific antigen (PSA).
A:Reference number: S05467; MUID:89282407; PMID:2471958
A:Accession: S05467
A:Molecule type: DNA
A:Residues: 1-29 <KL2>
A:Cross-references: UNIPARC:UPI0000172AC3; EMBL:X14810
R; Henttu, P.; Viikio, P.
Biochem. Biophys. Res. Commun. 160, 903-910, 1989
A:Title: cDNA coding for the entire human prostate specific antigen shows high homology to the rat prostate specific antigen cDNA
A:Reference number: A32546; MUID:89246551; PMID:2470373
A:Accession: A32546
A:Molecule type: mRNA
A:Residues: 1-72, 'T', 74-85, 'I', 87-174, 'P', 176-183, 'Q', 185-259, 'D', 261 <HEN>
A:Cross-references: UNIPARC:UPI0000172AC4; GB:M26663
R; Schulz, P.; Stucka, R.; Feldmann, H.; Combratio, G.; Klobbeck, H.G.; Fittler, F.
Nucleic Acids Res. 16, 6226, 1988
A:Title: Sequence of a cDNA clone encompassing the complete mature human prostate specific antigen
A:Reference number: S02239; MUID:88289366; PMID:2456523
A:Accession: S02239
A:Molecule type: mRNA
A:Residues: 1-72, 'T', 74-85, 'I', 87-174, 'P', 176-183, 'Q', 185-259, 'D', 261 <HEN>
A:Cross-references: UNIPARC:UPI0000172AC4; GB:M26663
R; Schulz, P.; Stucka, R.; Feldmann, H.; Combratio, G.; Klobbeck, H.G.; Fittler, F.
Nucleic Acids Res. 16, 6226, 1988
A:Title: Sequence of a cDNA clone encompassing the complete mature human prostate specific antigen
A:Reference number: A26757; MUID:87190978; PMID:2436946
A:Accession: A26757
A:Molecule type: mRNA
A:Residues: 5-261 <LU2>
A:Cross-references: UNIPARC:UPI000000044B
R; Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
Biochem. Biophys. Res. Commun. 155, 181-188, 1988
A:Title: Molecular cloning and characterization of novel prostate antigen cDNA's.
A:Reference number: A90144; MUID:88326297; PMID:2458104
A:Accession: C31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189523; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Tauda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: Molecular cloning of human prostate specific antigen cDNA.
A:Reference number: A26757; MUID:87190978; PMID:2436946
A:Accession: A26757
A:Molecule type: mRNA
A:Residues: 5-261 <LU2>
A:Cross-references: UNIPARC:UPI000000044B
R; Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
Biochem. Biophys. Res. Commun. 155, 181-188, 1988
A:Title: Molecular cloning and characterization of novel prostate antigen cDNA's.
A:Reference number: A90144; MUID:88326297; PMID:2458104
A:Accession: C31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189523; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Tauda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A:Title: Molecular cloning of human prostate specific antigen cDNA.
A:Reference number: A26757; MUID:87190978; PMID:2436946
A:Accession: A26757
A:Molecule type: mRNA
A:Residues: 5-261 <LU2>
A:Cross-references: UNIPARC:UPI000000044B
R; Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
Biochem. Biophys. Res. Commun. 155, 181-188, 1988
A:Title: Molecular cloning and characterization of novel prostate antigen cDNA's.
A:Reference number: A90144; MUID:88326297; PMID:2458104
A:Accession: C31567
A:Molecule type: mRNA
A:Residues: 5-261 <RL2>
A:Cross-references: UNIPARC:UPI000000044B; GB:M21895; NID:g189523; PIDN:AAAS9995.1; PID: R; Schaller, J.; Akiyama, K.; Tauda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987

A:Accession: A29586
A:Molecule type: DNA
A:Residues: 1-261 <SCH>
A:Cross-references: UNIPROT:P20151; UNIPARC:UPI000004CA0C; GB:M18157; NID:g186640; PIDN:
A>Note: the authors translated the codon TAC for residue 43 as Trp
C:Genetics:
A:Introns: 16/1; 69/2; 165/1; 210/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 80.0%; Score 40; DB 2; Length 261;
Best Local Similarity 77.8%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||: |||
DB 215 GPLVCGVL 223

RESULT 4
T35999
Probable aminoglycoside acetyltransferase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T35999
R:Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21574
A:Accession: T35999
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-262 <SEE>
A:Cross-references: UNIPROT:O9XAC9; UNIPARC:UPI00000DB235; EMBL:AL096839; PIDN:CAB50752.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SC06DB:SCC22.09
C:Superfamily: Escherichia coli aminoglycoside N3'-acetyltransferase

Query Match 80.0%; Score 40; DB 2; Length 262;
Best Local Similarity 88.9%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||: |||
DB 8 GPLVTRGTL 16

RESULT 5
G72548
Hypothetical protein APE1675 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72548
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <KAW>
A:Cross-references: UNIPROT:Q9YBC2; UNIPARC:UPI000005E041; DDBJ:AP000062; NID:G5105244;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1675

Query Match 78.0%; Score 39; DB 2; Length 155;
Best Local Similarity 77.8%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||: |||
DB 23 GPLITRGTL 31

RESULT 6
KQRTF
tissue kallikrein (EC 3.4.21.35) precursor - rat
N:Alternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004
C:Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R:Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A:Title: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of t
A:Reference number: A00944; MUID:83117659; PMID:6961406
A:Accession: A00944
A:Molecule type: mRNA
A:Residues: 1-265 <SWI>
A:Cross-references: UNIPROT:P00758; UNIPARC:UPI00000167958
A:Experimental source: pancreatic
R:Kato, H.; Nakanishi, E.; Enryoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A:Title: Characterization of serine proteinases isolated from rat submaxillary gland: wit
A:Reference number: A41429; MUID:88198057; PMID:3482210
A:Accession: A41429
A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-53, 'X', 55-87 <KAT>
A:Cross-references: UNIPARC:UPI0000172ABF
R:Gerald, W.L.; Chao, J.; Chao, L.
Biochim. Biophys. Acta 866, 1-14, 1986
A:Title: Immunological identification of rat tissue kallikrein cDNA and characterization
A:Reference number: A25137; MUID:86131678; PMID:3004582
A:Accession: A25137
A:Molecule type: mRNA
A:Residues: 115-265 <GER>
A:Cross-references: UNIPARC:UPI0000172AC0
R:Inoue, H.; Fukui, K.; Miyake, Y.
J. Biochem. 105, 834-840, 1989
A:Title: Identification and structure of the rat true tissue kallikrein gene expressed in
A:Reference number: JX0073; MUID:89327211; PMID:2753879
A:Accession: JX0073
A:Molecule type: DNA
A:Residues: 1-265 <INO>
A:Cross-references: UNIPARC:UPI0000167958; GB:D00448; NID:g220792; PIDN:BAA00346.1; PID:9
A:Experimental source: kidney
R:Ashley, P.L.; MacDonald, R.J.
Biochemistry 24, 4512-4520, 1985
A:Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A:Reference number: A23863; MUID:86051477; PMID:2998455
A:Accession: A23863
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <ASH>
A:Cross-references: UNIPARC:UPI0000167958; GB:M11563; NID:g205029; PIDN:AAA41464.1; PID:9
A:Experimental source: submaxillary gland
R:Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A:Title: Organization and expression of the rat kallikrein gene family.
A:Reference number: A33359; MUID:89214217; PMID:2708383
A:Accession: A33359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 5-265 <WIN>
A:Cross-references: UNIPARC:UPI000012DBE1; GB:M23874; GB:J04701; GB:M23875; GB:M23876; N
C:Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapeptide, from kin
C:Comment: The protein presumably assumes the two-chain form by cleavage between residue
C:Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release l
C:Genetics:
A:Introns: 20/1; 73/2; 169/1; 214/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; serine proteinase; zymogen

F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-28/Domain: activation peptide #status predicted <APT>
F:29-265/Product: tissue kallikrein, pancreatic #status predicted <MPT>
F:29-257/Domain: trypsin homology <TRY>
F:35-177,54-70,156-223,213-238/Disulfide bonds: #status predicted
F:69,124,217/Active site: His, Asp, Ser #status predicted

Query Match 78.0%; Score 39; DB 1; Length 265;
Best Local Similarity 66.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
DB 219 GPLICNGVL 227

RESULT 7
DBHU
complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
N:Alternate names: adipsin; C3 convertase activator
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: A40197; A00936; A60571; S66645
R:White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.; J. Biol. Chem. 267, 9210-9213, 1992
A:Title: Human adipsin is identical to complement factor D and is expressed at high level
A:Reference number: A40197; MUID:92250520; PMID:1374388
A:Accession: A40197
A:Molecule type: mRNA
A:Residues: 1-246 <WHI>
A:Cross-references: UNIPROT:P00746; UNIPARC:UPI0000172AB4; GB:M84526
R:Niemann, M.A.; Bhow, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
A:Title: Amino acid sequence of human D of the alternative complement pathway.
A:Reference number: A00936; MUID:85000441; PMID:6383466
A:Accession: A00936
A:Molecule type: protein
A:Residues: 19-44,'G',46-51,'Q',53-75,'TH',78,'P',80-83,'XXXITIE',90-172,86-91,185-235,'
A:Cross-references: UNIPARC:UPI0000172AE5
A:Note: a few residues were assigned from the previously published sequence of Reid et al
R:Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya
Mol. Immunol. 27, 637-644, 1990
A:Title: Molecular and functional identification and purification of complement component
A:Reference number: A60571; MUID:90370044; PMID:2395435
A:Accession: A60571
A:Molecule type: protein
A:Residues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>
A:Cross-references: UNIPARC:UPI0000172AE6
R:Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A:Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement
A:Reference number: S66645; MUID:196013156; PMID:7556615
A:Accession: S66645
A>Status: preliminary
A:Molecule type: protein
A:Residues: 19-44,'C',46-48 <BAL>
A:Cross-references: UNIPARC:UPI0000172AE7
C:Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
C:Genetics:
A:Gene: GDB:DF
A:Cross-references: GDB:132645; OMIM:134350
A:Map position: Xpter-Xqter
A:Superfamily: trypsin, trypsin homology
C:Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-246/Product: complement factor D (fragment) #status experimental <MAT>
F:19-241/Domain: trypsin homology <TRY>
F:44-60,141-207,172-189,197-222/Disulfide bonds: #status predicted
F:59,105,201/Active site: His, Asp, Ser #status predicted

Query Match 76.0%; Score 38; DB 1; Length 246;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
DB 203 GPLVCGVL 211

RESULT 8
S35711
semenogelase (EC 3.4.21.77) precursor - rhesus macaque
N:Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: S35711; S34239
R:Gauthier, E.R.; Chapdelaine, P.; Tremblay, R.R.; Dube, J.Y.
Biochim. Biophys. Acta 1174, 207-210, 1993
A:Title: Characterization of rhesus monkey prostate specific antigen cDNA.
A:Reference number: S35711; MUID:93363642; PMID:7689340
A:Accession: S35711
A:Molecule type: mRNA
A:Residues: 1-261 <GAU>
A:Cross-references: UNIPROT:P33619; UNIPARC:UPI000012DEE4; EMBL:X73560; NID:g311843; PID:
C:Comment: This enzyme preferentially cleaves after tyrosine residues.
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; prostate; serine proteinase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-24/Domain: propeptide #status predicted <PRO>
F:25-261/Product: semenogelase #status predicted <MAT>
F:25-253/Domain: trypsin homology <TRY>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 76.0%; Score 38; DB 1; Length 261;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
DB 215 GPLVCDGVL 223

RESULT 9
I49416
glandular kallikrein - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49416
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-46 <RES>
A:Cross-references: UNIPROT:Q62540; UNIPARC:UPI00000E8743; EMBL:U05716; NID:g497047; PID:
C:Superfamily: trypsin; trypsin homology

Query Match 74.0%; Score 37; DB 2; Length 46;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
DB 1 GPLICDGVL 9

RESULT 10
A05308
tissue kallikrein (EC 3.4.21.35), submandibular mGK-2 - mouse (fragment)
N:Alternate names: glandular kallikrein
C:Species: Mus musculus (house mouse)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1997 #text_change 22-Jun-1999
C:Accession: A05308
R:Mason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I.

Nature 303, 300-307, 1983
A;Title: Structure of mouse kallikrein gene family suggests a role in specific processing
A;Reference number: A009411; MUID:83219214; PMID:6602295
A;Accession: A05308
A;Molecule type: DNA
A;Residues: 1-96 <MAS>
A;Cross-references: UNIPARC:UPI000011E01B; GB:V00829; NID:G52775; PIDN:CAA24212.1; PID:9
A;Experimental source: Quakembush inbred strain
A;Note: this sequence has been translated from two exons (11-147 and 522-674) located up
C;Comment: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release
C;Genetics:
A;Gene: mGK-2
A;Map position: 7
A;Introns: 45/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland
F;1-88/Domain: trypsin homology (fragment) <TRY>

Query Match 74.0%; Score 37; DB 2; Length 96;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 50 GPLICDGV 58

RESULT 11
S15395
tissue kallikrein-related proteinase (EC 3.4.21.-) k10 - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #sequence_revision 19-Jul-1996 #text_change 17-Oct-1997
C;Accession: S15395; S15448
R;Gutman, N.; Elmoujahed, A.; Brillard, M.; Monegier du Sorbier, B.; Gauthier, F.
Eur. J. Biochem. 197, 425-429, 1991
A;Title: Microheterogeneity of rat submaxillary gland kallikrein k10, a member of the ka
A;Reference number: S15395; MUID:91224135; PMID:2026164
A;Accession: S15395
A;Molecule type: protein
A;Residues: 1-23;24-51;52-104 <GUT>
A;Cross-references: UNIPARC:UPI0000175BB8; UNIPARC:UPI0000175BB9; UNIPARC:UPI0000175BBA
A;Experimental source: submaxillary gland
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-104/Domain: trypsin homology (fragments) <TRY>
F;1-23/Product: tissue kallikrein-related protein k10 light chain (fragment) #status ex
F;24-51/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex
F;52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status ex

Query Match 74.0%; Score 37; DB 2; Length 104;
Best Local Similarity 66.7%; Pred. No. 9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 70 GPLICDGV 78

RESULT 12
B23863
tissue kallikrein (EC 3.4.21.35) S1, submaxillary - rat (fragment)
N;Alternate names: glandular kallikrein; kininogenin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
C;Accession: B23863
R;Ashley, P.L.; MacDonald, R.J.
Biochemistry 24, 4512-4520, 1985
A;Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
A;Reference number: A23863; MUID:86051477; PMID:2998455
A;Accession: B23863
A;Molecule type: mRNA
A;Residues: 1-156 <ASH>
A;Cross-references: UNIPROT:P15950; UNIPARC:UPI00001709DD; GB:M11564; NID:G205031; PIDN:

C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-148/Domain: trypsin homology (fragment) <TRY>

Query Match 74.0%; Score 37; DB 2; Length 156;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 110 GPLICDGV 118

RESULT 13
B32340
tissue kallikrein (EC 3.4.21.35) 3 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B32340
R;Shai, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.
Biochemistry 28, 5334-5343, 1989
A;Title: Characterization of genes encoding rat tonin and a kallikrein-like serine protease
A;Reference number: A32340; MUID:89375248; PMID:2550051
A;Accession: B32340
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <SHA>
A;Cross-references: UNIPROT:P15950; UNIPARC:UPI0000170B08; GB:M26534; NID:G206773; PIDN:
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-180/Domain: trypsin homology (fragment) <TRY>

Query Match 74.0%; Score 37; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 142 GPLICDGV 150

RESULT 14
S45356
probable serine proteinase (EC 3.4.21.-) ACO - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
C;Accession: S45356
R;Dihanich, M.; Spiess, M.
Biochim. Biophys. Acta 1218, 225-228, 1994
A;Title: A novel serine proteinase-like sequence from human brain.
A;Reference number: S45356; MUID:94289486; PMID:8018728
A;Accession: S45356
A;Molecule type: mRNA
A;Residues: 1-225 <DIH>
A;Cross-references: UNIPARC:UPI000016AFB3; EMBL:X75363; NID:G407137; PIDN:CAA53145.1; PI
A;Experimental source: Alzheimer's disease patient brain cortex
C;Genetics:
A;Gene: ACO
A;Introns: 175/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase

Query Match 74.0%; Score 37; DB 2; Length 225;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||:|
Db 180 GPLVCGGIL 188

RESULT 15
A27207

tissue kallikrein (EC 3.4.21.35), prostatic - guinea pig
N:Alternate names: glandular kallikrein
C:Species: Cavia porcellus (guinea pig)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27207
R:Dunbar, J.C.; Bradshaw, R.A.
Biochemistry 26, 3471-3478, 1987
A:Title: Amino acid sequence of guinea pig prostatic kallikrein.
A:Reference number: A27207; MUID:88000549; PMID:3307909
A:Accession: A27207
A:Molecule type: protein
A:Residues: 1-239 <DUN>
A:Cross-references: UNIPROT:PI2323; UNIPARC:UPI000012DEE2
A:Note: 50-Trp was also found
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-231/Domain: trypsin homology <TRY>
F:41,96,191/Active site: His, Asp, Ser #status predicted

Query Match 74.0%; Score 37; DB 2; Length 239;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 193 GPLICDGV 201

Search completed: March 11, 2006, 00:40:51
Job time : 14.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GPLVCRGTL 9

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	140	Q5R567_PONPY	Q5R567 pongo pygma
2	50	100.0	253	1 KLK7_HUMAN	P49862 homo sapien
3	45	90.0	250	1 KLK9_HUMAN	Q9UKQ9 homo sapien
4	45	90.0	251	2 Q9DBQ8_MOUSE	Q9DBQ8 mus musculus
5	44	88.0	210	2 Q63211_XENLA	Q63211 xenopus lae
6	44	88.0	251	1 KLK14_HUMAN	Q9PQ03 homo sapien
7	44	88.0	251	2 Q6B089_HUMAN	Q6B089 homo sapien
8	41	82.0	87	2 Q9CQ78_MOUSE	Q9CQ78 m mus muscu
9	41	82.0	249	2 Q9QYN4_MOUSE	Q9QYN4 mus musculus
10	41	82.0	253	2 Q5QBG5_9DIPT	Q5QBG5 culicoides
11	41	82.0	276	2 Q9QYN3_MOUSE	Q9QYN3 m hippostas
12	41	82.0	612	2 Q83WX7_STRBO	Q83WX7 streptomyc
13	41	82.0	621	2 Q8G3L1_BIFLO	Q8G3L1 bifidobacte
14	41	82.0	3201	2 Q9F828_9ACTO	Q9F828 micromonosp
15	41	82.0	3546	2 Q9F830_9ACTO	Q9F830 micromonosp
16	40	80.0	185	2 Q7Q831_ANOGA	Q7Q831 anopheles g
17	40	80.0	220	2 Q8NCW4_HUMAN	Q8NCW4 homo sapien
18	40	80.0	231	2 Q6GYJ5_STRCA	Q6GYJ5 struthio ca
19	40	80.0	248	2 Q5M813_XENTR	Q5M813 xenopus tro
20	40	80.0	254	2 Q9XSN6_PIG	Q9XSN6 sus scrofa
21	40	80.0	255	2 Q7Q235_ANOGA	Q7Q235 anopheles g
22	40	80.0	257	2 Q6LDS3_HUMAN	Q6LDS3 homo sapien
23	40	80.0	257	2 Q8QG86_BOTIN	Q8QG86 bothrops in
24	40	80.0	258	1 VSP3_BOTJA	Q9PTU8 bothrops ja
25	40	80.0	260	1 NRPN_RAT	Q8B780 rattus norv
26	40	80.0	260	2 Q71QJ2_TRIST	Q71QJ2 trimeresuru
27	40	80.0	260	2 Q71QI4_TRIST	Q71QI4 trimeresuru
28	40	80.0	260	2 Q71QH9_TRIST	Q71QH9 trimeresuru
29	40	80.0	261	1 KLK2_HUMAN	P20151 homo sapien
30	40	80.0	261	1 KLK3_HUMAN	P07288 homo sapien
31	40	80.0	261	2 Q546G3_HUMAN	Q546G3 homo sapien

32	40	80.0	262	2 Q9YAC9_STRCO	Q9YAC9 streptomyc
33	40	80.0	619	2 Q8KEH3_CHLFE	Q8KEH3 chlorobium
34	39	78.0	155	2 Q9YBC2_AERPE	Q9YBC2 aeropyrum p
35	39	78.0	161	2 Q5TUL3_ANOGA	Q5TUL3 anopheles g
36	39	78.0	176	2 Q52Q15_9PERC	Q52Q15 anoplarchus
37	39	78.0	178	2 Q52Q14_9PERC	Q52Q14 xiphister m
38	39	78.0	214	2 Q4SSW0_TETNG	Q4SSW0 tetraodon n
39	39	78.0	247	2 Q9W7Q5_PAROL	Q9W7Q5 paralichthy
40	39	78.0	249	2 Q5M910_XENTR	Q5M910 xenopus tro
41	39	78.0	249	2 Q5M8T8_XENTR	Q5M8T8 xenopus tro
42	39	78.0	252	2 Q5M908_XENTR	Q5M908 xenopus tro
43	39	78.0	254	2 Q5XG53_XENLA	Q5XG53 xenopus lae
44	39	78.0	261	1 KLK1_RAT	P00758 r nerve gro
45	39	78.0	297	2 Q9W174_DROME	Q9W174 drosophila

ALIGNMENTS

RESULT 1
Q5R567_PONPY Q5R567_PONPY PRELIMINARY; PRT; 140 AA.
AC Q5R567;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKF2p459E0918.
GN Name=DKF2p459E0918;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cortex;
RG The German CDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, CR860999; CAH93099.1; -; mRNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Hypothetical protein; Protease; Serine protease.
SQ SEQUENCE 140 AA; 15127 MW; 8DD6280252A39311 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 1 GPLVCRGTL 9
Db 94 GPLVCRGTL 102

RESULT 2
KLK7_HUMAN STANDARD; PRT; 253 AA.
ID KLK7_HUMAN Q8N5N9; Q8NFV7;
AC P49862; Q8N5N9 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 48, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (SC 3.4.21.-) (hK7) (Stratum corneum
DE chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 /FTRIDA_VSP_013581.
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A668 CRC64;

Query Match 100.0%; Score 50; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 3
KLK9_HUMAN STANDARD; PRT; 250 AA.
AC Q9UKQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-L3).
DE L3.
GN Names=KLK9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4.";
RT 19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20247258; PubMed=10783266; DOI=10.1006/geno.2000.6159;
RA Yousef G.M., Diamandis E.P.;
RT "The expanded human kallikrein gene family: locus characterization and molecular cloning of a new member, KLK-L3.";
RL Genomics 65:184-194 (2000).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McQuaig J., Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
RL Gene 257:119-130 (2000).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J., Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M., Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E., Canepeel S., Carrano A.V., Caolile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C., Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M., Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T., Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H., Kobayashi A., Larionov V., Leem S.-H., Lopez P., Lou Y., Lowry S., Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J., Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M., Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

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RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D., Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A., Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I., Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E., Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M., Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19.";
RL Nature 428:529-535 (2004).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal cord.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.
CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC
CC EMBL; AF135026; AAD26427.2; -; Genomic DNA.
CC EMBL; AF243527; AAG33362.1; -; Genomic DNA.
CC EMBL; AC011473; AAG23255.1; -; Genomic DNA.
CC HSSP; P00746; 1FDP.
CC MEROPS; S01.307; -.
CC Ensembl; ENSG00000129455; Homo sapiens.
CC HGNC; HGNC:6370; KLK9.
CC MIM; 605504; -.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
CC GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
CC InterPro; IPR001254; Peptidase_S1_S6.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; Trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS0240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC GlycoProtein; Hydrolyase; Protease; Serine protease; Signal.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 250 Kallikrein 9.
FT DOMAIN 23 249 Peptidase S1.
FT ACT_SITE 63 63 Charge relay system (By similarity).
FT ACT_SITE 111 111 Charge relay system (By similarity).
FT ACT_SITE 204 204 Charge relay system (By similarity).
FT CARBOHYD 131 131 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 211 211 N-linked (GlcNAc...) (Potential).
FT DISULFID 29 164 By similarity.
FT DISULFID 48 64 By similarity.
FT DISULFID 136 238 By similarity.
FT DISULFID 143 210 By similarity.
FT DISULFID 175 189 By similarity.
FT DISULFID 200 225 By similarity.
SQ SEQUENCE 250 AA; 27513 MW; F2785245B063E98B CRC64;

Query Match 90.0%; Score 45; DB 1; Length 250;
Best Local Similarity 88.9%; Pred. No. 2.5; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

QY 1 GPLVCRGTL 9
Db 206 GPLVCRGTL 214

RESULT 4
Q9DBQ8_MOUSE PRELIMINARY; PRT; 251 AA.
ID Q9DBQ8_MOUSE PRELIMINARY;
AC Q9DBQ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

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FT DISULFID 52 68 By similarity.
FT DISULFID 143 210 By similarity.
FT DISULFID 175 189 By similarity.
FT DISULFID 200 225 By similarity.
SQ SEQUENCE 251 AA; 27453 MW; 9087953BAFA7ED25 CRC64;
Query Match 88.0%; Score 44; DB 1; Length 251;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;
Indels 1; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
Db 206 GPLVCRGQL 214
RESULT 7
Q6B089 HUMAN
ID Q6B089 HUMAN PRELIMINARY; PRT; 251 AA.
AC Q6B089;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 13-Sep-2005 (TrEMBLrel. 31, Last annotation update)
DE Kallikrein 14, preproprotein.
GN Name=KLK14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL EMBL; BC074905; AAH74905.1; -; mRNA.
DR EMBL; BC074904; AAH74904.1; -; mRNA.
DR Ensemble; ENSG00000129437; Homo sapiens.
DR GO; GO:004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
DR DR InterPro; IPR001254; Peptidase_S1_S6.
DR DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM00020; TRY SP; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 251 AA; 27507 MW; C353A7D8B1960BD2 CRC64;
Query Match 88.0%; Score 44; DB 2; Length 251;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;
Indels 1; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
Db 206 GPLVCRGQL 214
RESULT 8
Q9CQ78 MOUSE
ID Q9CQ78 MOUSE PRELIMINARY; PRT; 87 AA.
AC Q9CQ78;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Mus musculus adult male tongue cDNA, RIKEN full-length
DE library, clone:2310081E03 product:protease, serine, 20, full insert
DE sequence (Mus musculus adult male tongue cDNA, RIKEN full-length
DE enriched library, clone:2310021N04 product:protease, serine, 20, full
DE insert sequence) (Fragment).
GN Name=2310015108Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085560; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Marzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wuzhah-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Clothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wu Ming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RN Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20530913; PubMed=10716861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RN Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sogabe Y., Suzuki H., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK019102; BAB31548.1; -; mRNA.
 DR HSSP; P00760; 1EZX.
 DR MEROPS; S01.257; -.
 DR MGI; MGI:1929977; 2310015108Rik.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR Pfam; PF00889; Trypsin; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Protease.
 FT NON_TER
 SQ SEQUENCE 87 AA; 9549 MW; B988D0CD62926EAA CRC64;
 Query Match 82.0%; Score 41; DB 2; Length 87;
 Best Local Similarity 77.8%; Pred. NO. 5;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GPLVCRGTL 9
 DB 42 GPLVCGSL 50
 RESULT 9
 Q9QYN4 MOUSE
 ID Q9QYN4.MOUSE PRELIMINARY; PRT; 249 AA.
 AC Q9QYN4;
 DT 01-WAY-2000 (TrEMBLrel. 13, Created)
 DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hippostasin.
 GN Name=2310015108Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
 RA Mitsui S., Okui A., Kominami K., Demura H., Yamaguchi N.;
 RT "cDNA cloning and tissue-specific splicing variants of mouse
 RT hippostasin/TLSP (PRSS20).";
 RN Biochim. Biophys. Acta 1494:206-210 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Yamaguchi N., Mitsui S.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB016226; BAA88825.1; -; mRNA.
 DR HSSP; P00760; 1EZX.
 DR MEROPS; S01.257; -.
 DR MGI; MGI:1929977; 2310015108Rik.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00889; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 249 AA; 27604 MW; F9FF9CB457D727D5 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 249;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 GPLVCRGTL 9
||| | | |
DB 204 GPLVCNGSL 212

RESULT 10

Q5QBG5 9D1PT
ID Q5QBG5 9D1PT PRELIMINARY; PRT; 253 AA.
AC Q5QBG5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Serine protease (Fragment).
OS Cullinoides sonorensis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Ceratopogonidae; Ceratopogoninae; Cullinoides; Monoculicoides.
OX NCBI_TaxID=179676;
RN [1]

NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=15796745;
RA Campbell C.L., Vandyke K.A., Letchworth G.J., Drolet B.S.,
RA Hanekamp T., Wilson W.C.;
RT "Midgut and salivary gland transcriptomes of the arbovirus vector
RT Cullinoides sonorensis (Diptera: Ceratopogonidae).";
RL Insect Mol. Biol. 14:121-136 (2005).
DR EMBL; AY752846; AAV84259.1; -; mRNA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0001095; P:negative regulation of blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Protease.
FT NON_TER
SQ SEQUENCE 253 AA; 27254 MW; 1A458EB8B5D32B48 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 253;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
||| | | |
DB 210 GPLACNGTL 218

RESULT 11

Q9QYN3_MOUSE
ID Q9QYN3_MOUSE PRELIMINARY; PRT; 276 AA.
AC Q9QYN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hippoboscidae prostate type (Mus musculus adult male tongue cDNA, RIKEN
DE full-length enriched library, clone:2310015108 product:protease,
DE serine, 20, full insert sequence) (Mus musculus adult male tongue
DE cDNA, RIKEN full-length enriched library, clone:2310040F07
DE product:protease, serine, 20, full insert sequence).
GN Name=2310015108Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
RA Mitsui S., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "cDNA cloning and tissue-specific splicing variants of mouse
RT hippostasin/TLSP (PRSS20).";
RL Biochim. Biophys. Acta 1494:206-210 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Blake J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osaoto N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,


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RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL; AE014295; AAN25531.1; -; Genomic_DNA.
DR HSSP; P08659; 1LCI.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; F:aldehyd dehydrog.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR Complete proteome; Ligase.
KW SEQUENCE 621 AA; 67948 MW; 5BCDDB4B5BF3083A CRC64;

Query Match 82.0%; Score 41; DB 2; Length 621;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRG 7
Db 436 GPLVCRG 442

RESULT 14
Q9F828_9ACTO
ID Q9F828_9ACTO PRELIMINARY; PRT; 3201 AA.
AC Q9F828_
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Megalomicin 6-deoxyerythronolide B synthase 3.
GN Name=megAIII;
OS Micromonospora megalomicina subsp. nigra.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micromonosporineae; Micromonosporaceae; Micromonospora.
OX NCBI_TaxID=136926;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NRRL3275;
RX MEDLINE=20430101; PubMed=10972798;
RA Volchegursky Y., Hu Z., Katz L., McDaniel R.;
RT "Biosynthesis of the anti-parasitic agent megalomicin: transformation
RT of erythromycin to megalomicin in Saccharopolyspora erythraea.";
RL Mol. Microbiol. 37:752-762(2000).
DR EMBL; AF263245; AAG13919.1; -; Genomic_DNA.
DR HSSP; Q03133; 1MO2.
DR SMR; Q9F828; 2932-3198.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0031177; F:phosphotransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR001227; ACP transferase.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR006163; Phosphanteth_bind.
DR HSSP; Q03133; 1MO2.
DR SMR; Q9F828; 2932-3198.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0031177; F:phosphotransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR001227; ACP transferase.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR006163; Phosphanteth_bind.
DR InterPro; IPR006162; Ppantne S.
DR InterPro; IPR000408; Reg chr condens.
DR InterPro; IPR001031; Thioesterase.

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DR Pfam; PF00698; Acyl_transf_1; 2.
DR Pfam; PF00106; adh_short; 2.
DR Pfam; PF00109; ketoacyl-synt; 2.
DR Pfam; PF02801; Ketoacyl-synt_C; 2.
DR Pfam; PF00550; PP-binding; 2.
DR Pfam; PF00975; Thioesterase; 1.
DR PROSITE; PS50075; ACP DOMAIN; 2.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
DR PROSITE; PS00012; PHOSPHANTHETHEINE; 2.
DR PROSITE; PS00626; RCI_2; UNKNOWN_1.
SQ SEQUENCE 3201 AA; 334783 MW; 44BDA30E14855650 CRC64;

Query Match 82.0%; Score 41; DB 2; Length 3201;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 1877 GPMVCRGGL 1885

RESULT 15
Q9F830_9ACTO
ID Q9F830_9ACTO PRELIMINARY; PRT; 3546 AA.
AC Q9F830_
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Megalomicin 6-deoxyerythronolide B synthase 1.
GN Name=megAI;
OS Micromonospora megalomicina subsp. nigra.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micromonosporineae; Micromonosporaceae; Micromonospora.
OX NCBI_TaxID=136926;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NRRL3275;
RX MEDLINE=20430101; PubMed=10972798;
RA Volchegursky Y., Hu Z., Katz L., McDaniel R.;
RT "Biosynthesis of the anti-parasitic agent megalomicin: transformation
RT of erythromycin to megalomicin in Saccharopolyspora erythraea.";
RL Mol. Microbiol. 37:752-762(2000).
DR EMBL; AF263245; AAG13917.1; -; Genomic_DNA.
DR HSSP; P72391; 1NM2.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0031177; F:phosphotransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR009081; ACP like.
DR InterPro; IPR001227; ACP transferase.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR006163; Phosphanteth_bind.
DR InterPro; IPR006162; Ppantne S.
DR Pfam; PF00698; Acyl_transf_1; 3.
DR Pfam; PF00106; adh_short; 2.
DR Pfam; PF00109; ketoacyl-synt; 2.
DR Pfam; PF02801; Ketoacyl-synt_C; 2.
DR Pfam; PF00550; PP-binding; 3.
DR PROSITE; PS50075; ACP DOMAIN; 3.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 2.
DR PROSITE; PS00012; PHOSPHANTHETHEINE; 2.
DR PROSITE; PS00013; LIPOCALIN; UNKNOWN_2.
DR PROSITE; PS00012; PHOSPHANTHETHEINE; 2.
SQ SEQUENCE 3546 AA; 371193 MW; 86C6794E95415BBC CRC64;

Query Match 82.0%; Score 41; DB 2; Length 3546;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9

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Db 2397 GPMVCRGGL 2405
||:|||||

Search completed: March 11, 2006, 00:38:52
Job time : 97.3333 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GPLVCRGTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	2	US-09-502-600-80
2	50	100.0	9	2	US-09-918-243-80
3	50	100.0	224	1	US-08-944-483-33
4	50	100.0	225	1	US-08-557-146-12
5	50	100.0	225	1	US-09-027-337-4
6	50	100.0	225	1	US-09-154-344-12
7	50	100.0	225	2	US-09-644-600-4
8	50	100.0	225	2	US-09-554-600A-4
9	50	100.0	253	1	US-08-557-146-2
10	50	100.0	253	1	US-08-824-874-3
11	50	100.0	253	1	US-09-154-344-2
12	50	100.0	253	2	US-08-930-188-2
13	50	100.0	253	2	US-09-210-084-3
14	50	100.0	253	2	US-09-764-762-3
15	50	100.0	253	4	PCT-US96-04294-2
16	50	100.0	265	2	US-09-949-016-7716
17	41	82.0	276	2	US-09-856-320A-4
18	41	82.0	3201	2	US-09-679-279-15
19	41	82.0	3546	2	US-09-679-279-13
20	40	80.0	20	1	US-08-472-228A-19
21	40	80.0	20	2	US-09-146-831-19
22	40	80.0	20	4	PCT-US96-09303-19
23	40	80.0	237	1	US-08-096-946-10
24	40	80.0	237	1	US-08-096-946-11
25	40	80.0	237	1	US-08-844-024-2
26	40	80.0	237	1	US-08-718-547-2
27	40	80.0	237	2	US-08-768-859A-1

28	40	80.0	237	2	US-08-768-859A-16	Sequence 16, Appl
29	40	80.0	237	2	US-08-768-859A-21	Sequence 21, Appl
30	40	80.0	237	2	US-08-767-820A-1	Sequence 1, Appl
31	40	80.0	237	2	US-08-767-820A-16	Sequence 16, Appl
32	40	80.0	237	2	US-08-767-820A-21	Sequence 21, Appl
33	40	80.0	237	2	US-08-622-046B-1	Sequence 1, Appl
34	40	80.0	237	2	US-08-622-046B-7	Sequence 7, Appl
35	40	80.0	237	2	US-08-622-046B-12	Sequence 12, Appl
36	40	80.0	237	2	US-08-944-483-37	Sequence 37, Appl
37	40	80.0	237	2	US-08-944-483-38	Sequence 38, Appl
38	40	80.0	237	2	US-09-100-264-3	Sequence 3, Appl
39	40	80.0	237	2	US-09-100-264-12	Sequence 12, Appl
40	40	80.0	237	2	US-09-303-339-2	Sequence 2, Appl
41	40	80.0	237	2	US-08-843-076D-1	Sequence 1, Appl
42	40	80.0	237	2	US-08-843-076D-7	Sequence 7, Appl
43	40	80.0	237	2	US-08-843-076D-8	Sequence 8, Appl
44	40	80.0	237	2	US-09-303-208-1	Sequence 1, Appl
45	40	80.0	237	2	US-09-303-208-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-502-600-80
; Sequence 80, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-502-600-80

Query Match 100.0%; Score 50; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||
DB 1 GPLVCRGTL 9

RESULT 2
US-09-918-243-80
; Sequence 80, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

;
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-918-243-80

Query Match 100.0%; Score 50; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

RESULT 3
US-08-944-483-33
; Sequence 33, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match 100.0%; Score 50; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 187

Db 178 GPLVCRGTL 186
RESULT 4
US-08-557-146-12
; Sequence 12, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 50; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 179 GPLVCRGTL 187

RESULT 5
US-09-027-337-4
; Sequence 4, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: TADG-15: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to

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; OTHER INFORMATION: similar domain in TAGD-15
US-09-027-337-4
Query Match      100.0%; Score 50; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 179 GPLVCRGTL 187

RESULT 6
US-09-154-344-12
; Sequence 12, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-09-154-344-12
Query Match      100.0%; Score 50; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 179 GPLVCRGTL 187

RESULT 7
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
```

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; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-644-600-4
Query Match      100.0%; Score 50; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 179 GPLVCRGTL 187

RESULT 8
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-09-654-600A-4
Query Match      100.0%; Score 50; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 179 GPLVCRGTL 187

RESULT 9
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-146-2

Query Match 100.0%; Score 50; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

RESULT 10
US-08-824-874-3
Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-08-824-874-3
Query Match 100.0%; Score 50; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

RESULT 11
US-09-154-344-2
Sequence 2, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 50; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215

RESULT 12
US-08-930-188-2
; Sequence 2, Application US/08930188
; Patent No. 6093397
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; APPLICANT: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,188
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/416,257
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Blalock, Donna K.
; REGISTRATION NUMBER: 38,082
; REFERENCE/DOCKET NUMBER: X9239
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-1090
; TELEFAX: 317-276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-188-2
Query Match 100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215
RESULT 13
US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3
Query Match 100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLVCRGTL 9
DB 207 GPLVCRGTL 215
RESULT 14
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

Db 207 GPLVCRGTL 215
 Search completed: March 11, 2006, 01:24:27
 Job time : 21.2222 secs

TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 532504
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-764-762-3

Query Match 100.0%; Score 50; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.24; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
 Db 207 GPLVCRGTL 215

RESULT 15
 PCT-US96-04294-2
 ; Sequence 2, Application PC/TUS9604294
 ; GENERAL INFORMATION:
 ; APPLICANT: Dixon, Eric P.
 ; APPLICANT: Johnstone, Edward M.
 ; APPLICANT: Little, Sheila P.
 ; TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
 ; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Eli Lilly and Company
 ; STREET: Lilly Corporate Center
 ; CITY: Indianapolis
 ; STATE: Indiana
 ; COUNTRY: United States of America
 ; ZIP: 46285
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/04294
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/416,257
 ; FILING DATE: 04-APR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Blalock, Donna K.
 ; REGISTRATION NUMBER: 38,082
 ; REFERENCE/DOCKET NUMBER: X9239
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 317-277-1090
 ; TELEFAX: 317-276-3861
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 253 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US96-04294-2

Query Match 100.0%; Score 50; DB 4; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.24; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-80

Perfect score: 50

Sequence: 1 GPLVCRGTL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	3	US-09-918-243-80
2	50	100.0	9	3	US-09-905-083-80
3	50	100.0	9	4	US-10-372-521-80
4	50	100.0	9	5	US-10-831-075-80
5	50	100.0	181	4	US-10-262-511-98
6	50	100.0	198	4	US-10-262-511-96
7	50	100.0	224	3	US-09-789-210-33
8	50	100.0	224	4	US-10-262-511-104
9	50	100.0	225	4	US-10-600-187-4
10	50	100.0	247	4	US-10-262-511-102
11	50	100.0	250	4	US-10-262-511-92
12	50	100.0	252	4	US-10-262-511-94
13	50	100.0	253	3	US-09-888-615-98
14	50	100.0	253	3	US-09-764-762-3
15	50	100.0	253	4	US-10-071-214-2
16	50	100.0	253	4	US-10-071-214-48
17	50	100.0	253	4	US-10-264-283-90
18	50	100.0	253	4	US-10-295-027-498
19	50	100.0	253	4	US-10-173-999-48
20	50	100.0	253	4	US-10-408-765A-639
21	50	100.0	253	5	US-10-643-795A-95
22	50	100.0	253	5	US-10-948-518-95
23	50	100.0	253	5	US-10-868-490A-1
24	50	100.0	257	4	US-10-344-394-38
25	47	94.0	249	4	US-10-071-214-47
26	45	90.0	247	3	US-09-764-898-284
27	45	90.0	247	3	US-09-764-847-742

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28 45 90.0 247 4 US-10-092-154-742 Sequence 742, App
29 45 90.0 250 4 US-10-055-569A-69 Sequence 69, Appl
30 45 90.0 250 4 US-10-344-394-29 Sequence 29, Appl
31 45 90.0 250 5 US-10-492-740-3 Sequence 3, Appli
32 45 90.0 251 3 US-09-764-898-212 Sequence 212, App
33 45 90.0 259 4 US-10-072-012-222 Sequence 222, App
34 44 88.0 243 4 US-10-071-214-46 Sequence 46, Appl
35 44 88.0 251 4 US-10-344-394-27 Sequence 27, Appl
36 44 88.0 267 5 US-10-480-988-20 Sequence 20, Appl
37 42 84.0 89 4 US-10-424-599-210636 Sequence 210636,
38 42 84.0 115 5 US-10-450-763-49720 Sequence 49720, A
39 41 82.0 23 4 US-10-071-214-6 Sequence 6, Appli
40 41 82.0 80 4 US-10-425-115-348061 Sequence 348061,
41 41 82.0 249 4 US-10-055-569A-68 Sequence 68, Appl
42 41 82.0 276 4 US-10-055-569A-67 Sequence 67, Appl
43 41 82.0 276 6 US-11-055-989-4 Sequence 4, Appli
44 40 80.0 54 3 US-09-860-739-5 Sequence 5, Appli
45 40 80.0 82 4 US-10-437-963-182803 Sequence 182803,

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ALIGNMENTS

RESULT 1
US-09-918-243-80
; Sequence 80, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-918-243-80

Query Match 100.0%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GPLVCRGTL 9
Db 1 GPLVCRGTL 9

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RESULT 2
US-09-905-083-80
; Sequence 80, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-905-083-80

Query Match 100.0%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||
DB 1 GPLVCRGTL 9

RESULT 3

US-10-372-521-80
; Sequence 80, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-10-372-521-80

Query Match 100.0%; Score 50; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||
DB 1 GPLVCRGTL 9

RESULT 4

US-10-831-075-80
; Sequence 80, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-10-831-075-80

Query Match 100.0%; Score 50; DB 5; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||
DB 1 GPLVCRGTL 9

RESULT 5

US-10-262-511-98
; Sequence 98, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 98
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-262-511-98

Query Match 100.0%; Score 50; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 133 GPLVCRGTL 141

RESULT 6

US-10-262-511-96

; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curasequid version 0.1
; SEQ ID NO 96

; LENGTH: 198

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 50; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 152 GPLVCRGTL 160

RESULT 7

US-09-789-210-33
; Sequence 33, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESS: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33

Query Match 100.0%; Score 50; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9

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Db      178 GPLVCRGTL 186
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RESULT 8
US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104
Query Match      100.0%; Score 50; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPLVCRGTL 9
Db      193 GPLVCRGTL 201
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RESULT 9
US-10-600-187-4
; Sequence 4, Application US/10600187
; Publication No. US20040086910A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/10/600,187
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/654,600A
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 09/027,337
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
US-10-600-187-4
Query Match      100.0%; Score 50; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPLVCRGTL 9
Db      179 GPLVCRGTL 187
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RESULT 10
US-10-262-511-102
; Sequence 102, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
```

APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 102
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-102

Query Match 100.0%; Score 50; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 193 GPLVCRGTL 201

RESULT 11
US-10-262-511-92
Sequence 92, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zernhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.

APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 92
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-92

Query Match 100.0%; Score 50; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 204 GPLVCRGTL 212

RESULT 12
US-10-262-511-94
Sequence 94, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Patturajan, Meera
APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zernhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen

```
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Stone, David J.
/ APPLICANT: Pena, Carol E. A.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Shimkets, Richard A.
/ APPLICANT: Rothenberg, Mark E.
/ APPLICANT: Leach, Martin D.
/ APPLICANT: Agee, Michele L.
/ APPLICANT: Berghs, Constance
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-462C
/ CURRENT APPLICATION NUMBER: US/10/262,511
/ CURRENT FILING DATE: 2003-05-28
/ PRIOR APPLICATION NUMBER: 60/326,483
/ PRIOR FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: 60/373,815
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 60/327,917
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/381,642
/ PRIOR FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/328,029
/ PRIOR FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: 60/381,038
/ PRIOR FILING DATE: 2002-05-16
/ PRIOR APPLICATION NUMBER: 60/328,056
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/373,260
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/373,826
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 60/327,435
/ PRIOR FILING DATE: 2001-10-05
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 439
/ SOFTWARE: CuraseqList version 0.1
/ SEQ ID NO 94
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-262-511-94

Query Match          100.0%; Score 50; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPLVCRGTL 9
Db      206  GPLVCRGTL 214
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RESULT 13
US-09-888-615-98
/ Sequence 98, Application US/09888615
/ Patent No. US20020064856A1
/ GENERAL INFORMATION:
/ APPLICANT: PLOWMAN, GREGORY
/ APPLICANT: WHYTE, DAVID
/ APPLICANT: CAENEPEEL, SEAN
/ APPLICANT: CHARYDCZAK, GLEN
/ APPLICANT: MANNING, GERARD
/ APPLICANT: SUDARSANAM, SUCHA
/ TITLE OF INVENTION: NOVEL PROTEASES
/ FILE REFERENCE: 038602/1214
/ CURRENT APPLICATION NUMBER: US/09/888,615
/ CURRENT FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/214,047
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 98
/ LENGTH: 253

Query Match          100.0%; Score 50; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPLVCRGTL 9
Db      207  GPLVCRGTL 215
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          |||||

RESULT 14
US-09-764-762-3
/ Sequence 3, Application US/09764762
/ Patent No. US20020068341A1
/ GENERAL INFORMATION:
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Lal, Preeti
/ TITLE OF INVENTION: NOVEL KALLIKREIN
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/764,762
/ FILING DATE: 16-Jan-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/210,084
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PP-0252 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 253 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 532504
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match          100.0%; Score 50; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPLVCRGTL 9
Db      207  GPLVCRGTL 215
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RESULT 15
US-10-071-214-2
/ Sequence 2, Application US/10071214
/ Publication No. US20030066099A1
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; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match      100.0%; Score 50; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GPLVCRGTL 9
Db      207 GPLVCRGTL 215

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Job time : 70.4444 secs

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OM protein - protein search, using sw model

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(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-80
Perfect score: 50
Sequence: 1 GPLVCRGTL 9

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Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New*

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- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB_PEP.*
- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB_PEP.*
- 4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB_PEP.*
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- 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB_PEP.*
- 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB_PEP.*
- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB_PEP.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	181	6	US-10-412-748-19
2	50	100.0	253	6	US-10-412-748-11
3	50	100.0	253	6	US-10-412-748-14
4	50	100.0	253	6	US-10-412-748-17
5	50	100.0	253	7	US-11-037-243-98
6	44	88.0	267	6	US-10-395-561-552
7	44	88.0	267	6	US-10-995-561-553
8	40	80.0	194	6	US-10-401-386B-12
9	40	80.0	237	6	US-10-401-386B-24
10	40	80.0	261	7	US-11-138-242A-8
11	40	80.0	261	7	US-11-150-066-8
12	40	80.0	261	7	US-11-033-039-358
13	40	80.0	261	7	US-11-155-288-10
14	40	80.0	269	6	US-10-401-386B-2
15	38	76.0	236	6	US-10-821-234-1274
16	38	76.0	237	6	US-10-401-386B-6
17	38	76.0	237	7	US-11-138-242A-5
18	38	76.0	237	7	US-11-150-066-5
19	38	76.0	260	6	US-10-131-826A-396
20	38	76.0	260	6	US-10-510-321-2
21	38	76.0	260	6	US-10-973-115B-396
22	38	76.0	260	7	US-11-183-914-7
23	38	76.0	261	7	US-11-138-242A-3
24	38	76.0	261	7	US-11-138-242A-10
25	38	76.0	261	7	US-11-150-066-3

26	38	76.0	261	7	US-11-150-066-10	Sequence 10, Appl
27	38	76.0	293	6	US-10-131-826A-456	Sequence 456, App
28	38	76.0	293	6	US-10-412-748-2	Sequence 2, Appli
29	38	76.0	293	6	US-10-412-748-7	Sequence 7, Appli
30	38	76.0	293	6	US-10-973-115B-456	Sequence 456, App
31	38	76.0	738	7	US-11-087-099-11986	Sequence 11986, A
32	37	74.0	15	7	US-11-234-786-512	Sequence 512, App
33	37	74.0	40	6	US-10-989-226-42	Sequence 42, Appl
34	37	74.0	40	7	US-11-066-967-69	Sequence 69, Appl
35	37	74.0	159	7	US-11-234-786-172	Sequence 172, App
36	37	74.0	205	7	US-11-234-786-176	Sequence 176, App
37	37	74.0	220	7	US-11-234-786-327	Sequence 327, App
38	37	74.0	254	7	US-11-234-786-523	Sequence 523, App
39	37	74.0	254	7	US-11-234-786-525	Sequence 525, App
40	37	74.0	320	7	US-11-037-243-90	Sequence 90, Appl
41	37	74.0	449	7	US-11-234-786-617	Sequence 617, App
42	36	72.0	283	7	US-11-072-512-2687	Sequence 2687, Ap
43	36	72.0	446	6	US-10-527-500-1	Sequence 1, Appli
44	36	72.0	451	7	US-11-087-099-1581	Sequence 1581, Ap
45	36	72.0	557	6	US-10-718-264-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19

Query Match 100.0%; Score 50; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.028; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 1 GPLVCRGTL 9
DB 135 GPLVCRGTL 143
RESULT 2
US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 50; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 50; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 50; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 5
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHARVDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 50; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 207 GPLVCRGTL 215

RESULT 6
US-10-995-561-552
; Sequence 552, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-552

Query Match      88.0%; Score 44; DB 6; Length 267;
Best Local Similarity 88.9%; Pred. No. 0.49;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPLVCRGTL 9
Db 222 GPLVCRGTL 230

RESULT 7
US-10-995-561-553
; Sequence 553, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
```


; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; PRIOR FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-553

Query Match 88.0%; Score 44; DB 6; Length 267;
Best Local Similarity 88.8%; Pred. No. 0.49;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GPLVCRGTL 9
Db 222 GPLVCRGQL 230
|||||

RESULT 8

US-10-401-386B-12
; Sequence 12, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: for Use
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28
; PRIOR FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2002-09-19
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-12

Query Match 80.0%; Score 40; DB 6; Length 194;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GPLVCRGTL 9
Db 148 GPLVCRGVL 156
|||||

RESULT 9

US-10-401-386B-24
; Sequence 24, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: for Use
; CURRENT APPLICATION NUMBER: US/10/401,386B
; PRIOR FILING DATE: 2003-03-28

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-24

Query Match 80.0%; Score 40; DB 6; Length 237;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 GPLVCRGTL 9
Db 191 GPLVCRGVL 199
|||||

RESULT 10

US-11-138-242A-8
; Sequence 8, Application US/11138242A
; Publication No. US20050266530A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Deborah J.
; APPLICANT: Snyder, Linda A.
; TITLE OF INVENTION: Cynomolgus Prostate Specific Antigen
; FILE REFERENCE: CEN5056 USA NP
; CURRENT APPLICATION NUMBER: US/11/138,242A
; PRIOR FILING DATE: 2005-05-26
; PRIOR FILING DATE: 2004-05-27
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-138-242A-8

Query Match 80.0%; Score 40; DB 7; Length 261;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
Db 215 GPLVCRGVL 223
|||||

RESULT 11

US-11-150-066-8
; Sequence 8, Application US/11150066
; Publication No. US20050276758A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Deborah J.
; APPLICANT: Snyder, Linda A.
; TITLE OF INVENTION: Method for Screening Agents Against Human Prostate Disease
; FILE REFERENCE: CEN5067 USA NP
; CURRENT APPLICATION NUMBER: US/11/150,066
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: 60/579,871
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-150-066-8

Query Match 80.0%; Score 40; DB 7; Length 261;

Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||||
DB 215 GPLVCNGVL 223

RESULT 12
US-11-033-039-358
; Sequence 358, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 358
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-358

Query Match 80.0%; Score 40; DB 7; Length 261;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||||
DB 215 GPLVCNGVL 223

RESULT 13
US-11-155-288-10
; Sequence 10, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANWK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-10

Query Match 80.0%; Score 40; DB 7; Length 261;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||||
DB 215 GPLVCNGVL 223

RESULT 14
US-10-401-386B-2
; Sequence 2, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-386B-2

Query Match 80.0%; Score 40; DB 6; Length 269;
Best Local Similarity 77.8%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||||
DB 223 GPLVCNGVL 231

RESULT 15
US-10-821-234-1274
; Sequence 1274, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1274
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1274

Query Match 76.0%; Score 38; DB 6; Length 236;
Best Local Similarity 77.8%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPLVCRGTL 9
|||||
DB 193 GPLVCNGVL 201

Search completed: March 11, 2006, 01:38:43
Job time : 9 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-86

Perfect score: 41

Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	4 AAE08291	Aae08291 Human str
2	41	100.0	9	8 ADR68847	Adr68847 Human str
3	41	100.0	136	4 ABG23378	Abg23378 Novel hum
4	41	100.0	198	6 ADA05736	Ada05736 Human NOV
5	41	100.0	198	8 ADN62900	Adn62900 Human NOV
6	41	100.0	253	2 AAR67888	Aar67888 Human str
7	41	100.0	253	2 AAU05383	Aau05383 Human amy
8	41	100.0	253	5 ABB84421	Abb84421 Human SCC
9	41	100.0	253	5 ABB84406	Abb84406 Human SCC
10	41	100.0	253	5 AAU82740	Aau82740 Amino aci
11	41	100.0	253	6 ABU07440	Abu07440 Protein d
12	41	100.0	253	6 ABU07471	Abu07471 Protein d
13	41	100.0	253	6 ABR58471	Abr58471 Human str
14	41	100.0	253	7 ADB80484	Adb80484 Ovarian c
15	41	100.0	253	7 ADJ68833	Adj68833 Human hea
16	41	100.0	253	7 ADN39180	Adn39180 Cancer/an
17	41	100.0	253	8 ADL06515	Adl06515 Human tum
18	41	100.0	253	8 ADN04182	Adn04182 Antipeori
19	41	100.0	253	8 ADR72880	Adr72880 Human ova
20	41	100.0	253	9 ADY67588	Ady67588 Human kal
21	41	100.0	253	9 AEC00353	Aec00353 Human kal
22	41	100.0	257	8 AAB21326	Aab21326 Human HSC
23	37	90.2	752	8 ADI28864	Adi28864 Human ser
24	36	87.8	9	4 AAE08320	Aae08320 Human str

25	36	87.8	9	8 ADR68877	Adr68877 Human str
26	36	87.8	210	8 ADR88035	Adr88035 Plant ful
27	36	87.8	567	8 ADY10906	Ady10906 Plant ful
28	36	87.8	818	5 ABB98135	Abb98135 Human PMM
29	36	87.8	818	5 AAU82753	Aau82753 Amino aci
30	35	85.4	346	8 ADT79403	Adt79403 Human BAC
31	35	85.4	475	4 AAE10657	Aae10657 Secreted
32	35	85.4	475	4 AAE02609	Aae02609 Human sec
33	35	85.4	475	5 ABB78618	Abb78618 Secreted
34	35	85.4	518	2 AAU61362	Aau61362 Aspartic
35	35	85.4	518	2 AAY13799	Aay13799 Human asp
36	35	85.4	518	2 AAY22239	Aay22239 Human CSP
37	35	85.4	518	2 AAY41714	Aay41714 Human PRO
38	35	85.4	518	3 AAY88424	Aay88424 Human asp
39	35	85.4	518	3 AAB44270	Aab44270 Human PRO
40	35	85.4	518	4 AAU07201	Aau07201 Human asp
41	35	85.4	518	4 AAE10628	Aae10628 Human asp
42	35	85.4	518	4 AAE10656	Aae10656 Human-Asp
43	35	85.4	518	4 AAE06858	Aae06858 Human Asp
44	35	85.4	518	4 AAE02608	Aae02608 Human Asp
45	35	85.4	518	4 AAE02580	Aae02580 Human asp

ALIGNMENTS

RESULT 1

AAE08291
ID AAE08291 standard; peptide; 9 AA.

AC AAE08291;

XX XX

DT 01-NOV-2001 (first entry)

DE Human stratum corneum chymotrypsin enzyme peptide #56 (residues 1-9).

XX Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;

KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;

KW antisease therapy; malignant hyperplasia.

XX OS Homo sapiens.

XX PN WC200159158-A1.

XX PD 16-AUG-2001.

XX PF 07-FEB-2001; 2001WO-US003977.

XX PR 11-FEB-2000; 2000US-00502600.

XX (UYAR-) UNIV ARKANSAS.

XX O'brien TJ;

XX WPI; 2001-514676/56.

DR Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

XX Claim 25; Page 114; 127pp; English.

XX The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

XX Sequence 9 AA;

SQ

Query Match 100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 1 MARSLLLPL 9

RESULT 2
ADR68847
ID ADR68847 standard; peptide; 9 AA.
AC ADR68847;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:86.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/63.
XX
PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
PS Claim 5; SEQ ID NO 86; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 41; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 1 MARSLLLPL 9

RESULT 3
ABG23378

ID ABG23378 standard; protein; 136 AA.
XX
AC ABG23378;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #23369.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS87565.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 53737; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 136 AA;

Query Match 100.0%; Score 41; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 7 MARSLLLPL 15

RESULT 4
ADA05736
ID ADA05736 standard; protein; 198 AA.
XX

ADA05736;
 06-NOV-2003 (first entry)
 Human NOV18c protein SEQ ID NO:96.
 human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 immunomodulator; cytostatic; nootropic; neuroprotective;
 antiparkinsonian; antilipaeamic; gene therapy; human disease;
 metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 neurodegenerative disorder; Alzheimer's disease; parkinson's disease;
 immune disorder; haematopoietic disorder; dyslipidaemia.
 Homo sapiens.
 WO2003029424-A2.
 10-APR-2003.
 02-OCT-2002; 2002WO-US031373.
 02-OCT-2001; 2001US-0326483P.
 05-OCT-2001; 2001US-0327435P.
 05-OCT-2001; 2001US-0327449P.
 09-OCT-2001; 2001US-0327517P.
 09-OCT-2001; 2001US-0328029P.
 09-OCT-2001; 2001US-0328044P.
 09-OCT-2001; 2001US-0328056P.
 12-OCT-2001; 2001US-0328849P.
 15-OCT-2001; 2001US-0329414P.
 17-OCT-2001; 2001US-0330142P.
 18-OCT-2001; 2001US-0330309P.
 22-OCT-2001; 2001US-0341058P.
 24-OCT-2001; 2001US-0339266P.
 24-OCT-2001; 2001US-0343629P.
 29-OCT-2001; 2001US-0349575P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381038P.
 17-MAY-2002; 2002US-0381042P.
 28-MAY-2002; 2002US-0381642P.
 28-MAY-2002; 2002US-0383656P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 01-OCT-2002; 2002US-00262511.
 (CURA-) CURAGEN CORP.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 Ji T, Gorwan L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ort W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 WPI; 2003-381626/36.
 N-PSDB; ADA05735.
 New NOVX polypeptides and nucleic acids, useful for diagnosing,
 preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
 cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 pharmacogenomics.
 Claim 1; Page 170; 586pp; English.
 The present invention describes NOVX proteins, where X can be 1 to 55
 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide

described above and a carrier; (2) a kit comprising, in one or more
 containers, the composition described above; (3) an isolated nucleic acid
 molecule which encodes a NOVX protein of the invention; (4) a vector
 comprising the nucleic acid molecule described above; (5) a cell
 comprising the above vector; (6) an antibody that immunospecifically
 binds to the polypeptide described above; (7) methods for determining the
 presence or amount of the above polypeptide or nucleic acid molecule in a
 sample; (8) methods for determining the presence of or predisposition to
 a disease associated with altered levels of expression of the above
 polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 method of identifying an agent that binds to the polypeptide described
 above; (10) a method for identifying a potential therapeutic agent for
 use in treating a pathology that is related to an aberrant expression or
 aberrant physiological interactions of the polypeptide; (11) a method of
 screening for a modulator of activity or of latency or predisposition to
 a pathology associated with the polypeptide; (12) a method for modulating
 the activity of the polypeptide described above; (13) methods of treating
 or preventing a pathology associated with the above polypeptide in a
 mammal; and (14) a method for producing the above polypeptide. NOVX
 sequences have antidiabetic, anorectic, antibacterial, virucide,
 immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
 and antilipaeamic activities, and can be used in gene therapy. The
 polypeptide is useful in manufacturing a medicament for treating a
 syndrome associated with a human disease. The polypeptide or the nucleic
 acid molecule may be used to diagnose, treat or prevent metabolic
 disorders such as diabetes or obesity, infections, cachexia, cancer,
 neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 disease, immune disorders, haematopoietic disorders and various
 dyslipidaemias. The nucleic acids can also be used as hybridisation
 probes, in chromosome mapping, tissue typing, preventive medicine and
 pharmacogenomics. The present sequence represents a human NOVX from the
 present invention.

Query Match 100.0%; Score 41; DB 6; Length 198;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
 |||||
 Db 1 MARSLLLPL 9

RESULT 5
 ADN62900
 ID ADN62900 standard; protein; 198 AA.
 XX ADN62900;
 AC ADN62900;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV18c.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
 XX
 XX 26-FEB-2004.
 PD
 XX
 PF 01-OCT-2002; 2002US-00262511.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILL/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATI/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIMW/) JI W.
 PA (MILL/) MILLER C B.
 PA (RST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGE E M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPIPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoj SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2004-213931/20.
 DR N-PSDB; ADM62899.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX

PS Claim 1; SEQ ID NO 96; 395pp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 198 AA;
 Query Match 100.0%; Score 41; DB 8; Length 198;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARSLLLPL 9
 Db 1 MARSLLLPL 9
 RESULT 6
 AAR67888
 ID AAR67888 standard; protein; 253 AA.
 XX
 AC AAR67888;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-AUG-1995 (first entry)
 XX
 DE Human stratum corneum chymotrophic recombinant enzyme (SCCE).
 XX
 KW Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;
 KW callosities; keratosis pilaris; ichthyoses; eczema.
 XX
 OS Homo sapiens.
 XX
 XX WO9500651-A1.
 XX
 PD 05-JAN-1995.
 XX
 XX 20-JUN-1994; 94WO-IB000166.
 XX
 PR 18-JUN-1993; 93DK-00000725.
 XX
 PA (SYMB-) SYMBICOM AB.
 XX
 XX Egelrud T, Hansson L;
 XX
 XX WPI; 1995-052088/07.
 DR N-PSDB; AAQ81203.
 XX

PT Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
PT related vectors, transformed cells and polypeptides, useful for treating
PT skin disorders, e.g. acne or psoriasis, and for identification of
PT specific inhibitors.

XX Disclosure; Page 97; 137pp; English.

XX The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
CC and skin care products, especially to treat and prevent acne, xeroderma,
CC or other hyperkeratotic conditions (e.g. callusities or keratosis
CC pilaris), ichthyoses, psoriasis, eczema, etc. It is produced
CC recombinantly following mammalian, insect, plant, or microorganism
CC transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

RESULT 7
AAW05383
ID AAW05383 standard; protein; 253 AA.

XX AAW05383;

XX 31-DEC-1996 (first entry)

XX Human amyloid precursor protein protease.

XX Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
XX therapy.

XX Homo sapiens.

XX WO9631122-A1.

XX 10-OCT-1996.

XX 02-APR-1996; 96WO-US004294.

XX 04-APR-1995; 95US-00416257.

XX (ELIL) LILLY & CO ELI.

XX Dixon EP, Johnstone EM, Little SP;

XX WPI; 1996-464694/46.

XX N-PSDB; AAT39783.

XX New isolated human amyloid precursor protein protease - used to develop
PT prods. for the treatment or diagnosis of associated conditions, esp.
PT Alzheimer's disease.

XX Claim 1; Page 44-45; 55pp; English.

XX Human amyloid precursor protein protease (AAW05383) is involved in the
CC processing or clearance of amyloid precursor protein to form beta-amyloid
CC peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783)
CC obt'd. from a human lung library. Recombinant protease can be produced in
CC transformed or transfected prokaryotic (partic. E. coli) or eukaryotic
CC (partic. AV-120 host cells. It is used to develop products for the design
CC and testing of cpds. useful for treating or preventing conditions
CC associated with beta-amyloid peptide, esp. Alzheimer's disease

XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

RESULT 8

AB884421

ID AB884421 standard; peptide; 253 AA.

XX AB884421;

XX 08-NOV-2002 (first entry)

XX Human SCCE protein N-terminal fragment SEQ ID 48.

XX SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

XX Homo sapiens.

XX WO200262135-A2.

XX 15-AUG-2002.

XX 08-FEB-2002; 2002WO-IB001300.

XX 09-FEB-2001; 2001CA-02332655.

XX 09-FEB-2001; 2001DK-00000218.

XX (EGEL/) EGELRUD T.

XX (HANS/) HANSSON L.

XX Egelrud T, Hansson L;

XX WPI; 2002-643380/69.

XX Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.

XX Example 6; Page 37; 74pp; English.

XX This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a
CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of
CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents the N-terminal
CC fragment of the human stratum corneum chymotryptic enzyme, SCCE
CC synonymous with human kallikrein 7 (KLK7), used in the development of the
CC transgenic mammals described in the invention

XX

SQ Sequence 253 AA;
Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
| | | | | | | | | |
Db 1 MARSLLLPL 9

RESULT 9
ABB84406
ID ABB84406 standard; protein; 253 AA.
XX ABB84406;
AC ABB84406;
DT 08-NOV-2002 (first entry)
XX
DE Human SCCE protein.
XX
KW SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
XX
OS Homo sapiens.
XX
XN WO200262135-A2.
XX
PD 15-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-IB001300.
XX
PR 09-FEB-2001; 2001CA-02332655.
PR 09-FEB-2001; 2001DK-00000218.
XX
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
XX Egelrud T, Hansson L;
XX WPI; 2002-643380/69.
DR N-PSDB; ABQ76226.
XX
PT Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
PS Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian
embryo having integrated within its genome, a heterologous nucleotide
sequence comprising at least a significant part of a nucleotide sequence
coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant.
operably linked to a promoter that drives expression of heterologous scce
or its variant in skin. The product of the invention is useful as a model
for the study of disease with the aim of improving treatment, to relieve
or ameliorate a pathogenic condition, for development or testing of a
cosmetic or a pharmaceutical formulation, and for the development of a
diagnostic method. It can also be used as a model for a skin disease or
skin cancer. The invention is also useful for screening or identifying a
compound or composition effective for the prevention or treatment of an
abnormal or unwanted phenotype, and for screening or identifying a
compound or composition effective for the prevention or treatment of
inflammatory skin diseases selected from diseases consisting of epidermal
hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
with epidermal hyperkeratosis. The mammal of the invention is also useful
as a model for further studies of itch mechanisms and the testing of
potential compounds and compositions for relieve of various skin diseases
where itch is a component. This sequence represents the human stratum
corneum chymotryptic enzyme, SCCE which is a serine protease synonymous

CC with human kallikrein 7 (KLK7) and is used in the development of the
CC transgenic mammals described in the invention
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
| | | | | | | | | |
Db 1 MARSLLLPL 9

RESULT 10
AAU82740
ID AAU82740 standard; protein; 253 AA.
XX
AC AAU82740;
XX
DT 23-APR-2002 (first entry)
XX
DE Amino acid sequence of novel human protease #39.
XX
KW Human; protease; cancer; immune-related disorder; cardiovascular disease;
KW neuronal-associated disease; metabolic disorder; inflammatory disorder;
KW nervous system disorder; sexual dysfunction; pain; mood disorder;
KW hypertension; psychotic disorder; neurological disorder; dyskinesia;
KW viral infection; human immunodeficiency virus; HIV; non-viral infection;
KW ocular disease; cytostatic; enzyme.
XX
OS Homo sapiens.
XX
XN WO200200860-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US020171.
XX
PR 26-JUN-2000; 2000US-0214047P.
XX
XX (SUGE-) SUGEN INC.
XX
PA Plowman G, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Charyczak G;
XX
XX WPI; 2002-139913/18.
DR N-PSDB; ABK31782.
XX
PT Nucleic acids encoding novel human proteases, useful for useful for
PT treating diseases and disorders such as cancers, immune-related diseases
PT and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
PT disorders.
XX
PS Claim 6; Fig 2N; 313pp; English.

The present invention relates to the isolation of novel human proteases,
and the nucleic acids encoding them. The sequences of the invention are
useful for treating diseases and disorders such as cancers (e.g. breast,
colon, lung), immune-related diseases and disorders (e.g. inflammatory
diseases and asthma), cardiovascular diseases (e.g. restenosis and
coronary thrombosis), brain or neuronal-associated diseases, metabolic
disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
rheumatoid arthritis and psoriasis), central or peripheral nervous system
diseases, migraines, pain, sexual dysfunction, mood disorders, attention
disorders, cognition disorders, hypotension, hypertension, psychotic
disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's
disease) and dyskinesias. The nucleic acids and polypeptides are also
useful for treating viral infections caused by human immunodeficiency
virus (HIV), and non-viral infections such as ocular disease (e.g.
glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
human proteases of the invention
XX

CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer
XX
SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 1 MARSLLLPL 9
|||||||

RESULT 12
ABU07471
ID ABU07471 standard; protein; 253 AA.
XX AC
ABU07471;
AC
DT 28-JAN-2003 (first entry)
XX
DE Protein differentially regulated in prostate cancer #74.
XX
KW Prostate cancer; gene expression; differential regulation;
KW molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
OS Homo sapiens.
XX
PN WO200281638-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010824.
XX
PR 06-APR-2001; 2001US-0281731P.
PR 06-APR-2001; 2001US-0281732P.
XX
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
PI Sun Z, Jay G;
XX
PI WPI; 2003-058520/05.
DR N-PSDB; ABX10375.
DR
XX
PT Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.
XX
PS Claim 1; Page 351; 416pp; English.
XX
XX The invention describes genes (I) which are differentially regulated in
XX prostate cancer. (I) is useful for diagnosing a prostate cancer in a
XX sample comprising prostate tissue, which involves determining the number
XX of target genes which are differentially-regulated in the sample, where
XX the number is indicative of the probability that the sample comprises
XX prostate cancer. (I) is useful for assessing a therapeutic or preventive
XX intervention in a subject having a prostate cancer, which involves
XX determining the expression levels in a sample comprising prostate tissue
XX of target genes which are differentially-regulated in prostate cancer.
XX Preferably, the expression levels of at least 10 genes are determined.
XX (I) is also useful for identifying agents that modulate a biological
XX activity of a polypeptide differentially-regulated in prostate cancer
XX cells, which involves contacting a polypeptide differentially-regulated

CC in prostate cancer cells with a test agent under conditions effective for
CC the test agent to modulate a biological activity of the polypeptide, and
CC determining whether the test agent modulates the biological activity. (I)
CC is useful as molecular markers, as drug targets, and for detecting,
CC diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC preventing or treating, determining predisposition to diseases and
CC conditions especially relating to prostate cancer. (I) and its expression
CC products are used in the diagnostic test to assay for presence of cancer
CC e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC of cancer, its stage of development, the nature of genetic defect, etc.
CC The polypeptide encoded by (I) can be used as target for therapy or drug
CC discovery. (I) can also be used for expressing the polypeptide and thus
CC for searching specific binding partners of the polypeptide. (I) is useful
CC in therapeutic applications to treat prostate cancer. The identification
CC of specific genes, and groups of genes, expressed in pathways
CC physiologically relevant to prostate cancer permits the definition of
CC functional and disease pathways and the delineation of targets in these
CC pathways which are useful in diagnostic, therapeutic, and clinical
CC applications. This is the amino acid sequence of a protein differentially
CC regulated in prostate cancer

XX SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLLPL 9
| | | | | | | |
Db 1 MARSLLLLPL 9

RESULT 13

ABR58471
ID ABR58471 standard; protein; 253 AA.

XX AC ABR58471;

XX DT 07-JUL-2003 (first entry)

DE DE Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.

XX KW Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.

XX OS Homo sapiens.

XX PN WO2003029469-A1.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031467.

XX PR 02-OCT-2001; 2001US-0327135P.

XX PR 30-MAY-2002; 2002US-0384531P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA, Mannion J;

XX DR WPI; 2003-372001/35.

XX PT New polynucleotide and polypeptide useful for diagnosing and/or treating
PT cancer, particularly ovarian cancer, and as a vaccine.

XX PS Claim 2; Page 157-158; 169pp; English.

XX CC The invention relates to a novel isolated polynucleotide. The

XX CC polynucleotides of the invention have cytostatic activity, and may have a
XX CC use in gene therapy, and in a vaccine. The composition and methods are
XX CC useful in diagnosing and/or treating cancer, particularly ovarian cancer.
XX CC The composition may also be used as a vaccine to prevent cancer. The
XX CC present sequence is used in the exemplification of the invention

XX SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLLPL 9
| | | | | | | |
Db 1 MARSLLLLPL 9

RESULT 14

ADB80484
ID ADB80484 standard; protein; 253 AA.

XX AC ADB80484;

XX DT 04-DEC-2003 (first entry)

DE DE Ovarian cancer-associated protein #24.

KW cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
KW post-operative chemotherapy; radiation therapy; tumour prognosis;
KW pre-cancerous lesion detection.

XX OS Homo sapiens.

XX PN WO2002102235-A2.

XX PD 27-DEC-2002.

XX PF 18-JUN-2002; 2002WO-US019297.

XX PR 18-JUN-2001; 2001US-0299234P.

XX PR 27-AUG-2001; 2001US-0315287P.

XX PR 05-SEP-2001; 2001US-0317544P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Mack DH, Gish KC;

XX DR WPI; 2003-167431/16.

XX DR N-PSDB; ADB80483.

XX PT Detecting an ovarian cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT polynucleotide that hybridizes to an ovarian cancer gene.

XX PS Claim 13; Page 291; 332pp; English.

XX CC The invention relates to a method of detecting an ovarian cancer-
XX CC associated transcript in a cell from a patient, by contacting a
XX CC biological sample from the patient with a polynucleotide that selectively
XX CC hybridizes to a sequence at least 80% identical to any of one of 80
XX CC nucleic acid sequences given in the specification. The method is useful
XX CC in diagnosing ovarian cancer and in identifying and using agents and/or
XX CC targets that inhibit ovarian cancer. The nucleic acid molecule,
XX CC polypeptide and the antibody may also be used in detecting ovarian
XX CC cancers, monitoring and early detection of relapse following treatment,
XX CC monitoring response to therapy, selecting patients for post-operative
XX CC chemotherapy or radiation therapy, in selection of pre-cancerous lesions,
XX CC and as vaccines. This sequence corresponds to one of the proteins used
XX CC for the detection method of the invention.

XX SQ Sequence 253 AA;

Query Match 100.0%; Score 41; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARLLLLPL 9
| | | | |
DB 1 MARLLLLPL 9

QY 1 MARLLLLPL 9
| | | | |
DB 1 MARLLLLPL 9

Search completed: March 11, 2006, 00:24:18
Job time : 88.6667 secs

RESULT 15
ADJ68833
ID ADJ68833 standard; protein; 253 AA.

XX AC ADJ68833;
XX DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID639.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.

OS Homo sapiens.

XX WO2003087768-A2.

XX 23-OCT-2003.

XX 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.

XX 17-JUN-2002; 2002US-0389987P.

XX 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOKOR.

XX (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

PI Warnock DE;

XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

PS Claim 1; SEQ ID NO 639; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 253 AA;

Query Match 100.0%; Score 41; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-86
Perfect score: 41
Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	253	2 A53968	serine proteinase
2	34	82.9	461	2 A46394	suppressor protein
3	33	80.5	397	2 B87343	conserved hypothet
4	33	80.5	571	2 E96550	hypothetical prote
5	33	80.5	582	2 I48673	matrix metalloprot
6	33	80.5	582	2 I84471	matrix metalloprot
7	32	78.0	81	2 B97856	hypothetical prote
8	32	78.0	126	2 C82169	DNA-binding protei
9	32	78.0	432	2 A83060	hypothetical prote
10	32	78.0	506	2 B87102	conserved membrane
11	32	78.0	921	2 T51136	ionotropic glutama
12	32	78.0	923	2 F84732	probable ligand-ga
13	32	78.0	1628	2 T38055	hypothetical prote
14	31	75.6	138	2 I48107	sodium channel alp
15	31	75.6	147	2 S28698	hypothetical prote
16	31	75.6	169	2 AB0627	cell division inhi
17	31	75.6	169	2 B29016	cell division inhi
18	31	75.6	294	2 B86450	hypothetical prote
19	31	75.6	346	2 T11364	NADH2 dehydrogenas
20	31	75.6	375	2 T71917	probable transamin
21	31	75.6	375	2 H64597	probable transamin
22	31	75.6	452	2 A83734	PTS system, n-acet
23	31	75.6	491	2 JC6197	stromelysin 3 (EC
24	31	75.6	556	1 S31330	inulinase (EC 3.2.
25	31	75.6	708	2 T43109	cytolysin B transp
26	31	75.6	2005	2 B25019	sodium channel pro
27	31	75.6	5059	2 T17464	rifamycin polyketi
28	30	73.2	72	2 JC2384	corazonin precursor
29	30	73.2	74	2 T17834	hypothetical prote

30	30	73.2	170	2 S43476	histone-like DNA-b
31	30	73.2	216	2 JE0297	DRE/CRT-binding pr
32	30	73.2	216	2 T51830	transcription fact
33	30	73.2	222	2 D82132	hypothetical prote
34	30	73.2	299	2 T17832	hypothetical prote
35	30	73.2	314	2 D85294	transcription acti
36	30	73.2	314	2 T05799	transcription acti
37	30	73.2	323	2 S47741	probable transcrip
38	30	73.2	323	2 B86025	probable transcrip
39	30	73.2	323	2 A91179	protein ZC155.4 [i
40	30	73.2	325	2 A88452	hypothetical prote
41	30	73.2	325	2 T25122	hypothetical prote
42	30	73.2	325	2 A97482	conserved hypothet
43	30	73.2	325	2 G12699	hypothetical prote
44	30	73.2	331	2 A87494	transmembrane glyc
45	30	73.2	354	2 A48931	

ALIGNMENTS

RESULT 1

A53968
serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 MARSLLLPL 9
| | | | | | | | | |
DB 1 MARSLLLPL 9

RESULT 2

A46394
suppressor protein SSL1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1531; protein YLR005W
C;Species: Saccharomyces cerevisiae
C;Date: 18-May-1994 #sequence_revision 19-Jul-1996 #text_change 31-Dec-2004
C;Accession: A46394; S64827
R;Yoon, H.; Miller, S.P.; Pabich, E.K.; Donahue, T.F.
Genes Dev. 6, 2463-2477, 1992
A;Title: SSL1, a suppressor of a HIS4 5'-UTR stem-loop mutation, is essential for transla
A;Reference number: A46394; MUID:94040711; PMID:1340463
A;Accession: A46394
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <YOO>
A;Cross-references: UNIPROT:Q04673; UNIPARC:UPI0000053049; GB:Z17385; NID:G2695; PID:G269
R;Vandenbol, M.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64742
A;Accession: S64827

A:Molecule type: DNA
A:Residues: 1-461 <V>N>
A:Cross-references: UNIPARC:UPI0000053049; EMBL:Z73177; NID:gl360293; PID:gl360294; MIPS
A>Note: experimental_source strain S28C
C:Genetics:
A:Gene: SGD:SSL1
A:Cross-references: SGD:S0003995; MIPS:YLR005W
A:Map position: 12R
C:Superfamily: tFIIH basal transcription factor complex, subunit SSL1
C:Keywords: transmembrane protein
F:356-372/Domain: transmembrane #status predicted <TMM>

Query Match 82.9%; Score 34; DB 2; Length 461;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MARSLLLPL 9
||| |||||
Db 216 MARGLLLPV 224

RESULT 3
B87343
conserved hypothetical protein CC0757 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87343
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: B87343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <STO>
A:Cross-references: UNIPROT:Q9AAM9; UNIPARC:UPI00000C7168; GB:AE005673; NID:gl3421992; E
C:Genetics:
A:Gene: CC0757

Query Match 80.5%; Score 33; DB 2; Length 397;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
||| |||||
Db 285 LARALLPL 293

RESULT 4
E96550
hypothetical protein Film15.13 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96550
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96550
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-571 <STO>
A:Cross-references: UNIPROT:Q9SYC9; UNIPARC:UPI000009EC28; GB:AE005173; NID:g4836937; PI
C:Genetics:

A:Gene: Film15.13
A:Map position: 1

Query Match 80.5%; Score 33; DB 2; Length 571;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
||| |||||
Db 332 MLRSLLVPL 340

RESULT 5
I48673
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C:Accession: I48673
R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel
A:Reference number: I38046; MUID:95224014; PMID:7708715
A:Accession: I48673
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: UNIPARC:UPI0000030971; EMBL:X83536; NID:g804999; PIDN:CAA58520.1; PII
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>
F:61-284/Domain: matrix metalloproteinase homology <MMP>
F:313-508/Domain: hemopexin repeat homology <PXN>
F:93,239,243,249/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status I
F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted

Query Match 80.5%; Score 33; DB 2; Length 582;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARSLLPL 9
: ||| |||||
Db 8 SRSLLPL 15

RESULT 6
I84471
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
N:Alternate names: membrane-type metalloproteinase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I84471; I61946
R:Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P.
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A:Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel
A:Reference number: I38046; MUID:95224014; PMID:7708715
A:Accession: I84471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: UNIPROT:Q10739; UNIPARC:UPI0000030970; EMBL:X83537; NID:g805012; PIDN
A:Accession: I61946
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-67, 'M', 69-254, 'A', 256-582 <RE2>
A:Cross-references: UNIPARC:UPI00001679D1; EMBL:X91785; NID:gl001926; PIDN:CAA62897.1; PI
C:Genetics:
A:Gene: mt-mmp
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>

A:Molecule type: mRNA
A:Residues: 1-921 <DAV>
A:Cross-references: UNIPROT:Q9SDQ4; UNIPARC:UPI00000A3CD0; EMBL:AF210701; PIDN:AAF21042.
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: glr5
A:Map position: 2

Query Match
Best Local Similarity 78.0%; Score 32; DB 2; Length 921;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|||||
Db 705 MARSRLVPL 713

RESULT 12
F84732
probable ligand-gated ion channel subunit [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: F84732
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84732
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-923 <STO>
A:Cross-references: UNIPROT:Q9SDQ4; UNIPARC:UPI000017A6D8; GB:AE002093; NID:g3831456; PI
C:Genetics:
A:Gene: At2g32400
A:Map position: 2

Query Match
Best Local Similarity 78.0%; Score 32; DB 2; Length 923;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
|||||
Db 707 MARSRLVPL 715

RESULT 13
T38055
hypothetical protein SPAC22F3.14c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T38055; T38177; S62429
R.Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1995
A:Reference number: Z21765
A:Accession: T38055
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-26 <LY1>
A:Cross-references: UNIPROT:Q09779; UNIPARC:UPI0000162020; EMBL:Z69239; PIDN:CAA93223.1;
R.Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21776
A:Accession: T38177
A:Molecule type: DNA
A:Residues: 8-1621 <LY2>
A:Cross-references: UNIPARC:UPI000017B1DE; EMBL:Z54285; NID:g1008429; PIDN:CAA91079.2; C
C:Genetics:
A:Gene: SPAC1D4.14
A:Map position: 1L

Query Match
Best Local Similarity 78.0%; Score 32; DB 2; Length 1628;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RSLLLPL 9
|||||
Db 583 RSLLLPL 589

RESULT 14
I48107
sodium channel alpha subunit - long-tailed hamster (fragment)
C:Species: Cricetulus longicaudatus (long-tailed hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48107
R.Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.
Am. J. Physiol. 264, 803-809, 1993
A:Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster
A:Reference number: I48107
A:Accession: I48107
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-138 <RES>
A:Cross-references: UNIPROT:Q60463; UNIPARC:UPI00000E7D6C; GB:M87540; NID:g191067; PIDN:
C:Genetics:
A:Gene: chol
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 75.6%; Score 31; DB 2; Length 138;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 8
|||||
Db 1 MARSVLVP 8

RESULT 15
S28698
hypothetical protein 16 - Agrobacterium tumefaciens plasmid pRI15955
C:Species: Agrobacterium tumefaciens
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S28698
R.Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1983
A:Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo
A:Reference number: S28683
A:Accession: S28698
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-147 <BAR>
A:Cross-references: UNIPROT:Q44395; UNIPARC:UPI00000BE55A; EMBL:X00493; NID:g39062; PIDN:
C:Genetics:
A:Gene: plasmid

Query Match 75.6%; Score 31; DB 2; Length 147;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 8
|||||
Db 1 MARYLLPL 8

Search completed: March 11, 2006, 00:40:53
Job time : 16.1111 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-86
Perfect score: 41
Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	41	100.0	66	2	Q6DTY1_HUMAN	Q6dt1 homo sapien
2	41	100.0	253	1	KLK7_HUMAN	P49862 homo sapien
3	36	87.8	855	1	POLS2_HUMAN	Q5k463 homo sapien
4	35	85.4	47	2	Q5DIH8_HUMAN	Q5di18 homo sapien
5	35	85.4	396	2	Q9NZL1_HUMAN	Q9nz11 homo sapien
6	35	85.4	468	2	Q9NZL2_HUMAN	Q9nz12 homo sapien
7	35	85.4	518	1	BACE2_HUMAN	Q9y520 homo sapien
8	35	85.4	593	2	Q4NGK9_GMCC	Q4ngk9 arthrobacte
9	35	85.4	1135	2	Q84W49_ARATH	Q84w49 arabidopsis
10	35	85.4	1192	2	Q9S7T0_ARATH	Q9s7t0 arabidopsis
11	34	82.9	118	2	Q7R254_NEUCR	Q7r254 neurospora
12	34	82.9	129	2	Q8H584_ORYSA	Q8h584 oryza sativ
13	34	82.9	322	2	Q7FP07_SYMPX	Q7fp07 symbiobacte
14	34	82.9	348	2	Q7UAK2_SYNPX	Q7u4k2 synchococc
15	34	82.9	439	2	Q6FTA5_CANGA	Q6fta5 candida gla
16	34	82.9	461	1	SSL1_YEAST	Q04673 saccharomyc
17	34	82.9	461	2	Q6B237_YEAST	Q6b237 saccharomyc
18	33	80.5	188	2	Q6SSD7_WHEAT	Q6ssd7 triticum ae
19	33	80.5	272	2	Q8LC74_ARATH	Q8lc74 arabidopsis
20	33	80.5	272	2	Q9FNC4_ARATH	Q9fnc4 arabidopsis
21	33	80.5	291	2	Q56Y44_ARATH	Q56y44 arabidopsis
22	33	80.5	295	2	Q8W2V5_ORYSA	Q8w2v5 oryza sativ
23	33	80.5	297	2	Q7P016_CHRYVO	Q7p016 chromobacte
24	33	80.5	323	2	Q5VJ91_9BURK	Q5vj91 brachymonas
25	33	80.5	368	2	Q8SAT6_ORYSA	Q8sat6 oryza sativ
26	33	80.5	397	2	Q9AA49_CAUCR	Q9aa49 caulobacter
27	33	80.5	424	2	Q827F2_STRAW	Q827f2 streptomyc
28	33	80.5	464	1	OTSA_RHISN	P55612 rhizobium s
29	33	80.5	526	2	Q9ZRH9_ORYSA	Q9zrh9 oryza sativ
30	33	80.5	531	2	Q6ZK46_ORYSA	Q6zk46 oryza sativ
31	33	80.5	571	2	Q9SYC9_ARATH	Q9syc9 arabidopsis

32	33	80.5	582	1	MMP14_MOUSE	P53690 mus musculu
33	33	80.5	582	1	MMP14_RAT	Q10739 rattus norv
34	33	80.5	582	2	Q8BTX2_MOUSE	Q8btx2 mus musculu
35	33	80.5	582	2	Q6DFU5_MOUSE	Q6dfu5 mus musculu
36	33	80.5	582	2	Q6IN06_RAT	Q6in06 rattus norv
37	33	80.5	809	2	Q8S23_ENCCU	Q8s23 encephalito
38	33	80.5	934	2	Q9DER4_CHICK	Q9der4 gallus gall
39	33	80.5	1048	2	Q6ZJF7_ORYSA	Q6zjf7 oryza sativ
40	33	80.5	1124	2	Q6ZBI6_ORYSA	Q6zbi6 oryza sativ
41	32	78.0	81	2	Q92G73_RICCN	Q92g73 rickettsia
42	32	78.0	126	2	Q9KRE6_VIBCH	Q9kre6 vibrio chol
43	32	78.0	139	2	Q658A9_ORYSA	Q658a9 oryza sativ
44	32	78.0	149	2	Q69YF9_HUMAN	Q69yf9 homo sapien
45	32	78.0	149	2	Q8KAK3_CHLTE	Q8kak3 chlorobium

ALIGNMENTS

RESULT 1
Q6DTY1_HUMAN
ID Q6DTY1_HUMAN PRELIMINARY; PRT; 66 AA.
AC Q6DTY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kallikrein 7 splice variant 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Kishi T., Michael I.P., Diamandis E.P.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY646152; AAT6047.1; -, mRNA.
SQ SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;

Query Match 100.0%; Score 41; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 0.99; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 MARSLLLPL 9
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Db 1 MARSLLLPL 9

RESULT 2
KLK7_HUMAN
ID KLK7_HUMAN STANDARD; PRT; 253 AA.
AC P49862; Q8NSN9; Q8NFV7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (hk7) (Stratum corneum
chymotryptic enzyme) (hSCCE).
GN Name=KLK7; Synonyms=PRSS6, SCCE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
RC TISSUE=Skin;
RX MEDLINE=94308225; PubMed=8034709;
RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
RA Egelrud T.;
RT "Cloning, expression, and characterization of stratum corneum
chymotryptic enzyme. A skin-specific human serine proteinase.";
RL J. Biol. Chem. 269:19420-19426(1994).

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Query Match 100.0%; Score 41; DB 1; Length 253;
 Best Local Similarity 100.0%; Pred. NO. 3.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
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 Db 1 MARSLLLPL 9

RESULT 3

ID POLS2 HUMAN STANDARD; PRT; 855 AA.
 AC Q5K4E3; Q8NEY4;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DE 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Polypeptide-2 precursor (EC 3.4.21.-) (Polyserine protease-2) (Protease
 DE serine 36).
 GN Name=PRSS36;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], ENZYME ACTIVITY, ENZYME REGULATION,
 RP SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND N-GLYCOSYLATION.
 RC TISSUE=Liver;
 RX PubMed=15536082; DOI=10.1074/jbc.M409139200;
 RA Cal S., Quesada V., Llamazares M., Diaz-Perales A., Garabaya C.,
 RA Lopez-Otin C.;
 RA "Human polypeptide-2, a novel enzyme with three tandem serine protease
 RT domains in a single polypeptide chain.";
 RL J. Biol. Chem. 280:1953-1961(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hoshiro T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K.,
 RA Yamazaki M., Ninomiya K., Iehibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuba T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 CC -1- FUNCTION: Serine protease. Hydrolyzes the peptides N-t-Boc-Gln-
 CC Ala-Arg-AMC and N-t-Boc-Gln-Gly-Arg-AMC and, to a lesser extent,
 CC N-t-Boc-Ala-Phe-Lys-AMC and N-t-Boc-Val-Lys-AMC. Has a
 CC preference for substrates with an Arg instead of a Lys residue in

CC Position Pl.
 CC -1- ENZYME REGULATION: Inhibited by serine proteinase inhibitor 4-(2-
 CC aminocethyl)-benzenesulfonyl fluoride, but not with EDTA or E-64.
 CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix. Not attached
 CC to membranes.
 CC -1- TISSUE SPECIFICITY: Expressed in fetal kidney, skeletal muscle,
 CC liver, placenta and heart. Also expressed in tumor cell lines
 CC derived from lung and colon adenocarcinomas.
 CC -1- DOMAIN: The first serine protease domain is catalytically active,
 CC whereas the second domain lacks the essential His residue of the
 CC catalytic triad at position 363, and the third domain lacks the
 CC essential Asp residue of the catalytic triad at position 679. The
 CC second and third domains are therefore predicted to be inactive
 CC (by similarity).
 CC -1- PTM: The 3 protease domains are not proteolytically cleaved.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- SIMILARITY: Contains 3 peptidase S1 domains.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 51.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AJ627034; CAF25303.1; -; mRNA.
 CC EMBL; AK075142; BAC11431.1; ALT_FRAME; mRNA.
 CC HSSP; P00750; 1RTP.
 CC MEROPS; S01.414; -.
 CC HGNC; HGNC:26906; PRSS36.
 CC InterPro; IPR001254; Peptidase_S1_S6.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; Trypsin; 3.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_SPC; 3.
 CC PROSITE; PS02440; TRYPSIN_DOM; 3.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Extracellular matrix; Glycoprotein; Hydrolase; Protease; Repeat;
 KW Serine protease; Signal; Zymogen.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 46 Potential.
 FT CHAIN 47 855 Peptidase-2.
 FT DOMAIN 47 291 Peptidase S1 1.
 FT DOMAIN 323 555 Peptidase S1 2.
 FT DOMAIN 590 808 Peptidase S1 3.
 FT ACT_SITE 87 87 Charge relay system (By similarity).
 FT ACT_SITE 139 139 Charge relay system (By similarity).
 FT ACT_SITE 243 243 Charge relay system (By similarity).
 FT CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 217 217 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 317 317 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 402 402 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 407 407 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 421 421 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 508 508 By similarity.
 FT DISULFID 72 88 By similarity.
 FT DISULFID 173 249 By similarity.
 FT DISULFID 206 228 By similarity.
 FT DISULFID 239 267 By similarity.
 FT DISULFID 348 364 By similarity.
 FT DISULFID 444 516 By similarity.
 FT DISULFID 505 534 By similarity.
 FT DISULFID 616 631 By similarity.
 FT DISULFID 711 772 By similarity.
 FT DISULFID 739 751 By similarity.
 SQ SEQUENCE 855 AA; 91921 MW; D1AF788019BD3A71 CRC64;

Query Match

87.8%; Score 36; DB 1; Length 855;

Best Local Similarity	88.9%;	Pred. No. 1.4e+02;	
Matches	8;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARSLLLPL 9
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Db 1 MARHLLLPL 9

RESULT 4

QSDIH8_HUMAN	QSDIH8_HUMAN PRELIMINARY;	PRT;	47 AA.
ID	QSDIH8		
AC	QSDIH8;		
DT	10-MAY-2005 (TrEMBLrel. 30, Created)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)		
DE	BACE2 (Fragment).		
GN	Name=BACE2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
NCBI_TaxID=9606;			
[1]			
RP	NUCLEOTIDE SEQUENCE.		
RN			

Sun X., Wang Y., Qing H., Christensen M.A., Liu Y., Zhou W., Tong Y., Xia C., Huang Y., Zhang S., Liu X., Song W.; "distal transcriptional regulation and function of the human BACE2 and BACE1 genes."; FASEB J. 19:739-749(2005).
EMBL; AY769996; AAX14808.1; - ; Genomic_DNA.
NON TER 47
SEQUENCE 47 AA; 4914 MW; C4SFBC50BB70971B CRC64;

Qy 1 MARSLLLPL 9
:|:|:|:|
Db 4 LARALLLPL 12

RESULT 5

Q9NZL1_HUMAN	
ID	Q9NZL1_HUMAN PRELIMINARY; PRT; 396 AA.
AC	Q9NZL1;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Apartyl protease.
GN	Name=BACE2;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]

RX MEDLINE=20422477; PubMed=10965118;
 RA Solana A., Estivill X., de la Luna S.;
 RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
 RT Alzheimer's amyloid precursor protein beta-secretase.";
 RL Cytogenet. Cell Genet. 89:177-184(2000).
 DR ENBL; AF188277; AAF35836.1; -; mRNA.
 DR HSSP; P56817; 1FKN.
 DR Dr
 DR Ensembl; ENSG0000182240; Homo sapiens.
 DR GO: GO:0016021; C:integral to membrane; ISS.

DR HSSP; P56817; 1FKN.
DR Ensembl; ENSG00000181181.
DR GO: GO:0016021; C:innate immunity; MF:molecular function; BP:biological process; KEGG: K04406; K04407; K04408; K04409; K04410; K04411; K04412; K04413; K04414; K04415; K04416; K04417; K04418; K04419; K04420; K04421; K04422; K04423; K04424; K04425; K04426; K04427; K04428; K04429; K04430; K04431; K04432; K04433; K04434; K04435; K04436; K04437; K04438; K04439; K04440; K04441; K04442; K04443; K04444; K04445; K04446; K04447; K04448; K04449; K04450; K04451; K04452; K04453; K04454; K04455; K04456; K04457; K04458; K04459; K04460; K04461; K04462; K04463; K04464; K04465; K04466; K04467; K04468; K04469; K04470; K04471; K04472; K04473; K04474; K04475; K04476; K04477; K04478; K04479; K04480; K04481; K04482; K04483; K04484; K04485; K04486; K04487; K04488; K04489; K04490; K04491; K04492; K04493; K04494; K04495; K04496; K04497; K04498; K04499; K04500; K04501; K04502; K04503; K04504; K04505; K04506; K04507; K04508; K04509; K04510; K04511; K04512; K04513; K04514; K04515; K04516; K04517; K04518; K04519; K04520; K04521; K04522; K04523; K04524; K04525; K04526; K04527; K04528; K04529; K04530; K04531; K04532; K04533; K04534; K04535; K04536; K04537; K04538; K04539; K04540; K04541; K04542; K04543; K04544; K04545; K04546; K04547; K04548; K04549; K04550; K04551; K04552; K04553; K04554; K04555; K04556; K04557; K04558; K04559; K04560; K04561; K04562; K04563; K04564; K04565; K04566; K04567; K04568; K04569; K04570; K04571; K04572; K04573; K04574; K04575; K04576; K04577; K04578; K04579; K04580; K04581; K04582; K04583; K04584; K04585; K04586; K04587; K04588; K04589; K04590; K04591; K04592; K04593; K04594; K04595; K04596; K04597; K04598; K04599; K04600; K04601; K04602; K04603; K04604; K04605; K04606; K04607; K04608; K04609; K04610; K04611; K04612; K04613; K04614; K04615; K04616; K04617; K04618; K04619; K04620; K04621; K04622; K04623; K04624; K04625; K04626; K04627; K04628; K04629; K04630; K04631; K04632; K04633; K04634; K04635; K04636; K04637; K04638; K04639; K04640; K04641; K04642; K04643; K04644; K04645; K04646; K04647; K04648; K04649; K04650; K04651; K04652; K04653; K04654; K04655; K04656; K04657; K04658; K04659; K04660; K04661; K04662; K04663; K04664; K04665; K04666; K04667; K04668; K04669; K04670; K04671; K04672; K04673; K04674; K04675; K04676; K04677; K04678; K04679; K04680; K04681; K04682; K04683; K04684; K04685; K04686; K04687; K04688; K04689; K04690; K04691; K04692; K04693; K04694; K04695; K04696; K04697; K04698; K04699; K04700; K04701; K04702; K04703; K04704; K04705; K04706; K04707; K04708; K04709; K04710; K04711; K04712; K04713; K04714; K04715; K04716; K04717; K04718; K04719; K04720; K04721; K04722; K04723; K04724; K04725; K04726; K04727; K04728; K04729; K04730; K04731; K04732; K04733; K04734; K04735; K04736; K04737; K04738; K04739; K04740; K04741; K04742; K04743; K04744; K04745; K04746; K04747; K04748; K04749; K04750; K04751; K04752; K04753; K04754; K04755; K04756; K04757; K04758; K04759; K04760; K04761; K04762; K04763; K04764; K04765; K04766; K04767; K04768; K04769; K04770; K04771; K04772; K04773; K04774; K04775; K04776; K04777; K04778; K04779; K04780; K04781; K04782; K04783; K04784; K04785; K04786; K04787; K04788; K04789; K04790; K04791; K04792; K04793; K04794; K04795; K04796; K04797; K04798; K04799; K04800; K04801; K04802; K04803; K04804; K04805; K04806; K04807; K04808; K04809; K04810; K04811; K04812; K04813; K04814; K04815; K04816; K04817; K04818; K04819; K04820; K04821; K04822; K04823; K04824; K04825; K04826; K04827; K04828; K04829; K04830; K04831; K04832; K04833; K04834; K04835; K04836; K04837; K04838; K04839; K04840; K04841; K04842; K04843; K04844; K04845; K04846; K04847; K04848; K04849; K04850; K04851; K04852; K04853; K04854; K04855; K04856; K04857; K04858; K04859; K04860; K04861; K04862; K04863; K04864; K04865; K04866; K04867; K04868; K04869; K04870; K04871; K04872; K04873; K04874; K04875; K04876; K04877; K04878; K04879; K04880; K04881; K04882; K04883; K04884; K04885; K04886; K04887; K04888; K04889; K04890; K04891; K04892; K04893; K04894; K04895; K04896; K04897; K04898; K04899; K04900; K04901; K04902; K04903; K04904; K04905; K04906; K04907; K04908; K04909; K04910; K04911; K04912; K04913; K04914; K04915; K04916; K04917; K04918; K04919; K04920; K04921; K04922; K04923; K04924; K04925; K04926; K04927; K04928; K04929; K04930; K04931; K04932; K04933; K04934; K04935; K04936; K04937; K04938; K04939; K04940; K04941; K04942; K04943; K04944; K04945; K04946; K04947; K04948; K04949; K04950; K04951; K04952; K04953; K04954; K04955; K04956; K04957; K04958; K04959; K04960; K04961; K04962; K04963; K04964; K04965; K04966; K04967; K04968; K04969; K04970; K04971; K04972; K04973; K04974; K04975; K04976; K04977; K04978; K04979; K04

RESULT 7

RESULT	BACE2_HUMAN	ID	BACE2_HUMAN	STANDARD;	PRT;	518 AA.
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AC Q9Y5Z0; O9UJ76;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Beta secretase 2 precursor (BC 3.4.23.45) (Beta-site App-cleaving
DE enzyme 2) (Aspartyl protease 1) (Asp 1) (ASPI) (Membrane-associated
DE aspartic protease 1) (Memapsin-1) (Down region aspartic protease).
GN Names=BACE2; Synonyms=ASP21; ORFNames=UNQ418/PRO852;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
RY Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomaselli A.G., Parodi L.A., Henrikson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
RT secretase activity.";
RL Nature 402:533-537(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP CHARACTERIZATION.
RX MEDLINE=22088158; PubMed=12093293; DOI=10.1021/bi025926t;
RY Turner R.T. III, Loy J.A., Nguyen C., Devasamudram T., Ghosh A.K.,
RA Koelsch G., Tang J.;
RT "Specificity of memapsin 1 and its implications on the design of
RT memapsin 2 (beta-secretase) inhibitor selectivity.";
RL Biochemistry 41:8742-8746(2002).
CC -I- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC Alzheimer's amyloid precursor protein.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: Belongs to the peptidase A1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF200342; AAF17078.1; -; mRNA.
CC EMBL; AF117892; AAD45240.1; -; mRNA.
CC EMBL; AF050171; AAD45963.1; -; mRNA.
CC EMBL; AF178532; AAF29494.1; -; mRNA.
CC EMBL; AF204944; AAF26368.1; -; mRNA.
CC EMBL; AF200192; AAF13714.1; -; mRNA.
CC EMBL; AY358927; AAQ89286.1; -; mRNA.
CC EMBL; AL163284; CAB90458.1; -; Genomic DNA.
CC EMBL; AL163285; CAB90554.1; -; Genomic DNA.
CC EMBL; BC014453; AAL14453.1; -; mRNA.
CC HSP; P56817; 1M4H.
CC MEROPS; A01.041; -.

RA
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RY Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schilhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.B.,
RA Minoshima S., Shimizu N., Nordisk G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [9]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP CHARACTERIZATION.
RX MEDLINE=22088158; PubMed=12093293; DOI=10.1021/bi025926t;
RY Turner R.T. III, Loy J.A., Nguyen C., Devasamudram T., Ghosh A.K.,
RA Koelsch G., Tang J.;
RT "Specificity of memapsin 1 and its implications on the design of
RT memapsin 2 (beta-secretase) inhibitor selectivity.";
RL Biochemistry 41:8742-8746(2002).
CC -I- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
CC Alzheimer's amyloid precursor protein.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: Belongs to the peptidase A1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF200342; AAF17078.1; -; mRNA.
CC EMBL; AF117892; AAD45240.1; -; mRNA.
CC EMBL; AF050171; AAD45963.1; -; mRNA.
CC EMBL; AF178532; AAF29494.1; -; mRNA.
CC EMBL; AF204944; AAF26368.1; -; mRNA.
CC EMBL; AF200192; AAF13714.1; -; mRNA.
CC EMBL; AY358927; AAQ89286.1; -; mRNA.
CC EMBL; AL163284; CAB90458.1; -; Genomic DNA.
CC EMBL; AL163285; CAB90554.1; -; Genomic DNA.
CC EMBL; BC014453; AAL14453.1; -; mRNA.
CC HSP; P56817; 1M4H.
CC MEROPS; A01.041; -.

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DR Ensembl: ENSG00000182240; Homo sapiens.
DR HGNC: HGNC:934; BACE2.
DR MIM: 605668; -.
DR GO: GO:0016021; C:integral to membrane; NAS.
DR GO: GO:0005624; C:membrane fraction; TAS.
DR GO: GO:0004190; F:aspartic-type endopeptidase activity; IDA.
DR GO: GO:0006509; P:membrane protein ectodomain proteolysis; IDA.
DR GO: GO:0042985; P:negative regulation of amyloid precursor pr. . .; IMP.
DR GO: GO:0016486; P:peptide hormone processing; NAS.
DR GO: GO:0006464; P:protein modification; TAS.
DR GO: GO:0009306; P:protein secretion; TAS.
DR InterPro: IPR009119; Pept Al_BACE.
DR InterPro: IPR009121; Pept Al_BACE2.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR009007; Pept_Aspartc_cat.
DR InterPro: IPR001461; Peptidase_Al.
DR PANTHER: PTHR13683:SF15; Pept Al_BACE; 1.
DR PANTHER: PTHR13683:Peptidase_Al; 1.
DR Pfam: PF00026; Asp; 1.
DR PRINTS: PR01817; BACE2.
DR PRINTS: PR01815; BACEFAMILY.
DR PRINTS: PR00792; PEPSIN.
DR PROSITE: PS00141; ASP_PROTEASE; 2.
DR KX Aspartyl protease; Glycoprotein; Hydrolase; Protease; Signal;
KW Transmembrane; Zymogen.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 ? Potential.
FT CHAIN 21 518 Beta secretase 2.
FT TOPO_DOM 21 473 Extracellular (Potential).
FT TRANSMEM 474 494 Potential.
FT TOPO_DOM 495 518 Cytoplasmic (Potential).
FT ACT_SITE 110 110 By similarity.
FT ACT_SITE 303 303 By similarity.
FT CARBOHYD 170 170 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 366 366 N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 36 36 A -> T (in Ref. 6).
SQ SEQUENCE 518 AA; 56180 MW; 2E903150823760D3 CRC64;

Query Match 85.4%; Score 35; DB 1; Length 518;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 4 LARALLPL 12

RESULT 8
Q4NGK9_9M1CC PRELIMINARY; PRT; 593 AA.
AC Q4NGK9_9M1CC PRELIMINARY; PRT; 593 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE ATP-binding region, ATPase-like; Histidine kinase A, N-terminal.
GN ORFNames=ArthDRAFT_2772;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococciaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lipidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Iserani S., Pfluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FB24;
RC US DOE Joint Genome Institute (JGI-PGF);
RG US DOE Joint Genome Institute (JGI-PGF);
RA Larimer F., Land M.;

RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: RAHG01000005; EAL96513.1; -; Genomic_DNA.
KW ATP-binding; Kinase.
SQ SEQUENCE 593 AA; 64710 MW; 2D81CDA7841B21C CRC64;

Query Match 85.4%; Score 35; DB 2; Length 593;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 199 LARSLLPLV 207

RESULT 9
Q84W49_ARATH PRELIMINARY; PRT; 1135 AA.
AC Q84W49;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein At3g01780 (Fragment).
GN Name=At3g01780;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BT004227; AAO42242.1; -; mRNA.
DR InterPro: IPR002048; EF-hand.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1135 1135
SQ SEQUENCE 1135 AA; 126119 MW; C5FDDC178D1E2D96 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1135;
Best Local Similarity 77.8%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 237 MARSLLPLV 245

RESULT 10
Q9S7T0_ARATH PRELIMINARY; PRT; 1192 AA.
AC Q9S7T0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE F28J7.11 protein (F4P13.33 protein).
GN Name=F28J7.11; Synonym=F4P13.33;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OX NCBI_TaxID=3702;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC010797; AAF013433.1; -; Genomic_DNA.
DR EMBL; AC009325; AAF01560.1; -; Genomic_DNA.
DR InterPro; IPR002048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
SQ SEQUENCE 1192 AA; 132863 MW; 4F67B124CBAPF154 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1192;
Best Local Similarity 77.8%; Pred. No. 31e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 237 MARSLVLPV 245
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RESULT 11
Q7R254 NEUCR PRELIMINARY; PRT; 118 AA.
ID Q7R254;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DE Predicted protein (Hypothetical protein G21B4.400).
GN Names=NCU04420.1; Synonyms=G21B4.400;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR748;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter R.J., Osmani S.A.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gherre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA German Neurospora genome project;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000720; EAA28261.1; -; Genomic_DNA.
DR EMBL; BX908908; CAF06025.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 118 AA; 12596 MW; D1F84E47108B2145 CRC64;

Query Match 82.9%; Score 34; DB 2; Length 118;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC010797; AAF013433.1; -; Genomic_DNA.
DR EMBL; AC009325; AAF01560.1; -; Genomic_DNA.
DR InterPro; IPR002048; EF-hand.
DR PROSITE; PS00018; EF_HAND; UNKNOWN 1.
SQ SEQUENCE 1192 AA; 132863 MW; 4F67B124CBAPF154 CRC64;

Query Match 85.4%; Score 35; DB 2; Length 1192;
Best Local Similarity 77.8%; Pred. No. 31e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 237 MARSLVLPV 245
|||||:

RESULT 12
Q8H584 ORYSA PRELIMINARY; PRT; 129 AA.
ID Q8H584;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DE Hypothetical protein OJ1656_E11.113 (Hypothetical protein
DE P0496D04.53).
GN Names=OJ1656_E11.113; Synonyms=P0496D04.53;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OJ1656_E11.113";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0496D04.53";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003843; BAC24850.1; -; Genomic_DNA.
DR EMBL; AP004670; BAD30793.1; -; Genomic_DNA.
DR Gramene; O8H584; -.
KW Hypothetical protein.
SQ SEQUENCE 129 AA; 13891 MW; 6334E639E1A6DEAE CRC64;

Query Match 82.9%; Score 34; DB 2; Length 129;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 8
Db 40 LARSLLLP 47
|||||:

RESULT 13
Q67P07 SYMTH PRELIMINARY; PRT; 322 AA.
ID Q67P07;
AC Q67P07;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Ferrichrome ABC transporter permease protein.
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=JAM14863;
RC PubMed=15393646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RT bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AP006840; BAD40586.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.

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DR Pfam; PF01032; FecCD; 1.
KW Complete proteome.
SQ SEQUENCE 322 AA; 34949 MW; 80157DE1532812D9 CRC64;

Query Match      82.9%; Score 34; DB 2; Length 322;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db |||||:|

RESULT 14
Q7U4K2_SYNXP PRELIMINARY; PRT; 348 AA.
ID Q7U4K2;
AC Q7U4K2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ldpA protein.
GN OrderedLocuNames=SYNW2065;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825637; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsa B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.B., Regala W., Allen E.B., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
CC -!- SUBUNIT: The cyanobacterial PSI reaction center is composed of one
CC copy each of psaA,B,C,D,E,F,I,J,K,L,M and X, and forms trimeric
CC complexes (By similarity).
CC -!- SUBCELLULAR LOCATION: Tightly associated with stromal side of the
CC thylakoid membrane (By similarity).
DR EMBL; BX569694; CAB08580.1; -; Genomic_DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
DR Pfam; PF00037; Fer4; 1.
DR PRINTS; PR00353; 4FE4SFERDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
KW Metal-binding; Thylakoid; Transport.
SQ SEQUENCE 348 AA; 37531 MW; 1E1903BE684081A95 CRC64;

Query Match      82.9%; Score 34; DB 2; Length 348;
Best Local Similarity 77.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db |||||:|

RESULT 15
Q6FTA5_CANGA PRELIMINARY; PRT; 439 AA.
ID Q6FTA5_CANGA;
AC Q6FTA5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|Q04673|Saccharomyces cerevisiae YLR005w SSL1.
GN OrderedLocuNames=CRGJ0G04059g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
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[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 2001 / CBS 138;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaut J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenn S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR380953; CAG59466.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR004595; Ssl1.
DR InterPro; IPR007198; Ssl1_like.
DR InterPro; IPR012170; TFIIF_SSL1.
DR InterPro; IPR002035; VWF_A.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF04056; Ssl1; 1.
DR PIRSF; PIRSF015919; TFIIF_SSL1; 1.
DR SMART; SM00327; VWA; 1.
DR TIGRFAMs; TIGR00622; Ssl1; 1.
DR PROSITE; PS00234; VWFA; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 439 AA; 49183 MW; 07D1A63D1575D894 CRC64;

Query Match      82.9%; Score 34; DB 2; Length 439;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db |||||:|

Search completed: March 11, 2006, 00:38:56
Job time : 99.3333 secs
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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-86
Perfect score: 41
Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	100.0	9	2	US-09-502-600-86
2	41	100.0	9	2	US-09-318-243-86
3	41	100.0	253	1	US-08-557-146-2
4	41	100.0	253	1	US-08-824-874-3
5	41	100.0	253	1	US-09-154-344-2
6	41	100.0	253	2	US-08-930-188-2
7	41	100.0	253	2	US-09-210-084-3
8	41	100.0	253	2	US-09-764-762-3
9	41	100.0	253	4	PCT-US96-04294-2
10	41	100.0	265	2	US-09-949-016-7716
11	36	87.8	9	2	US-09-502-600-116
12	36	87.8	9	2	US-09-318-243-116
13	35	85.4	475	2	US-09-668-314C-67
14	35	85.4	518	2	US-08-999-723-2
15	35	85.4	518	2	US-09-434-427-2
16	35	85.4	518	2	US-09-548-372D-2
17	35	85.4	518	2	US-09-548-367D-2
18	35	85.4	518	2	US-09-551-853D-2
19	35	85.4	518	2	US-09-215-450-19
20	35	85.4	518	2	US-09-416-901B-2
21	35	85.4	518	2	US-09-548-376D-2
22	35	85.4	518	2	US-09-886-143-2
23	35	85.4	518	2	US-09-794-927A-2
24	35	85.4	518	2	US-09-548-373D-2
25	35	85.4	518	2	US-09-795-847B-2
26	35	85.4	518	2	US-09-869-414-2
27	35	85.4	518	2	US-09-548-366F-2

28 35 85.4 518 2 US-09-548-368D-2 Sequence 2, Appli
29 35 85.4 518 2 US-09-794-925A-2 Sequence 2, Appli
30 35 85.4 518 2 US-09-806-194A-2 Sequence 2, Appli
31 35 85.4 518 2 US-09-668-314C-2 Sequence 2, Appli
32 35 85.4 518 2 US-09-668-314C-66 Sequence 66, Appli
33 35 85.4 518 2 US-09-548-365-2 Sequence 2, Appli
34 35 85.4 518 2 US-09-794-743-2 Sequence 2, Appli
35 35 85.4 518 2 US-09-999-833A-196 Sequence 196, App
36 35 85.4 518 2 US-10-020-445A-196 Sequence 196, App
37 35 85.4 541 2 US-09-949-016-11075 Sequence 11075, A
38 32 78.0 43 2 US-09-149-476-355 Sequence 355, App
39 32 78.0 123 2 US-09-270-767-33977 Sequence 33977, A
40 32 78.0 123 2 US-09-270-767-49194 Sequence 49194, A
41 32 78.0 175 2 US-09-869-388-8 Sequence 8, Appli
42 32 78.0 204 2 US-09-134-000C-3659 Sequence 3659, Ap
43 32 78.0 226 2 US-09-869-388-10 Sequence 10, Appli
44 32 78.0 227 2 US-09-869-388-6 Sequence 6, Appli
45 32 78.0 230 2 US-09-869-388-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-502-600-86
; Sequence 86, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-C
; CURRENT FILING DATE: 2000-02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-502-600-86

Query Match 100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 2
US-09-918-243-86
; Sequence 86, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

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;
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-918-243-86

Query Match      100.0%; Score 41; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 3
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-557-146-2

Query Match      100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 4
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3

Query Match      100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 5
US-09-154-344-2
; Sequence 2, Application US/09154344
; Patent No. 5981256
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
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Db 1 MARSLLLPL 9

RESULT 6
US-08-930-188-2
Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2

Query Match 100.0%; Score 41; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

RESULT 7
US-09-210-084-3
Sequence 3, Application US/09210084
Patent No. 6197511
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-09-210-084-3

Query Match 100.0%; Score 41; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
| | | | |
Db 1 MARSLLLPL 9

RESULT 8
US-09-764-762-3
Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5

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;/
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
;/ STREET: 3174 Porter Drive
;/ CITY: Palo Alto
;/ STATE: CA
;/ COUNTRY: USA
;/ ZIP: 94304
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: DOS
;/ SOFTWARE: FastSeq for Windows Version 2.0
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;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/764,762
;/ FILING DATE: 16-Jan-2001
;/ CLASSIFICATION: <Unknown>
;/
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 09/210,084
;/ FILING DATE: <Unknown>
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;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Billings, Lucy J.
;/ REGISTRATION NUMBER: 36,749
;/ REFERENCE/DOCKET NUMBER: PF-0252 US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 415-855-0555
;/ TELEFAX: 415-845-4166
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;/ INFORMATION FOR SEQ ID NO: 3:
;/
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 253 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ IMMEDIATE SOURCE:
;/ CLONE: GenBank
;/ LIBRARY: 532504
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;/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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;/ US-09-764-762-3
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;/ Query Match 100.0%; Score 41; DB 2; Length 253;
;/ Best Local Similarity 100.0%; Pred. No. 0.49;
;/ Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;/ QY 1 MARSLLLPL 9
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;/ Db 1 MARSLLLPL 9
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;/ RESULT 9
;/ PCT-US96-04294-2
;/ Sequence 2, Application PC/TUS9604294
;/ GENERAL INFORMATION:
;/ APPLICANT: Dixon, Eric P.
;/ APPLICANT: Johnstone, Edward M.
;/ APPLICANT: Little, Sheila P.
;/ TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
;/ TITLE OF INVENTION: RELATED NUCLEIC ACIDS
;/ NUMBER OF SEQUENCES: 3
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Eli Lilly and Company
;/ STREET: Lilly Corporate Center
;/ CITY: Indianapolis
;/ STATE: Indiana
;/ COUNTRY: United States of America
;/ ZIP: 46285
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
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;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US96/04294
;/ FILING DATE:
;/ CLASSIFICATION:
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;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/416,257
;/ FILING DATE: 04-APR-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Blalock, Donna K.
;/ REGISTRATION NUMBER: 38,082
;/ REFERENCE/DOCKET NUMBER: X9239
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 317-277-1090
;/ TELEFAX: 317-276-3861
;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 253 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ PCT-US96-04294-2
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;/ Query Match 100.0%; Score 41; DB 4; Length 253;
;/ Best Local Similarity 100.0%; Pred. No. 0.49;
;/ Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;/ QY 1 MARSLLLPL 9
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;/ Db 1 MARSLLLPL 9
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;/ RESULT 10
;/ US-09-949-016-7716
;/ Sequence 7716, Application US/09949016
;/ Patent No. 6812339
;/ GENERAL INFORMATION:
;/ APPLICANT: VENTER, J. Craig et al.
;/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;/ FILE REFERENCE: CL001307
;/ CURRENT APPLICATION NUMBER: US/09/949,016
;/ CURRENT FILING DATE: 2000-04-14
;/ PRIOR APPLICATION NUMBER: 60/241,755
;/ PRIOR FILING DATE: 2000-10-20
;/ PRIOR APPLICATION NUMBER: 60/237,768
;/ PRIOR FILING DATE: 2000-10-03
;/ PRIOR APPLICATION NUMBER: 60/231,498
;/ PRIOR FILING DATE: 2000-09-08
;/ NUMBER OF SEQ ID NOS: 207012
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 7716
;/ LENGTH: 265
;/ TYPE: PRT
;/ ORGANISM: Human
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;/ US-09-949-016-7716
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;/ Query Match 100.0%; Score 41; DB 2; Length 265;
;/ Best Local Similarity 100.0%; Pred. No. 0.51;
;/ Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;/ QY 1 MARSLLLPL 9
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;/ Db 13 MARSLLLPL 21
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;/ RESULT 11
;/ US-09-502-600-116
;/ Sequence 116, Application US/09502600A
;/ Patent No. 6294344
;/ GENERAL INFORMATION:
;/ APPLICANT: O'Brien, Timothy J.
;/ TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
;/ TITLE OF INVENTION: Ovarian Cancer
;/ FILE REFERENCE: D6223CIP-C
;/ CURRENT FILING DATE: 2000-02-11
;/ CURRENT APPLICATION NUMBER: US/09/502,600A
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; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-502-600-116

Query Match      87.8%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ARSLLLPL 9
Db      1 ARSLLLPL 8

RESULT 12
US-09-918-243-116
; Sequence 116, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 2-10 of the SCCE protein
US-09-918-243-116

Query Match      87.8%; Score 36; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ARSLLLPL 9
Db      1 ARSLLLPL 8

RESULT 13
US-09-668-314C-67
; Sequence 67, Application US/09668314C
; Patent No. 6844148
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314C
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-668-314C-67

Query Match      85.4%; Score 35; DB 2; Length 475;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      4 LARALLPL 12

RESULT 14
US-08-999-723-2
; Sequence 2, Application US/08999723A
; Patent No. 6025180
; GENERAL INFORMATION:
; APPLICANT: Powell, David J.
; APPLICANT: Southan, Christopher
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Evans, Joanne R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH70262
; CURRENT APPLICATION NUMBER: US/08/999,723A
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-999-723-2

Query Match      85.4%; Score 35; DB 2; Length 518;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLLPL 9
Db      4 LARALLPL 12

RESULT 15
US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASPI
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
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US-09-434-427-2

Query Match 85.4%; Score 35; DB 2; Length 518;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
Db :||:|||||
4 LARALLLPL 12

Search completed: March 11, 2006, 01:24:28
Job time : 22.2222 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-86
Perfect score: 41
Sequence: 1 MARSLLLPL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	3	US-09-918-243-86
2	41	100.0	9	3	US-09-905-083-86
3	41	100.0	9	4	US-10-372-521-86
4	41	100.0	9	5	US-10-831-075-86
5	41	100.0	136	5	US-10-450-763-53737
6	41	100.0	198	4	US-10-262-511-96
7	41	100.0	253	3	US-09-888-615-98
8	41	100.0	253	3	US-09-764-762-3
9	41	100.0	253	4	US-10-071-214-2
10	41	100.0	253	4	US-10-071-214-48
11	41	100.0	253	4	US-10-264-283-90
12	41	100.0	253	4	US-10-295-027-498
13	41	100.0	253	4	US-10-173-999-48
14	41	100.0	253	4	US-10-408-765A-639
15	41	100.0	253	5	US-10-643-795A-95
16	41	100.0	253	5	US-10-948-518-95
17	41	100.0	253	5	US-10-868-490A-1
18	41	100.0	257	4	US-10-344-394-38
19	37	90.2	752	5	US-10-612-466B-6
20	36	87.8	9	3	US-09-918-243-116
21	36	87.8	9	3	US-09-905-083-116
22	36	87.8	9	4	US-10-372-521-116
23	36	87.8	9	5	US-10-831-075-116
24	36	87.8	99	4	US-10-424-599-279409
25	36	87.8	172	4	US-10-424-599-239079
26	36	87.8	210	4	US-10-425-114-50699
27	36	87.8	542	4	US-10-425-115-318442

28 36 87.8 567 4 US-10-425-114-66721 Sequence 66721, A
29 36 87.8 818 3 US-09-888-615-111 Sequence 111, App
30 36 87.8 818 5 US-10-433-757-13 Sequence 13, Appl
31 35 85.4 232 4 US-10-424-599-262566 Sequence 262566,
32 35 85.4 346 4 US-10-791-488A-4 Sequence 4, Appli
33 35 85.4 475 5 US-10-817-979-67 Sequence 67, Appli
34 35 85.4 517 5 US-10-749-714-2 Sequence 2, Appli
35 35 85.4 518 3 US-09-794-927-2 Sequence 2, Appli
36 35 85.4 518 3 US-09-795-847-2 Sequence 2, Appli
37 35 85.4 518 3 US-09-794-743-2 Sequence 2, Appli
38 35 85.4 518 3 US-09-794-748-2 Sequence 2, Appli
39 35 85.4 518 3 US-09-794-925-2 Sequence 2, Appli
40 35 85.4 518 3 US-09-215-450-19 Sequence 19, Appli
41 35 85.4 518 3 US-09-681-442-2 Sequence 2, Appli
42 35 85.4 518 3 US-09-978-295A-196 Sequence 196, App
43 35 85.4 518 3 US-09-886-143-2 Sequence 2, Appli
44 35 85.4 518 3 US-09-978-697-196 Sequence 196, App
45 35 85.4 518 3 US-09-978-192A-196 Sequence 196, App

ALIGNMENTS

RESULT 1
US-09-918-243-86
; Sequence 86, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-918-243-86

Query Match 100.0%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 2
US-09-905-083-86
; Sequence 86, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-905-083-86

Query Match      100.0%; Score 41; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 3
US-10-372-521-86
; Sequence 86, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-10-372-521-86

Query Match      100.0%; Score 41; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 4
US-10-831-075-86
; Sequence 86, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-10-831-075-86

Query Match      100.0%; Score 41; DB 5; Length 9;
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 1 MARSLLLPL 9

RESULT 5
US-10-450-763-53737
; Sequence 53737, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 53737
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (51)..(78)
; OTHER INFORMATION: Serine proteases trypsin family, histidine proteins. domain
; OTHER INFORMATION: Identified by eMATRIX, accession number BL00134A, p-value=6.143e-
; OTHER INFORMATION: 20, raw score of 11.96
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (36)..(133)
; OTHER INFORMATION: Trypsin domain identified by Pfam, accession name trypsin, E-
; OTHER INFORMATION: value=3.2e-31, Pfam score of 101.0
US-10-450-763-53737

Query Match      100.0%; Score 41; DB 5; Length 136;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 7 MARSLLLPL 15

RESULT 6
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
```



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; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 96
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96

Query Match      100.0%; Score 41; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 4.9; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 MARSLPL 9
Db      1 MARSLPL 9

RESULT 7
US-09-888-615-98
; Sequence 98, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98

Query Match      100.0%; Score 41; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 MARSLPL 9
Db      1 MARSLPL 9

RESULT 8
US-09-764-762-3
; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/09/764,762
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,084
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3

Query Match      100.0%; Score 41; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 MARSLPL 9
Db      1 MARSLPL 9

RESULT 9
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US-10-071-214-2
; Sequence 2, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-071-214-2

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 10
US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: EGELRUD, Torbjorn
; TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
; FILE REFERENCE: HANSSON=3A
; CURRENT APPLICATION NUMBER: US/10/071,214
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,422
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00218
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from
; OTHER INFORMATION: homo sapiens.
US-10-071-214-48

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 11
US-10-264-283-90
; Sequence 90, Application US/10264283
; Publication No. US20030144494A1
; GENERAL INFORMATION:
; APPLICANT: Aigate, Paul A.
; APPLICANT: Mannion, Jane
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.590
; CURRENT APPLICATION NUMBER: US/10/264,283
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 90
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-283-90

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARSLLLPL 9
Db      1 MARSLLLPL 9

RESULT 12
US-10-295-027-498
; Sequence 498, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 498
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-498

Query Match      100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLPL 9
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Db 1 MARSLPL 9

RESULT 13
US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US20040005563A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-48

Query Match 100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLPL 9
| | | | |
Db 1 MARSLPL 9

RESULT 14
US-10-408-765A-639
; Sequence 639, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojn D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 639
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639

Query Match 100.0%; Score 41; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLPL 9
| | | | |
Db 1 MARSLPL 9

RESULT 15
US-10-643-795A-95
; Sequence 95, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAUGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 95
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-643-795A-95

Query Match 100.0%; Score 41; DB 5; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARSLPL 9
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Db 1 MARSLPL 9

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Title: US-09-905-083A-86

Perfect score: 41

Sequence: 1 MARSLLLPL 9

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Searched: 161667 seqs, 27834885 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pdb.*
- 4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pdb.*
- 5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pdb.*
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- 8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	253	6	US-10-412-748-11
2	41	100.0	253	6	US-10-412-748-14
3	41	100.0	253	6	US-10-412-748-17
4	41	100.0	253	7	US-11-037-243-98
5	36	87.8	818	7	US-11-037-243-111
6	35	85.4	138	7	US-11-096-568A-1854
7	32	78.0	303	7	US-11-198-819-2
8	31	75.6	23	7	US-11-175-690-33
9	30	73.2	216	6	US-10-798-579A-2
10	30	73.2	216	6	US-10-883-512-95
11	30	73.2	216	6	US-10-883-512-96
12	30	73.2	216	6	US-10-838-616-59
13	30	73.2	216	6	US-10-714-887-426
14	30	73.2	216	6	US-10-887-475B-2
15	30	73.2	216	7	US-11-114-672-12
16	30	73.2	219	6	US-10-883-512-92
17	30	73.2	242	7	US-11-096-568A-20677
18	30	73.2	354	6	US-10-821-234-1618
19	30	73.2	561	7	US-11-087-099-10415
20	30	73.2	577	7	US-11-074-176-184
21	29	70.7	250	7	US-11-087-099-2477
22	29	70.7	251	6	US-10-883-512-81
23	29	70.7	251	7	US-11-087-099-7434
24	29	70.7	259	7	US-11-096-568A-10450
25	29	70.7	336	7	US-11-096-568A-5367

26	29	70.7	372	7	US-11-096-568A-5366	Sequence 5366, Ap
27	29	70.7	464	7	US-11-096-568A-18302	Sequence 18302, A
28	29	70.7	494	7	US-11-096-568A-16301	Sequence 16301, A
29	29	70.7	514	7	US-11-096-568A-16300	Sequence 16300, A
30	29	70.7	661	7	US-11-072-512-2645	Sequence 2645, Ap
31	29	70.7	783	7	US-11-082-389-354	Sequence 354, App
32	28	68.3	89	7	US-11-096-568A-5658	Sequence 5658, Ap
33	28	68.3	113	7	US-11-096-568A-5657	Sequence 5657, Ap
34	28	68.3	142	7	US-11-096-568A-5656	Sequence 5656, Ap
35	28	68.3	182	7	US-11-096-568A-26809	Sequence 26809, A
36	28	68.3	214	7	US-11-096-568A-26808	Sequence 26808, A
37	28	68.3	280	7	US-11-096-568A-23041	Sequence 23041, A
38	28	68.3	289	7	US-11-096-568A-278	Sequence 278, App
39	28	68.3	351	6	US-10-467-657-5272	Sequence 5272, Ap
40	28	68.3	353	7	US-11-096-568A-24235	Sequence 24235, A
41	28	68.3	367	7	US-11-096-568A-18566	Sequence 18566, A
42	28	68.3	371	7	US-11-096-568A-29391	Sequence 29391, A
43	28	68.3	412	7	US-11-096-568A-28435	Sequence 28435, A
44	28	68.3	426	7	US-11-096-568A-20044	Sequence 20044, A
45	28	68.3	449	7	US-11-096-568A-28434	Sequence 28434, A

ALIGNMENTS

RESULT 1

US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-11

Query Match 100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY	1	MARSLLLPL	9
DB	1	MARSLLLPL	9

RESULT 2

US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV1172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLPL 9
Db      1 MARSLLPL 9
|||||

RESULT 3
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAV172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 41; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MARSLLPL 9
Db      1 MARSLLPL 9
|||||

RESULT 4
US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; PRIOR FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 41; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MARSLLPL 9
Db      1 MARSLLPL 9
|||||

RESULT 5
US-11-037-243-111
; Sequence 111, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 111
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-111

Query Match      87.8%; Score 36; DB 7; Length 818;
Best Local Similarity 88.9%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MARSLLPL 9
Db      1 MARSLLPL 9
|||||

RESULT 6
US-11-096-568A-1854
; Sequence 1854, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1854
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(138)
; OTHER INFORMATION: Ceres Seq. ID no. 15179472
US-11-096-568A-1854

Query Match      85.4%; Score 35; DB 7; Length 138;
Best Local Similarity 88.9%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MARSLLPL 9
Db      1 MARSLLPL 9
|||||

RESULT 7
```

US-11-198-819-2
; Sequence 2, Application US/11198819
; Publication No. US20050287582A1
; GENERAL INFORMATION:
; APPLICANT: Adema, Gorse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-AUG-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-11-198-819-2

Query Match 78.0%; Score 32; DB 7; Length 303;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 1 MGRPLLLPL 9

RESULT 8
US-11-175-690-33
; Sequence 33, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201

US-11-198-819-2
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-33

Query Match 75.6%; Score 31; DB 7; Length 23;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 3 LAYSLLLPL 11

RESULT 9
US-10-798-579A-2
; Sequence 2, Application US/10798579A
; Publication No. US20060005281A1
; GENERAL INFORMATION:
; APPLICANT: Kirin Beer Kabushiki Kaisha; Japan International Research Center for
; APPLICANT: Agricultural Sciences
; TITLE OF INVENTION: A production of plants having improved rooting efficiency and vase
; TITLE OF INVENTION: using environmental stress-resistant gene
; FILE REFERENCE: PH-2034
; CURRENT APPLICATION NUMBER: US/10/798,579A
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: JP 2003-071082
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-798-579A-2

Query Match 73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 185 MAEGMLLPL 193

RESULT 10
US-10-883-512-95
; Sequence 95, Application US/10883512
; Publication No. US20060005265A1
; GENERAL INFORMATION:
; APPLICANT: Bughrara, Suleiman
; APPLICANT: Han, Zhao
; APPLICANT: Wang, Yuexia
; TITLE OF INVENTION: Ryegrass CBF3 Gene: Identification and Isolation
; FILE REFERENCE: MSU-08807
; CURRENT APPLICATION NUMBER: US/10/883,512
; CURRENT FILING DATE: 2004-07-01
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95

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; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-883-512-95

Query Match      73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 185 MAEGMLLPL 193

RESULT 11
US-10-883-512-96
; Sequence 96, Application US/10883512
; Publication No. US20060005265A1
; GENERAL INFORMATION:
; APPLICANT: Bughrara, Suleiman
; APPLICANT: Han, Zhou
; APPLICANT: Wang, Yuexia
; TITLE OF INVENTION: Ryegrass CBF3 Gene: Identification and Isolation
; FILE REFERENCE: MSU-08807
; CURRENT APPLICATION NUMBER: US/10/883,512
; CURRENT FILING DATE: 2004-07-01
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 96
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-883-512-96

Query Match      73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 185 MAEGMLLPL 193

RESULT 12
US-10-838-616-59
; Sequence 59, Application US/10838616
; Publication No. US20060008874A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: CREELMAN, Robert A
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
; FILE REFERENCE: MBI-0069CIP
; CURRENT APPLICATION NUMBER: US/10/838,616
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/685,922
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 09/810,836
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22

; LENGTH: 216
; TYPE: PRT

; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 59
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-838-616-59

Query Match      73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
Db 185 MAEGMLLPL 193

RESULT 13
US-10-714-887-426
; Sequence 426, Application US/10714887
; Publication No. US20060015972A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: CANALES, Roger
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omaira
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
; FILE REFERENCE: MBI0058-CIP
; CURRENT APPLICATION NUMBER: US/10/714,887
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 426
; LENGTH: 216
; TYPE: PRT
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; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: CBF3 polypeptide
US-10-714-887-426

Query Match 73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 185 MAEGMLLPL 193

RESULT 14
US-10-887-475B-2
; Sequence 2, Application US/10887475B
; Publication No. US20060015973A1
; GENERAL INFORMATION:
; APPLICANT: SHINOZAKI, Kazuko;
; APPLICANT: KASUGA, Mie;
; APPLICANT: SAKUMA, Yoh
; TITLE OF INVENTION: Environmental stress-tolerant plants
; FILE REFERENCE: 382.1029CIP
; CURRENT APPLICATION NUMBER: US/10/887,475B
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: US 10/664,771
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 09/301,217
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: JP 10-292348
; PRIOR FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 2
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-887-475B-2

Query Match 73.2%; Score 30; DB 6; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARSLLLPL 9
DB 185 MAEGMLLPL 193

RESULT 15
US-11-114-672-12
; Sequence 12, Application US/11114672
; Publication No. US20060026716A1
; GENERAL INFORMATION:
; APPLICANT: Sivasankar, Sobhana
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Xu, Deping
; TITLE OF INVENTION: Transcriptional Activators Involved in
; TITLE OF INVENTION: Abiotic Stress Tolerance
; FILE REFERENCE: 1084
; CURRENT APPLICATION NUMBER: US/11/114,672
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: US 60/565,430
; PRIOR FILING DATE: 2004-04-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-114-672-12

Query Match 73.2%; Score 30; DB 7; Length 216;
Best Local Similarity 66.7%; Pred. No. 40;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MARSLLLPL 9
DB 185 MAEGMLLPL 193

Search completed: March 11, 2006, 01:38:43
Job time : 8 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:10:50 ; Search time 86.6667 Seconds
(without alignments)
45.628 Million cell updates/sec

Title: US-09-905-083A-99
Perfect score: 42
Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	4 AAE08334	Aae08334 Human str
2	42	100.0	9	4 AAE08304	Aae08304 Human str
3	42	100.0	9	8 ADR68891	Adr68891 Human str
4	42	100.0	9	8 ADR68860	Adr68860 Human str
5	42	100.0	97	6 ADA05740	Ada05740 Human NOV
6	42	100.0	97	8 ADN62904	Adn62904 Human NOV
7	42	100.0	144	8 ADI39727	Adi39727 Stratum c
8	42	100.0	144	8 ADI37151	Adi37151 Stratum c
9	42	100.0	181	6 ADA05738	Ada05738 Human NOV
10	42	100.0	181	8 ADN62902	Adn62902 Human NOV
11	42	100.0	198	6 ADA05736	Ada05736 Human NOV
12	42	100.0	198	8 ADN62900	Adn62900 Human NOV
13	42	100.0	224	6 ADA05744	Ada05744 Human NOV
14	42	100.0	224	8 ADN62908	Adn62908 Human NOV
15	42	100.0	224	9 ADV21100	Adv21100 Human str
16	42	100.0	225	4 AAB98502	Aab98502 Human Str
17	42	100.0	247	6 ADA05742	Ada05742 Human NOV
18	42	100.0	247	8 ADN62906	Adn62906 Human NOV
19	42	100.0	250	6 ADA05732	Ada05732 Human NOV
20	42	100.0	250	8 ADN62896	Adn62896 Human NOV
21	42	100.0	252	6 ADA05734	Ada05734 Human NOV
22	42	100.0	252	8 ADN62898	Adn62898 Human NOV
23	42	100.0	253	2 AAR67888	Aar67888 Human str
24	42	100.0	253	2 AAW05383	Aaw05383 Human amy

ALIGNMENTS

RESULT 1
AAE08334
ID AAE08334 standard; peptide; 9 AA.
XX AAE08334;
AC AAE08334;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #99 (residues 91-99).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW anticense therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
FN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX (UYAR-) UNIV ARKANSAS.
XX O'brien TJ;
XX
DR WPI; 2001-514676/56.
XX
PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.
XX
PS Disclosure; Page 124; 127pp; English.
XX
CC The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used CC to treat a cancer selected from ovarian, breast, lung, colon, prostate CC and other cancers in which SCCE is overexpressed. The present sequence is CC human SCCE peptide
XX
SQ Sequence 9 AA;

Abb84421 Human SCC
Abb84406 Human SCC
Aau82740 Amino aci
Abu07440 Protein d
Abu07471 Protein d
Abr58471 Human str
Adb80484 Ovarian c
Adj68833 Human hea
Adn39180 Cancer/tum
Adl06515 Human tum
Adn04182 Antipsori
Adr72880 Human ova
Ade00353 Human kal
Aab21326 Human HSC
Abb84422 Rat SCCE
Abg23378 Novel hum
Aae08302 Human str
Adr68858 Human str
Abg68630 Stratum c
Abb84423 Murine SC

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Query Match      100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 2
AAE08304
ID AAE08304 standard; peptide; 9 AA.
XX
AC AAE08304;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human stratum corneum chymotrypsin enzyme peptide #69 (residues 91-99).
XX
KW Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour;
KW cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
KW antisease therapy; malignant hyperplasia.
XX
OS Homo sapiens.
XX
PN WO200159158-A1.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US003977.
XX
PR 11-FEB-2000; 2000US-00502600.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ;
XX
DR WPI; 2001-514676/56.
XX
PT Diagnosing cancer comprises detecting stratum corneum chymotrypsin
PT enzyme.
XX
PS Claim 25; Page 117; 127pp; English.
XX
CC The invention relates to diagnosing cancer especially ovarian cancer, by
CC screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are
CC considered to be an integral part of tumour growth and metastasis, and
CC therefore, markers indicative of their presence or absence are useful for
CC the diagnosis of cancer. The method is useful for diagnosing cancer,
CC carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used
CC to treat a cancer selected from ovarian, breast, lung, colon, prostate
CC and other cancers in which SCCE is overexpressed. The present sequence is
CC human SCCE peptide
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 3
ADR68891
ID ADR68891 standard; peptide; 9 AA.
XX
AC ADR68891;
XX
DT 02-DEC-2004 (first entry)
XX

DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:130.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
XX
PF 20-FEB-2004; 2004WO-US005134.
XX
PR 21-FEB-2003; 2003US-00372521.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'brien TJ, Cannon MJ, Santin A;
XX
DR WPI; 2004-653294/63.
XX
PT Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for
PT vaccinating an individual against SCCE, and in monitoring and developing
PT immunotherapies for ovarian and other malignancies.
XX
PS Disclosure; SEQ ID NO 130; 117pp; English.
XX
CC The invention relates to a novel method for vaccinating an individual
CC against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating
CC an individual with a SCCE peptide, which elicits an immune response in
CC the individual. A peptide of the invention acts as a stratum corneum
CC chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating
CC an individual against SCCE, particularly an individual having, suspected
CC or at risk of getting ovarian, lung, prostate, pancreatic or colon
CC cancer. The oligonucleotide is useful for treating a neoplastic state in
CC an individual, such as ovarian, breast, lung, colon, prostate, or
CC pancreatic cancer, and other cancers in which SCCE is overexpressed. The
CC peptides are also useful in the monitoring and development of
CC immunotherapies for ovarian and other malignancies. The present sequence
CC represents a peptide fragment of serine protease SCCE (stratum corneum
CC chymotrytic enzyme).
XX
SQ Sequence 9 AA;

Query Match      100.0%; Score 42; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 4
ADR68860
ID ADR68860 standard; peptide; 9 AA.
XX
AC ADR68860;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:99.
XX
KW serine protease; stratum corneum chymotrytic enzyme; SCCE;
KW immune response; ovarian cancer; lung cancer; prostate cancer;
KW pancreatic cancer; colon cancer.
XX
OS Homo sapiens.
XX
PN WO2004075723-A2.
XX
PD 10-SEP-2004.
```


CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 42; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORIKASKSF 9
DB 72 ORIKASKSF 80
|||||

RESULT 6
ADN62904
ID ADN62904 standard; protein; 97 AA.
XX AC ADN62904;
DT 01-JUL-2004 (first entry)
XX DE Human NOV18e.
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.

XX
OS Homo sapiens.
XX US2004038223-A1.
XX 26-FEB-2004.
XX 01-OCT-2002; 2002US-00262511.
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.
XX 09-OCT-2001; 2001US-0327917P.
XX 09-OCT-2001; 2001US-0328029P.
XX 09-OCT-2001; 2001US-0328044P.
XX 09-OCT-2001; 2001US-0328056P.
XX 12-OCT-2001; 2001US-0328849P.
XX 15-OCT-2001; 2001US-0329414P.
XX 17-OCT-2001; 2001US-0330142P.
XX 18-OCT-2001; 2001US-0330309P.
XX 22-OCT-2001; 2001US-0341058P.
XX 24-OCT-2001; 2001US-0339266P.
XX 24-OCT-2001; 2001US-0343629P.
XX 29-OCT-2001; 2001US-0349575P.
XX 01-NOV-2001; 2001US-0346357P.
XX 17-APR-2002; 2002US-0373260P.
XX 19-APR-2002; 2002US-0373815P.
XX 19-APR-2002; 2002US-0373817P.
XX 19-APR-2002; 2002US-0373826P.
XX 19-APR-2002; 2002US-0373884P.
XX 22-APR-2002; 2002US-0374977P.
XX 16-MAY-2002; 2002US-0381037P.
XX 16-MAY-2002; 2002US-0381038P.
XX 16-MAY-2002; 2002US-0381042P.
XX 17-MAY-2002; 2002US-0381542P.
XX 28-MAY-2002; 2002US-0383656P.
XX 29-MAY-2002; 2002US-0383631P.
XX 25-JUN-2002; 2002US-0391335P.
(SMIT/) SMITHSON G.

PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG W.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (ROTH/) ROTHENBERG R A.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX WPI; 2004-213931/20.
DR N-PSDB; ADN62903.
XX
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 100; 395pp; English.
XX
XX The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient our
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate and preventing their expression. NOVX
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disorders, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic

CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.

SQ Sequence 97 AA;

Query Match 100.0%; Score 42; DB 8; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 |||||
 Db 72 QRIKASKSF 80

RESULT 7

ADI39727
 ID ADI39727 standard; protein; 144 AA.

XX AC ADI39727;

XX DT 15-APR-2004 (first entry)

XX DE Stratum corneum chymotryptic enzyme (sccc) catalytic domain.

XX KW Immune T cell; dendritic cell; extracellular serine protease;

XX KW tumour antigen derived gene-14; TADG-14; carcinoma;

XX KW stratum corneum chymotryptic enzyme; sccc.

XX OS Unidentified.

XX XX US6642013-B1.

XX XX 04-NOV-2003.

XX XX 18-JUL-2000; 2000US-00618259.

XX XX 21-AUG-1997; 97US-00915659.

XX XX 21-AUG-1998; 98US-00137944.

XX PA (UYAR-) UNIV ARKANSAS MEDICAL SCI.

XX XX O'brien TJ, Underwood LJ;

XX XX WPI; 2004-118109/12.

XX PT Production of activated immune cells or dendritic cells by exposing
 PT immune cells to tumor antigen derived gene protein fragment consisting of
 PT amino acid sequences.

XX PS Example 1; SEQ ID NO 4; 44pp; English.

XX CC The present invention relates to novel activated immune T cells or
 CC dendritic cells directed toward extracellular serine protease termed
 CC tumour antigen derived gene-14 (TADG-14). The method of the invention
 CC involves exposing the immune cells to a TADG-14 protein fragment, where
 CC exposure to the TADG-14 protein fragment activates the immune cells. The
 CC invention is used for the production of activated immune T cells or
 CC dendritic cells. The invention allows screening to identify proteases
 CC overexpressed in carcinoma. The present sequence is stratum corneum
 CC chymotryptic enzyme (sccc) catalytic domain. This sequence is used in the
 CC invention.

XX SQ Sequence 144 AA;

Query Match 100.0%; Score 42; DB 8; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 |||||
 Db 28 QRIKASKSF 36

RESULT 8

ADI37151
 ID ADI37151 standard; protein; 144 AA.

XX AC ADI37151;

XX DT 06-MAY-2004 (first entry)

XX DE Stratum corneum chymotryptic enzyme (sccc) catalytic domain.

XX KW Serine protease; tumour antigen derived gene-14; TADG-14;

XX KW neoplastic state; cancer; ovary; breast; lung; colon; prostate;

XX KW chymotryptic enzyme; sccc; enzyme.

XX OS Homo sapiens.

XX XX US2003199010-A1.

XX XX 23-OCT-2003.

XX XX 13-JUN-2003; 2003US-00461787.

XX XX 21-AUG-1997; 97US-00915659.

XX XX 21-AUG-1998; 98US-00137944.

XX XX 18-JUL-2000; 2000US-00618259.

XX PA (UYAR-) UNIV ARKANSAS.

XX XX O'brien TJ, Underwood LJ;

XX XX WPI; 2004-141550/14.

XX PT Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful
 PT for treating neoplastic state (such as ovarian cancer, breast cancer,
 PT lung cancer, colon cancer, prostate cancer) in an individual.

XX PS Example 1; SEQ ID NO 4; 46pp; English.

XX CC The invention relates to extracellular serine protease termed tumour
 CC antigen derived gene-14 (TADG-14) and its nucleic acid. Composition
 CC comprising TADG-14 peptide is useful for treating a neoplastic state in
 CC an individual. The neoplastic state is chosen from ovarian cancer, breast
 CC cancer, lung cancer, colon cancer, prostate cancer in which TADG-14 is
 CC overexpressed. The present sequence is Stratum corneum chymotryptic
 CC enzyme (sccc) catalytic domain. This sequence is used in the
 CC exemplification of the invention.

XX SQ Sequence 144 AA;

Query Match 100.0%; Score 42; DB 8; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 |||||
 Db 28 QRIKASKSF 36

RESULT 9

ADA05738
 ID ADA05738 standard; protein; 181 AA.

XX AC ADA05738;

XX DT 06-NOV-2003 (first entry)

XX DE Human NOV18d protein SEQ ID NO:98.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

XX KW immunomodulator; cytostatic; neuroprotective;

XX KW antiparkinsonian; antilipemic; gene therapy; human disease;

KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; haematopoietic disorder; dyslipidaemia.
XX Homo sapiens.
XX WO2003029424-A2.
XX PD 10-APR-2003.
XX PF 02-OCT-2002; 2002WO-US031373.
XX PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383556P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
PR 01-OCT-2002; 2002US-00262511.
XX PA (CURA-) CURAGEN CORP.
XX PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dippippo VA;
PI Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
XX WPI; 2003-381626/36.
DR N-PSDB; ADA05737.
XX PT New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX Claim 1; Page 171; 586pp; English.
XX The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above

CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipidemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.
XX SQ Sequence 181 AA;
Query Match 100.0%; Score 42; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.54; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
QY 1 QRIKASKSF 9
Db 72 QRIKASKSF 80
|||||||
RESULT 10
ADN62902
ID ADN62902 standard; protein; 181 AA.
XX AC ADN62902;
XX DT 01-JUL-2004 (first entry)
XX DE Human NOV18d.
XX KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX OS Homo sapiens.
XX PN US2004038223-A1.
XX PD 26-FEB-2004.
XX PF 01-OCT-2002; 2002US-00262511.
XX PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.

29-OCT-2001; 2001US-0349575P.
 01-NOV-2001; 2001US-0346357P.
 17-APR-2002; 2002US-0373260P.
 19-APR-2002; 2002US-0373815P.
 19-APR-2002; 2002US-0373817P.
 19-APR-2002; 2002US-0373826P.
 19-APR-2002; 2002US-0373884P.
 22-APR-2002; 2002US-0374977P.
 16-MAY-2002; 2002US-0381037P.
 16-MAY-2002; 2002US-0381039P.
 16-MAY-2002; 2002US-0381042P.
 17-MAY-2002; 2002US-0381642P.
 28-MAY-2002; 2002US-0383656P.
 29-MAY-2002; 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 (SMIT/) SMITHSON G.
 (MILL/) MILLET I.
 (PEYM/) PEYMAN J. A.
 (KEKU/) KEKUDA R.
 (JUUJ/) JU J.
 (LILL/) LI L.
 (GUOX/) GUO X.
 (PATT/) PATTURAJAN M.
 (SPYT/) SPYTEK K. A.
 (EDIN/) EDINGER S. R.
 (ELLE/) ELLERMAN K.
 (WALY/) MALYANKAR U. M.
 (ORTT/) ORT T.
 (GORM/) GORMAN L.
 (ZERH/) ZERHUSEN B. D.
 (ANDE/) ANDERSON D. W.
 (ZHON/) ZHONG M.
 (CATT/) CATTERTON E.
 (JIWV/) JI W.
 (MILL/) MILLER C. E.
 (RAST/) RASTELLI L.
 (STON/) STONE D. J.
 (PENA/) PENA C. E. A.
 (SHEN/) SHENOY S. G.
 (SHIM/) SHIMKETS R. A.
 (ROTH/) ROTHENBERG M. E.
 (LEAC/) LEACH M. D.
 (AGEE/) AGEE M. L.
 (BERG/) BERGHS C.
 (DIPI/) DIPIPPO V. A.
 (EISE/) EISEN A.
 (GANG/) GANGOLLI E. A.
 (RIEG/) RIEGER D. K.
 (SPAD/) SPADERNA S. K.
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
 Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 WPI: 2004-213931/20.
 N-PSDB: ADN62901.
 Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 Claim 1; SEQ ID NO 98; 395pp; English.
 The invention relates to isolated NOVX polypeptides and polynucleotides.
 NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 treat a medical condition in human related to the aberrant expression and
 activity of NOVX polypeptides. For example, NOVX polypeptides and
 polynucleotides may be used to treat disorders associated with decreased
 expression or activity of NOVX by supplementing the patient our
 production or to rectify mutations. Conversely, antisense NA molecules

CC may be administered to down regulate expression of NOVX polypeptides by
 binding with the cells own genes and preventing their expression. NOVX
 polynucleotides and complementary sequences may also be used as DNA
 probes in diagnostic assays to detect and quantitate the presence of
 similar sequences in samples, and so which patients may be in need of
 restorative therapy. NOVX polypeptides may also be used as antigens in
 the production of antibodies and in assays to identify modulators
 (agonists and antagonists) of the expression and activity of NOVX. The
 anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 used to modulate NOVX polynucleotide expression and activity of NOVX
 polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 diagnostic agents for detecting the presence of NOVX in samples. NOVX
 polypeptides and polynucleotides may be used in this way to prevent,
 diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 disorders, Alzheimer's Disease, cancer, cancer-associated cachexia, neurodegenerative
 haematopoietic disorders, and the various dyslipidaemias, metabolic
 disturbances associated with obesity, the metabolic syndrome X and
 wasting disorders associated with chronic diseases and various cancers.
 They may also be used as antibacterial agents. The present sequence
 represents the amino acid sequence of a human NOVX protein.

SQ Sequence 181 AA;
 Query Match 100.0%; Score 42; DB 8; Length 181;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
 Db 72 QRIKASKSF 80

RESULT 11
 ADA05736
 ID ADA05736 standard; protein; 198 AA.
 XX
 AC ADA05736;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human NOV18c protein SEQ ID NO:96.
 XX
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO2003029424-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 02-OCT-2002; 2002WO-US031373.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.

01-NOV-2001; 2001US-0346357P.
17-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373884P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-0383831P.
25-JUN-2002; 2002US-0391335P.
01-OCT-2002; 2002US-00262511.
(CURA-) CURAGEN CORP.
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CB, Rastelli L, Stone DU, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
WPI; 2003-381626/36.
N-PSDB; ADA05735.
New NOVX polypeptides and nucleic acids, useful for diagnosing,
preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
cancer or dyslipidemia, and in chromosome mapping, tissue typing or
pharmacogenomics.
Claim 1; Page 170; 586pp; English.
The present invention describes NOVX proteins, where X can be 1 to 55
(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide described above; (13) methods of treating
or preventing a pathology associated with the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide. NOVX
sequences have antidiabetic, anorectic, antibacterial, virucide,
immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
and antilipase activities, and can be used in gene therapy. The
polypeptide is useful in manufacturing a medicament for treating a
syndrome associated with a human disease. The polypeptide or the nucleic
acid molecule may be used to diagnose, treat or prevent metabolic
disorders such as diabetes or obesity, infections, cachexia, cancer,
neurodegenerative disorders such as Alzheimer's disease or Parkinson's
disease, immune disorders, hematopoietic disorders and various
dyslipidaemias. The nucleic acids can also be used as hybridisation
probes, in chromosome mapping, tissue typing, preventive medicine and
pharmacogenomics. The present sequence represents a human NOVX from the
present invention.
Sequence 198 AA;
Query Match 100.0%; Score 42; DB 6; Length 198;

Best Local Similarity 100.0%; Pred. No. 0.59; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99
RESULT 12
ADN62900
ID ADN62900 standard; protein; 198 AA.
XX
AC ADN62900;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human NOV18c.
XX
KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
OS Homo sapiens.
XX
PN US2004038223-A1.
XX
PD 26-FEB-2004.
XX
PF 01-OCT-2002; 2002US-00262511.
XX
PR 02-OCT-2001; 2001US-0326483P.
PR 05-OCT-2001; 2001US-0327435P.
PR 05-OCT-2001; 2001US-0327449P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
(SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KERU/) KERUDA R.
PA (JUJU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.

PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERH/) ZERHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIMW/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGEE/) AGEE M L.
 PA (BERG/) BERGHS C.
 PA (DIPI/) DIPPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.

PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
 PI Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2004-213931/20.
 DR N-PSDB; ADNG2899.

XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

XX Claim 1; SEQ ID NO 96; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 198 AA;

Query Match 100.0%; Score 42; DB 8; Length 198;

Best Local Similarity 100.0%; Pred. NO. 0.59; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

Qy 1 QRIKASKSF 9
 Db |||||
 91 QRIKASKSF 99

RESULT 13

ADA05744
 ID ADA05744 standard; protein; 224 AA.

XX AC ADA05744;

XX DT 06-NOV-2003 (first entry)

XX DE Human NOV18g protein SEQ ID NO:104.

XX KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytotatic; nootropic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003029424-A2.

XX PD 10-APR-2003.

XX PF 02-OCT-2002; 2002WO-US031373.

XX PR 02-OCT-2001; 2001US-0326483P.

XX PR 05-OCT-2001; 2001US-0327435P.

XX PR 05-OCT-2001; 2001US-0327449P.

XX PR 09-OCT-2001; 2001US-0327917P.

XX PR 09-OCT-2001; 2001US-0328029P.

XX PR 09-OCT-2001; 2001US-0328044P.

XX PR 09-OCT-2001; 2001US-0328056P.

XX PR 12-OCT-2001; 2001US-0328849P.

XX PR 15-OCT-2001; 2001US-0329414P.

XX PR 17-OCT-2001; 2001US-0330142P.

XX PR 18-OCT-2001; 2001US-0330309P.

XX PR 22-OCT-2001; 2001US-0341058P.

XX PR 24-OCT-2001; 2001US-0339266P.

XX PR 29-OCT-2001; 2001US-0343629P.

XX PR 29-OCT-2001; 2001US-0349575P.

XX PR 01-NOV-2001; 2001US-0346357P.

XX PR 17-APR-2002; 2002US-0373260P.

XX PR 19-APR-2002; 2002US-0373815P.

XX PR 19-APR-2002; 2002US-0373817P.

XX PR 19-APR-2002; 2002US-0373826P.

XX PR 19-APR-2002; 2002US-0373884P.

XX PR 22-APR-2002; 2002US-0374977P.

XX PR 16-MAY-2002; 2002US-0381037P.

XX PR 16-MAY-2002; 2002US-0381038P.

XX PR 16-MAY-2002; 2002US-0381042P.

XX PR 17-MAY-2002; 2002US-0381642P.

XX PR 28-MAY-2002; 2002US-0383656P.

XX PR 29-MAY-2002; 2002US-0383831P.

XX PR 25-JUN-2002; 2002US-0391335P.

XX PR 01-OCT-2002; 2002US-00262511.

XX (CURA-) CURAGEN CORP.

XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;

XX Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;

XX Ort T, Gorman L, Zehrusen BD, Anderson DW, Zhong M, Catterton E;

XX Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;

XX Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;

XX Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

XX WPI; 2003-381626/36.

DR N-PSDB; ADA05743.

XX New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 172; 586pp; English.
XX
CC The present invention describes NOVX proteins, where X can be 1 to 55
CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC described above and a carrier; (2) a kit comprising, in one or more
CC containers, the composition described above; (3) an isolated nucleic acid
CC molecule which encodes a NOVX protein of the invention; (4) a vector
CC comprising the nucleic acid molecule described above; (5) a cell
CC comprising the above vector; (6) an antibody that immunospecifically
CC binds to the polypeptide described above; (7) methods for determining the
CC presence or amount of the above polypeptide or nucleic acid molecule in a
CC sample; (8) methods for determining the presence of or predisposition to
CC a disease associated with altered levels of expression of the above
CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC method of identifying an agent that binds to the polypeptide described
CC above; (10) a method for identifying a potential therapeutic agent for
CC use in treating a pathology that is related to an aberrant expression or
CC aberrant physiological interactions of the polypeptide; (11) a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide; (12) a method for modulating
CC the activity of the polypeptide described above; (13) methods of treating
CC or preventing a pathology associated with the above polypeptide in a
CC mammal; and (14) a method for producing the above polypeptide. NOVX
CC sequences have antidiabetic, anorectic, antibacterial, virucide,
CC immunomodulator, cytosstatic, nootropic, neuroprotective, antiparkinsonian
CC and antilipemic activities, and can be used in gene therapy. The
CC polypeptide is useful in manufacturing a medicament for treating a
CC syndrome associated with a human disease. The polypeptide or the nucleic
CC acid molecule may be used to diagnose, treat or prevent metabolic
CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, hematopoietic disorders and various
CC dyslipidaemias. The nucleic acids can also be used as hybridisation
CC probes, in chromosome mapping, tissue typing, preventive medicine and
CC present invention.
XX
XX Sequence 224 AA;
SQ

Query Match 100.0%; Score 42; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 77 QRIKASKSF 85
|||||||

RESULT 14
ADN62908
ID ADN62908 standard; protein; 224 AA.
XX
AC ADN62908;
XX
XX 01-JUL-2004 (first entry)
DT
XX Human NOV18g.
DE
XX human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
KW wasting disorder.
XX
XX Homo sapiens.
OS
XX US2004038223-A1.
PI

XX 26-FEB-2004.
PD
XX 01-OCT-2002; 2002US-00262511.
PF
XX
XX 02-OCT-2001; 2001US-0326483P.
PR
XX 05-OCT-2001; 2001US-0327435P.
PR
XX 05-OCT-2001; 2001US-0327449P.
PR
XX 09-OCT-2001; 2001US-0327917P.
PR
XX 09-OCT-2001; 2001US-0328029P.
PR
XX 09-OCT-2001; 2001US-0328044P.
PR
XX 09-OCT-2001; 2001US-0328056P.
PR
XX 12-OCT-2001; 2001US-0328849P.
PR
XX 15-OCT-2001; 2001US-0329414P.
PR
XX 17-OCT-2001; 2001US-0330142P.
PR
XX 18-OCT-2001; 2001US-0330309P.
PR
XX 22-OCT-2001; 2001US-0341058P.
PR
XX 24-OCT-2001; 2001US-0339266P.
PR
XX 24-OCT-2001; 2001US-0343629P.
PR
XX 29-OCT-2001; 2001US-0349575P.
PR
XX 01-NOV-2001; 2001US-0346357P.
PR
XX 17-APR-2002; 2002US-0373260P.
PR
XX 19-APR-2002; 2002US-0373815P.
PR
XX 19-APR-2002; 2002US-0373817P.
PR
XX 19-APR-2002; 2002US-0373826P.
PR
XX 19-APR-2002; 2002US-0373884P.
PR
XX 22-APR-2002; 2002US-0374977P.
PR
XX 16-MAY-2002; 2002US-0381037P.
PR
XX 16-MAY-2002; 2002US-0381038P.
PR
XX 16-MAY-2002; 2002US-0381042P.
PR
XX 28-MAY-2002; 2002US-0383656P.
PR
XX 29-MAY-2002; 2002US-0383831P.
PR
XX 25-JUN-2002; 2002US-0391335P.
XX
XX (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (JUGU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERH/) ZERHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIWW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (FENA/) FENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
XX Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;

PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2004-213931/20.
 DR N-PSDB; ADN62907.
 XX
 XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 FT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 XX Claim 1; SEQ ID NO 104; 395pp; English.

XX The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.

XX Sequence 224 AA;

Query Match 100.0%; Score 42; DB 8; Length 224;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 Db 77 QRIKASKSF 85
 |||||

RESULT 15
 ADV21100
 ID ADV21100 standard; protein; 224 AA.

XX AC ADV21100;

XX 24-FEB-2005 (first entry)

XX Human stratum corneum chymotrypsin protein.

XX Protein purification; PS133 protein; serine protease; prostate disease;
 KW andrology; genitourinary disease; prostatic cancer; cytostatic;
 KW protein therapy; chymotrypsin; enzyme.

XX Homo sapiens.

XX Key Location/Qualifiers

XX 26..42

FT Domain /note = Catalytically functional motif

FT Domain 83..87

FT /note = Catalytically functional motif

FT Domain 174..179
 FT /note = Catalytically functional motif
 XX US2004241646-A1.

XX PD 02-DEC-2004.

XX 20-FEB-2001; 2001US-00789210.

XX 06-OCT-1997; 97US-00944483.

XX (COHE/) COHEN M.

XX (COLP/) COLPITTS T L.

XX (FRIE/) FRIEDMAN P N.

XX (GRAN/) GRANADOS E.

XX (KLAS/) KLAS M R.

XX (RUSS/) RUSSELL J C.

XX (STEM/) STEWART K D.

XX (STRO/) STROUPE S D.

XX Cohen M, Colpitts TL, Friedman PN, Granados E, Klass MR;

PI Russell JC, Stewart KD, Stroupe SD;

XX WPI; 2005-011614/01.

XX GENBANK; L33404.

XX New isolated polypeptides, useful for detecting, diagnosing, staging,
 FT monitoring, prognosticating, preventing or treating, or determining
 FT predisposition to diseases or conditions of the prostate such as prostate
 FT cancer.

XX Example 1; SEQ ID NO 33; 96pp; English.

XX The invention relates to PS133 protein, a member of the human serine
 CC protease family and its corresponding nucleic acid sequence. PS133
 CC polypeptide is useful for detecting, diagnosing, staging, monitoring, to
 CC prognosticating, preventing or treating or determining predisposition to
 CC diseases or conditions of the prostate such as prostatic cancer. The
 CC present sequence is the human stratum corneum chymotrypsin protein. This
 CC sequence is used to align with PS133 consensus protein.

XX Sequence 224 AA;

Query Match 100.0%; Score 42; DB 9; Length 224;
 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
 Db 62 QRIKASKSF 70
 |||||

Search completed: March 11, 2006, 00:24:19
 Job time : 87.6667 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:24:40 ; Search time 14.1111 Seconds
(without alignments)
61.367 Million cell updates/sec

Title: US-09-905-083A-99
Perfect score: 42
Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	253	2 A53968	serine proteinase
2	34	81.0	373	2 D89004	protein T24A6.11 [
3	33	78.6	427	2 A49518	kallistatin precu
4	32	76.2	895	2 D72571	probable DNA-direc
5	31	73.8	248	2 A40625	tetrachloro-p-hydr
6	31	73.8	298	2 S32368	beta-SNAP protein
7	31	73.8	302	2 T50147	mak16-like protein
8	31	73.8	362	2 F81409	probable phosphate
9	30	71.4	142	2 C39610	BET1 protein - yea
10	30	71.4	321	2 C71463	probable p-loop AT
11	30	71.4	331	2 H97051	probable dehydroge
12	30	71.4	427	2 T48159	hypothetical prote
13	30	71.4	517	2 T40129	hypothetical prote
14	30	71.4	627	2 C68850	neutral endopeptid
15	30	71.4	627	2 A47098	lactococcal enope
16	30	71.4	627	2 F53290	endopeptidase Pepo
17	30	71.4	875	2 T19678	hypothetical prote
18	30	71.4	985	2 D82776	pyruvate dehydroge
19	30	71.4	1102	2 H84545	probable ubiquitin
20	30	71.4	3660	1 S02041	dystrophin, muscle
21	29	69.0	65	2 AF2269	hypothetical prote
22	29	69.0	141	1 B46322	1eK protein - toba
23	29	69.0	172	2 H81251	NADH2 dehydrogenas
24	29	69.0	182	2 C64176	hypothetical prote
25	29	69.0	203	2 C90678	thiogalactoside ac
26	29	69.0	203	2 G85528	thiogalactoside ac
27	29	69.0	268	2 E84339	quinolinate phosph
28	29	69.0	349	2 AE2568	WD repeat protein
29	29	69.0	368	2 T22587	hypothetical prote

30	29	69.0	463	2 G97300	aspartyl/asparagin
31	29	69.0	484	2 JCS282	phosphoglucanase d
32	29	69.0	526	1 G71081	probable helicase
33	29	69.0	563	2 B82883	hypothetical prote
34	29	69.0	584	2 T48273	hypothetical prote
35	29	69.0	585	2 I37216	calicin - human (f
36	29	69.0	669	2 AB2028	hypothetical prote
37	29	69.0	691	2 T46476	hypothetical prote
38	29	69.0	717	2 AC1419	DNA topoisomerase
39	29	69.0	738	2 E86294	hypothetical prote
40	29	69.0	743	2 C86168	hypothetical prote
41	29	69.0	759	2 S67164	probable membrane
42	29	69.0	940	2 A40985	projectin - fruit
43	29	69.0	1018	2 T15297	hypothetical prote
44	29	69.0	1742	2 S24600	projectin - fruit
45	29	69.0	6658	2 T13931	projectin - fruit

ALIGNMENTS

RESULT 1

A53968
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; UNIPARC:UPI0000001BC4; GB:L33404; NID:G521214; PIDN:R
C;Genetics:
A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRI>

Query Match	100.0%;	Score 42;	DB 2;	Length 253;
Best Local Similarity	100.0%;	Pred. No. 0.092;		
Matches	9;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Qy	1 QRIKASKSF 9
Db	91 QRIKASKSF 99

RESULT 2

D89004
protein T24A6.11 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89004
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: D89004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <STO>
A;Cross-references: UNIPROT:O61942; UNIPARC:UPI000017A667; GB:chr_V; PIDN:AAC17798.1; PII
A;Note: contains similarity to C4-type zinc fingers
C;Genetics:
A;Gene: T24A6.11

A;Map position: 5

Query Match 81.0%; Score 34; DB 2; Length 373;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
|:|:|:|:|:
Db 9 QEIKSKSP 17

RESULT 3

A49518
Kallistatin precursor - human
N;Alternate names: proteinase inhibitor 4; tissue kallikrein inhibitor
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
C;Accession: A49518; A55560; A45093
R;Chai, K.X.; Chen, L.M.; Chao, J.; Chao, L.
J. Biol. Chem. 268, 24498-24505, 1993
A;Title: Kallistatin: a novel human serine proteinase inhibitor. Molecular cloning, tissue
A;Reference number: A49518; MUID:94043294; PMID:8227002
A;Accession: A49518
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-427 <CHA>
A;Cross-references: UNIPROT:P29622; UNIPARC:UPI000012DC02; GB:L19684; NID:G425145; PIDN:
R;Chai, K.X.; Ward, D.C.; Chao, J.; Chao, L.
Genomics 23, 370-378, 1994
A;Title: Molecular cloning, sequence analysis, and chromosomal localization of the human
A;Reference number: A55560; MUID:95137583; PMID:7835886
A;Accession: A55560
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-427 <CH2>
A;Cross-references: UNIPARC:UPI000012DC02; GB:L28101; NID:G609489; PIDN:AAC41706.1; PID:
R;Zhou, G.X.; Chao, L.; Chao, J.
J. Biol. Chem. 267, 25873-25880, 1992
A;Title: Kallistatin: a novel human tissue kallikrein inhibitor. Purification, character
A;Reference number: A45093; MUID:93100304; PMID:1334408
A;Accession: A45093
A;Molecule type: protein
A;Residues: 389-403 <ZHO>
A;Cross-references: UNIPARC:UPI00000353AC; PIDN:AAB24557.1; PID:G261993
A;Note: sequence extracted from NCBI backbone (NCBIP:120847)
C;Genetics:
A;Gene: GDB:PI4; KLST
A;Cross-references: GDB:266537; OMIM:147935
A;Map position: 14q31-14q32.1
C;Superfamily: serpin
C;Keywords: blocked amino end; glycoprotein; pyroglutamic acid; serine proteinase inhibi
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-427/Product: kallistatin #status predicted <MAT>
F;21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;33.108.157.238/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;308/Inhibitory site: Phe (tissue kallikrein) #status experimental

Query Match 78.6%; Score 33; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
|:|:|:|:|:
Db 355 QKLEASKSF 363

RESULT 4

D72571
Probable DNA-directed RNA polymerase subunit A' APE1853 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72571
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A74450; MUID:99310339; PMID:10382966
A;Accession: D72571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-895 <KAW>
A;Cross-references: UNIPROT:Q9YAU1; UNIPARC:UPI000005E0F5; DDBJ:AP000062; NID:G5105244; I
C;Genetics:
A;Gene: APE1853
C;Superfamily: Halobacterium DNA-directed RNA polymerase chain A

Query Match 76.2%; Score 32; DB 2; Length 895;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKS 8
|:|:|:|:|:
Db 885 QRVKASKA 892

RESULT 5

A40625
tetracloro-p-hydroquinone reductive dehalogenase (EC 1.-.-.-) - Flavobacterium sp.
N;Alternate names: glutathione S-transferase homolog; TECH reductive dehalogenase
C;Species: Flavobacterium sp.
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A40625
R;Orser, C.S.; Dutton, J.; Lange, C.; Jablonski, P.; Xun, L.; Hargis, M.
J. Bacteriol. 175, 2640-2644, 1993
A;Title: Characterization of a Flavobacterium glutathione S-transferase gene involved re
A;Reference number: A40625; MUID:93239690; PMID:8478329
A;Accession: A40625
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-248 <ORS>
A;Cross-references: UNIPARC:UPI000017A939; GB:M98559; NID:G148689; PIDN:AAA24921.1; PID:
A;Experimental source: ATCC 39723
A;Note: sequence extracted from NCBI backbone (NCBIN:130432, NCBIP:130433)
C;Keywords: oxidoreductase

Query Match 73.8%; Score 31; DB 2; Length 248;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
|:|:|:|:|:
Db 227 QRMKARRSF 235

RESULT 6

S32368
beta-SNAP protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
R;Whiteheart, S.W.; Griff, I.C.; Brunner, M.; Clary, D.O.; Mayer, T.; Buhrow, S.A.; Rothm
Nature 362, 353-355, 1993
A;Title: SNAP family of NSF attachment proteins includes a brain-specific isoform.
A;Reference number: S32367; MUID:93205122; PMID:8455721
A;Accession: S32368
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <WHI>
A;Cross-references: UNIPROT:P81126; UNIPARC:UPI0000135B11
C;Superfamily: alpha-soluble NSF attachment protein

Query Match 73.8%; Score 31; DB 2; Length 298;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

A;Title: Identification and structure of four yeast genes (SLY) that are able to suppress
A;Reference number: A39610; MUID:91117254; PMID:1990290
A;Accession: C39610
A:Molecule type: DNA
A;Residues: 1-142 <DAS>
A;Cross-references: UNIPROT:P22804; UNIPARC:UPI000012689C; EMBL:X54237; NID:94483; PIDN:1
R;Rowley, N.
submitted to the EMBL Data Library, August 1994
A;Reference number: S48442
A;Accession: S48453
A:Molecule type: DNA
A;Residues: 1-142 <ROW>
A;Cross-references: UNIPARC:UPI000012689C; GB:Z47047; EMBL:Z38113; NID:9603997; PID:g763;
R;Voss, H.; Tamames, J.; Teodoru, C.; Valencia, A.; Sensen, C.; Wilmann, S.; Schwager, C.
Yeast 11, 61-78, 1995
A;Title: Nucleotide sequence and analysis of the centromeric region of yeast chromosome 1
A;Reference number: S50795; MUID:95282515; PMID:7762303
A;Accession: S58677
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-142 <VOS>
A;Cross-references: UNIPARC:UPI000012689C; EMBL:X79743
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
C;Genetics:
A;Gene: SGD:BET1; SLY12
A;Cross-references: SGD:S0001266; MIPS:YII004C
A;Map position: 9L
A;Introns: 4/2
C;Keywords: transmembrane protein
F;126-142/Domain: transmembrane #status predicted <TMM>

Query Match 71.4%; Score 30; DB 2; Length 142;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRIKASKS 8
Db 67 QRIKALKS 74

RESULT 10
C71463
probable p-loop ATPase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 31-Dec-2004
C;Accession: C71463
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: C71463
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-321 <ARN>
A;Cross-references: UNIPROT:O84847; UNIPARC:UPI00000D33B9; GB:AE001357; GB:AE001273; NID
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: mesJ
C;Superfamily: cell cycle control PP-loop ATPase MesJ/YaeO

Query Match 71.4%; Score 30; DB 2; Length 321;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRIKASKSP 9
Db 277 ERLVASKSF 285

RESULT 11
H97051
probable dehydrogenase, YULF B. subtilis ortholog [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97051
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <KUR>
A;Cross-references: UNIPROT:Q97JP2; UNIPARC:UPI000000CA131; GB:AE001437; PIDN:AAK79203.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1231
C;Superfamily: Escherichia coli yojR protein

Query Match 71.4%; Score 30; DB 2; Length 331;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKS 8
DB 303 QRLKVS KS 310
||| |||

RESULT 12
T48159
hypothetical protein T1008.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48159
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224486
A;Accession: T48159
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <BEV>
A;Cross-references: UNIPROT:Q9M035; UNIPARC:UPI000000A2376; EMBL:AL161746
A;Experimental source: cultivar Columbia; BAC clone T1008
C;Genetics:
A;Map position: 5
A;Introns: 317/1
A;Note: T1008.80

Query Match 71.4%; Score 30; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKS 9
DB 140 RRVKASVS F 148
:||| |||

RESULT 13
T40129
hypothetical protein SPBC2F12.12c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40129
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1997
A;Reference number: 221907
A;Accession: T40129
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-517 <WOO>
A;Cross-references: UNIPROT:O14342; UNIPARC:UPI0000013A210; EMBL:Z97211; PIDN:CAB10159.1;
A;Experimental source: strain 972H-; cosmid c2F12
C;Genetics:
A;Gene: SPDB:SPBC2F12.12c
A;Map position: 2

A;Introns: 42/3; 126/3; 157/3; 308/3

Query Match 71.4%; Score 30; DB 2; Length 517;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QRIKASKS 9
DB 187 QRIAPKSF 195
||| |||

RESULT 14
C86850
neutral endopeptidase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86850
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <STO>
A;Cross-references: UNIPROT:Q07744; UNIPARC:UPI0000165F0B; GB:AE005176; PID:g12724829; P1
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: pepO

Query Match 71.4%; Score 30; DB 2; Length 627;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RIKASKS 9
DB 570 RMKASKS 577
|:|||||

RESULT 15
A47098
lactococcal endopeptidase (EC 3.4.-.-) - Lactococcus lactis subsp. cremoris (strain P8-2-
C;Species: Lactococcus lactis subsp. cremoris
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A47098
R;Mierau, I.; Tan, P.S.T.; Haandrikman, A.J.; Kok, J.; Leenhouts, K.J.; Konings, W.N.; Ve
J. Bacteriol. 175, 2087-2096, 1993
A;Title: Cloning and sequencing of the gene for a lactococcal endopeptidase, an enzyme w
A;Reference number: A47098; MUID:93209954; PMID:8458851
A;Accession: A47098
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <MIE>
A;Cross-references: UNIPROT:Q09145; UNIPARC:UPI000016F8B8; GB:L04938; NID:g2933013; PIDN:f
C;Genetics:
A;Gene: pepO
C;Keywords: hydrolase; oligopeptide transport

Query Match 71.4%; Score 30; DB 2; Length 627;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RIKASKS 9
DB 570 RMKASKS 577
|:|||||

Search completed: March 11, 2006, 00:40:54
Job time : 15.1111 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:11:15 ; Search time 95.2222 Seconds
(without alignments)
66.684 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	253	1 KLK7_HUMAN	P49862 homo sapien
2	36	85.7	249	1 KLK7_MOUSE	Q91ve3 mus musculus
3	34	81.0	107	1 Y1897_PASMU	Q9cju4 pasteurella
4	34	81.0	294	2 Q88037_PSEPK	Q88037 pseudomonas
5	34	81.0	296	2 Q4K21_PSEF5	Q4ka21 pseudomonas
6	34	81.0	683	2 Q82XB0_NITEU	Q82xb0 nitrosomonas
7	33	78.6	310	2 Q678H2_5VIRU	Q678h2 lymphocysti
8	33	78.6	314	1 RLAO_THEAC	P57692 thermoplasm
9	33	78.6	427	1 KAIN_HUMAN	P29622 homo sapien
10	33	78.6	427	1 KAIN_PONPY	Q5rcr2 pongo pygma
11	33	78.6	445	2 Q54TF9_DICDI	Q54tf9 dictyosteli
12	33	78.6	513	2 Q54H89_DICDI	Q54h89 dictyosteli
13	33	78.6	671	2 Q8EUP9_MYCPE	Q8eup9 mycoplasma
14	33	78.6	1618	2 Q4S703_TETNG	Q4s703 tetraodon n
15	32	76.2	161	1 RL10_MYCPE	Q8evj0 mycoplasma
16	32	76.2	240	2 Q6PDR5_ACTAD	Q6fdr5 acinetobact
17	32	76.2	274	2 Q4QB71_LEIMA	Q4qb71 leishmania
18	32	76.2	362	2 Q4HKD5_CAMLA	Q4hkds campylobact
19	32	76.2	458	2 Q7RKQ8_PLAFO	Q7rkq8 plasmodium
20	32	76.2	467	2 Q8IBN4_PLAF7	Q8ibn4 plasmodium
21	32	76.2	474	2 Q7VRX5_CANBF	Q7vrxx5 candidatus
22	32	76.2	490	2 Q8SAQ6_CHLRE	Q8saq6 chlamydomon
23	32	76.2	571	2 Q5X079_LEGEL	Q5x079 legionella
24	32	76.2	684	2 Q818K2_HOLDI	Q818k2 holotrichia
25	32	76.2	761	2 Q6D7X6_ERWCT	Q6d7x6 erwinia car
26	32	76.2	772	2 Q62HP6_BURNA	Q62hp6 burkholderi
27	32	76.2	772	2 Q63W23_BURPS	Q63w23 burkholderi
28	32	76.2	793	2 Q7QXV1_GIALA	Q7qxv1 giardia lam
29	32	76.2	895	2 Q9YAU1_AERPE	Q9yau1 aeropyrum p
30	32	76.2	909	2 Q4P5Q8_USTWA	Q4p5q8 ustilago ma
31	32	76.2	3395	2 Q5CW22_CRYPV	Q5cw22 cryptospori

32	31	73.8	143	2	Q4RULO_TETNG	Q4rulo tetraodon n
33	31	73.8	155	2	Q6DGM1_BRABE	Q6dgm1 brachydanio
34	31	73.8	176	2	Q6AXN0_RAT	Q6axn0 rattus norv
35	31	73.8	176	2	Q6P3B2_MOUSE	Q6p3b2 mus musculu
36	31	73.8	177	2	Q8TB05_HUMAN	Q8tb05 homo sapien
37	31	73.8	200	2	Q4S4E7_TETNG	Q4s4e7 tetraodon n
38	31	73.8	201	2	Q519U9_ENTHI	Q519u9 entamoeba h
39	31	73.8	212	2	Q71MF6_HUMAN	Q71mf6 homo sapien
40	31	73.8	235	2	Q6FB10_ACTAD	Q6fb10 acinetobact
41	31	73.8	247	1	PCPC_SPHCR	Q03520 sphingobium
42	31	73.8	248	2	Q937X0_9SPHN	Q937x0 sphingomona
43	31	73.8	254	2	Q975X7_SULTO	Q975x7 sulfolobus
44	31	73.8	276	2	Q8N8N1_HUMAN	Q8n8n1 homo sapien
45	31	73.8	298	1	SNAB_BOVIN	P81126 bos taurus

ALIGNMENTS

RESULT 1
 ID KLK7_HUMAN STANDARD; PRT; 253 AA.
 AC P49862; Q8N5N9; Q8NFV7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Kallikrein 7 precursor (EC 3.4.21.-) (hK7) (Stratum corneum
 chymotryptic enzyme) (hSCCE).
 GN Name=KLK7; Synonyms=PRSS6, SCCE;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 23-53.
 RC TISSUE=Skin;
 RX MEDLINE=94308225; PubMed=8034709;
 RA Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
 RA Egelrud T.;
 RT "Cloning, expression, and characterization of stratum corneum
 chymotryptic enzyme. A skin-specific human serine proteinase.";
 RT J. Biol. Chem. 269:19420-19426(1994).
 RL [2]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
 RC TISSUE=Keratinocyte;
 RX PubMed=10974542; DOI=10.1016/S0378-1119(00)00280-8;
 RA Yousef G.M., Scorilas A., Magklara A., Soosaipillai A.,
 RA Diamandis E.P.;
 RA "The KLK7 (PRSS6) gene, encoding for the stratum corneum chymotryptic
 enzyme is a new member of the human kallikrein gene family - genomic
 characterization, mapping, tissue expression and hormonal
 regulation.";
 RL Gene 254:119-128(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
 RA Can L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
 RA Moss P., Preper B., Wang K.;
 RA "Sequencing and expression analysis of the serine protease gene
 cluster located in chromosome 19q13 region.";
 RT Gene 257:119-130(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
 RA Wallbrandt P., Egelrud T.;
 RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
 mice; a model for chronic itchy dermatitis";
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION,
 RC TISSUE SPECIFICITY.
 TISSUE=Ovarian carcinoma;

RX MEDLINE=22623266; PubMed=12738725;
RA Dong Y., Kaushal A., Brattand M., Nicklin J., Clements J.A.;
RT "Differential splicing of KLK5 and KLK7 in epithelial ovarian cancer
produces novel variants with potential as cancer biomarkers.";
RL Clin. Cancer Res. 9:1710-1720(2003).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=95314630; PubMed=7794273;
RA Skytt A., Stromqvist M., Egelrud T.;
RT "Primary substrate specificity of recombinant human stratum corneum
chymotryptic enzyme.";
RL Biochem. Biophys. Res. Commun. 211:586-589(1995).
CC -I- FUNCTION: May catalyze the degradation of intercellular cohesive
structures in the cornified layer of the skin in the continuous
shedding of cells from the skin surface. Specific for amino acid
residues with aromatic side chains in the P1 position. SCCE
cleaves insulin B chain at 6-Leu-Cys-7, 16-Tyr-|-Leu-17, 25-
Phe-|-Tyr-26, and 26-Tyr-|-Phe-27. Could play a role in the
activation of precursors to inflammatory cytokines.
CC -I- SUBCELLULAR LOCATION: Secreted. In ovarian carcinoma, secreted and
also observed at the apical membrane and in cytoplasm at the
invasive front.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=P49862-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=P49862-2; Sequence=VSP_013581;
CC -I- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
expressed by keratinocytes in the epidermis. Also expressed in the
brain, mammary gland, cerebellum, spinal cord and kidney. Lower
levels in salivary glands, uterus, thymus, thyroid, placenta,
trachea and testis. Up-regulated in ovarian carcinoma, especially
late-stage serous carcinoma, compared with normal ovaries and
benign adenomas (at the protein level).
CC -I- INDUCTION: By estrogens and glucocorticoids in a breast carcinoma
cell line.
CC -I- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
subfamily.
CC -I- SIMILARITY: Contains 1 peptidase S1 domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; L33404; AAC37551.1; -; mRNA.
DR EMBL; AF166330; AAD49718.1; -; Genomic_DNA.

DR EMBL; AF243527; AAG33360.1; -; Genomic DNA.
DR EMBL; AF332583; AAK69624.1; -; Genomic_DNA.
DR EMBL; AF411214; AAN03662.1; -; mRNA.
DR EMBL; AF411215; AAN03663.1; -; mRNA.
DR EMBL; BC032005; AAH32005.1; -; mRNA.
DR PIR; A53968; A53968.
DR HSSP; P00760; IEZX.
DR MEROPS; S01.300; -.
DR Ensembl; ENSG00000169035; Homo sapiens.
DR HGNC; HGNC:6368; KLK7.
DR H-InvDB; HIX0015373; -.
DR MIM; 604438; -.
DR GO; GO:0008236; F-serine-type peptidase activity; TAS.
DR GO; GO:0008544; P-epidermis development; TAS.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM0020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease; Signal; Zymogen.
FT SIGNAL 1 22
FT PROPEP 23 29 Activation peptide.
FT CHAIN 30 253 Kallikrein 7.
FT DOMAIN 30 250 Peptidase S1.
FT ACT_SITE 70 70 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 205 205 Charge relay system (By similarity).
FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
FT DISULFID 36 137 By similarity.
FT DISULFID 55 71 By similarity.
FT DISULFID 144 211 By similarity.
FT DISULFID 176 190 By similarity.
FT DISULFID 201 226 By similarity.
FT DISULFID ? 239 By similarity.
FT VARSPPLIC 1 72 Missing (in isoform 2).
FT CONFLICT 226 226 C -> W (in Ref. 6; AAH32005).
FT SEQUENCE 253 AA; 27525 MW; 2D68B6B15A76A668 CRC64;
SQ
Query Match 100.0%; Score 42; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRIKASKSF 9
Db 91 QRIKASKSF 99
RESULT 2
KLK7 MOUSE
ID KLK7 MOUSE STANDARD; PRT; 249 AA.
AC Q91VE3; Q9R048;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic
enzyme) (Thymopain).
GN Name=KLK7; Synonyms=Prss6, Scce;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC TISSUE=Thymus;
RA Yamaguchi N.;
RT "A novel cDNA cloning of mouse serine protease, thymopain.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

[2]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=129/SvJ;
 RA Hansson L., Baeckman A., Ny A., Edlund M., Edholm E., Tornell J.,
 RA Wallbrandt P., Egelrud T.;
 RT "Epidermal overexpression of stratum corneum chymotryptic enzyme in
 RT mice; a model for chronic itchy dermatitis.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakada I., Osato Y., Saio R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru N., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Ciothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Santana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wu L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zvolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirokane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Iotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FBV/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [5]
 RN NUCLEOTIDE SEQUENCE OF 1-234, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6; TISSUE=Tail;
 RX MEDLINE=99399282; PubMed=10469296;
 RX DOI=10.1046/j.1523-1747.1999.00662.x;
 RA Baeckman A., Stranden P., Brattand M., Hansson L., Egelrud T.;
 RT "Molecular cloning and tissue expression of the murine analog to human
 RT stratum corneum chymotryptic enzyme.";

RL J. Invest. Dermatol. 113:152-155 (1999).
 CC -1- FUNCTION: May catalyze the degradation of intercellular cohesive
 CC structures in the cornified layer of the skin in the continuous
 CC shedding of cells from the skin surface. Specific for amino acid
 CC residues with aromatic side chains in the P1 position. SCCE
 CC cleaves insulin B chain at 6-Leu-Cys-7, 16-Tyr-Leu-17, 25-
 CC Phe-Tyr-26, and 26-Tyr-Thr-27. Could play a role in the
 CC activation of precursors to inflammatory cytokines.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in skin and, at lower levels, in
 CC lung, kidney, brain, heart and spleen. In skin, expressed in high
 CC suprabasal keratinocytes and in the luminal parts of hair
 CC follicles. Not detected in liver and skeletal muscle.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 CC subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AB008371; BAB55604.1; -; mRNA.
 DR EMBL; AF339930; AAK69652.1; -; Genomic DNA.
 DR EMBL; AK029477; BAC26467.1; -; mRNA.
 DR EMBL; AK077406; BAC36787.1; -; mRNA.
 DR EMBL; BC027823; AAH27823.1; -; mRNA.
 DR EMBL; AF124299; AAF01139.1; -; mRNA.
 DR HSSP; P00760; 1EZX.
 DR MEROPS; S01.300; -;
 DR Ensembl; ENSMUSG00000030713; Mus musculus.
 DR MGI; MGI:1346336; K1k7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR001254; Peptidase_S1_S6.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; Trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 25 Activation peptide (By similarity).
 FT CHAIN 26 249 Kallikrein 7 (By similarity).
 FT REGION 26 246 Serine protease (By similarity).
 FT ACT_SITE 66 66 Charge relay system (By similarity).
 FT ACT_SITE 108 108 Charge relay system (By similarity).
 FT ACT_SITE 201 201 Charge relay system (By similarity).
 FT DISULFID 51 67 By similarity.
 FT DISULFID 140 207 By similarity.
 FT DISULFID 172 186 By similarity.
 FT DISULFID 197 222 By similarity.
 FT CONFLICT 215 217 VSW -> ASR (in Ref. 5).
 SQ SEQUENCE 249 AA; 27257 MW; 0D4E380F12D14F87 CRC64;
 Query Match 85.7%; Score 36; DB 1; Length 249;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QRIKASKSF 9
 Db 87 QKIKATKSF 95
 RESULT 3
 ID Y1897_PASMU STANDARD; PRT; 107 AA.
 AC Q9CJU4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Hypothetical lipoprotein PM1897 precursor.

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GN OrderedLocusNames=PM1897;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.B., Paustian M.L., Whitam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE006227; AK03981.1; -; Genomic DNA.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
CC Palmitate; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 107 Hypothetical protein PM1897.
FT LIPID 18 18 N-palmitoyl cysteine (Potential).
FT LIPID 18 18 S-diacylglycerol cysteine (Potential).
SQ SEQUENCE 107 AA; 12214 MW; 920C61E14A10F405 CRC64;
Query Match 81.0%; Score 34; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QRIKASKSF 9
DB 27 QRIEASESF 35
RESULT 4
Q88Q37_PSEPK PRELIMINARY; PRT; 294 AA.
AC Q88Q37;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulator AmpR, putative.
GN OrderedLocusNames=PP0661;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Meinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfel E.K., Scanlan D., Tran K.,
RA Moazzaz A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedter H., Lauber J., Stjepandic D., Hohnsbeil J., Straetz M., Heim S.,
RA Kiewitz C., Elsen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
CC -!- SIMILARITY: Contains 1 HTH lyser-type DNA-binding domain.
DR EMBL; AS016776; AAN6286.1; -; Genomic DNA.
DR TIGR; PP0661; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
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DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR000847; HTH_LySR.
DR InterPro; IPR005119; LySR_subst_bd.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF00126; HTH 1; 1.
DR Pfam; PF03466; LySR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS50931; HTH_LYSR; 1.
KW Activator; Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 294 AA; 32996 MW; 33695F24D26560EF CRC64;
Query Match 81.0%; Score 34; DB 2; Length 294;
Best Local Similarity 77.8%; Pred. No. 59;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRIKASKSF 9
DB 259 QRIEASESF 267
RESULT 5
Q4KA21_PSEF5
ID Q4KA21_PSEF5 PRELIMINARY; PRT; 296 AA.
AC Q4KA21;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Transcriptional regulator, LySR family.
GN ORFNames=PFL3812;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=PF-5;
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Ghinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY93076.1; -; Genomic DNA.
SQ SEQUENCE 296 AA; 33530 MW; 3941F0F1EA3E92F0 CRC64;
Query Match 81.0%; Score 34; DB 2; Length 296;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRIKASKSF 9
DB 259 QRIEASESF 267
RESULT 6
Q82XB0_NITEU
ID Q82XB0_NITEU PRELIMINARY; PRT; 683 AA.
AC Q82XB0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sensory transduction histidine kinases.
GN OrderedLocusNames=NE0377;
OS Nitrosomonas europaea
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 19718 / IF0 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Savavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whitaker M.M., Atp D.J.;
RA "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321857; CAD84288.1; -; Genomic_DNA.
DR HSP; Q56310; I15D.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR004358; His_kin_like_C.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; HiskA; 1.
DR PRINTS; PR00344; BCTRUSENSOR.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HiskA; 1.
DR PROSITE; PS01019; HIS_KIN; 1.
KW Complete proteome; Kinase.
SQ SEQUENCE 683 AA; 77013 MW; 69895958B6543ED4 CRC64;

Query Match 81.0%; Score 34; DB 2; Length 683;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
DB 548 QRIASKSF 556

RESULT 7
Q678H2_9VIRU PRELIMINARY; PRT; 310 AA.
ID Q678H2_9VIRU PRELIMINARY; PRT; 310 AA.
AC Q678H2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Lymphocystis disease virus - isolate China.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
OX NCBI_TaxID=256729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
RA Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
RT "Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
RT China.";
RL J. Virol. 78:6982-6994(2004).
DR EMBL; AY380826; AAU10885.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001545; Gly_hormoneB.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 310 AA; 34349 MW; 714DAC2A33E42C11 CRC64;

Query Match 78.6%; Score 33; DB 2; Length 310;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
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Db 183 QRIKSKNF 191
|:|:|:|:|
RESULT 8
RLAO_THEAC STANDARD; PRT; 314 AA.
ID _RLAO_THEAC STANDARD; PRT; 314 AA.
AC P57692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acidic ribosomal protein P0 homolog (L10E).
GN Names:rpP0; OrderedLocNames=ra0359;
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC NCBI_TaxID=2303;
OX NCBI_TaxID=2303;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
CC -!- FUNCTION: Ribosomal protein P0 is the functional equivalent of
CC E.coli protein L10.
CC -!- SIMILARITY: Belongs to the ribosomal protein L10P family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC EMBL; AL445064; CAC11503.1; -; Genomic_DNA.
DR HAMAP; MF_00280; -; 1.
DR InterPro; IPR001790; Ribosomal_L10.
DR Pfam; PF00466; Ribosomal_L10; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 314 AA; 34583 MW; F40D048680E0B6EB CRC64;

Query Match 78.6%; Score 33; DB 1; Length 314;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKS 8
DB 17 QRIKASRS 24
|:|:|:|:|

RESULT 9
KAIN_HUMAN STANDARD; PRT; 427 AA.
ID _KAIN_HUMAN STANDARD; PRT; 427 AA.
AC P29622; Q53XB5; Q86TR9; Q96B25;
DT 01-SEP-1993 (Rel. 25, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kallistatin precursor (Serpin A4) (Kallikrein inhibitor) (Protease
DE inhibitor 4).
GN Names:SERPIN4; Synonyms=XST, PI4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
RX MEDLINE=94043294; PubMed=8227002;
RA Chai K.X., Chen L.-M., Chao J., Chao L.;
RT "Kallistatin: a novel human serine proteinase inhibitor. Molecular
RT cloning, tissue distribution, and expression in Escherichia coli.";
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DR PANTHER: PTHR11461; Prot_inh_serpin; 1.
 DR Pfam: PF00079; Serpin; 1.
 DR SMART: SM00093; SERPIN; 1.
 DR PROSITE: PS00284; SERPIN; 1.
 KW Glycoprotein; Protease inhibitor; Serine protease inhibitor; Serpin;
 KW SIGNAL.
 FT CHAIN 1 20 Potential.
 FT SITE 21 427 Kallistatin.
 FT CARBOHYD 388 389 Reactive bond (By similarity).
 FT CARBOHYD 33 33 N-linked (GLNac. . .) (Potential).
 FT CARBOHYD 108 108 N-linked (GLNac. . .) (Potential).
 FT CARBOHYD 157 157 N-linked (GLNac. . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GLNac. . .) (Potential).
 SQ SEQUENCE 427 AA; 48558 MW; 24E05E0197F27ED CRC64;
 Query Match 78.6%; Score 33; DB 1; Length 427;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QRIKASKSF 9
 DB 355 OKLEASKSF 363
 RESULT 11
 Q54TF9_DICDI PRELIMINARY; PRT; 445 AA.
 AC Q54TF9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS ORFNames=DD0204663;
 GN Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Farbrother P., Desany B., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum";
 RL Nature 0:0-0(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAP10100075; EAL66649.1; -; Genomic DNA.
 DR GO; GO:0031072; F:heat shock protein binding; IEA.
 DR GO; GO:0051082; F:unfolded protein binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 KW Chaperone; Hypothetical protein.
 SQ SEQUENCE 445 AA; 50097 MW; BD1A93FAF109CA13 CRC64;
 Query Match 78.6%; Score 33; DB 2; Length 445;
 Best Local Similarity 77.8%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
 DB 103 KRIKACKSF 111
 RESULT 12
 Q54H89_DICDI PRELIMINARY; PRT; 513 AA.
 AC Q54H89;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=DD0219472;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Farbrother P., Desany B., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum";
 RL Nature 0:0-0(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAP101000218; EAL62638.1; -; Genomic DNA.
 DR EMBL; AAP101000218; EAL62638.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 513 AA; 58802 MW; 994053C8156F1DDC CRC64;
 Query Match 78.6%; Score 33; DB 2; Length 513;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QRIKASKSF 9
 DB 489 KRVKSKSF 497
 RESULT 13
 Q8EUP9_MYCPE PRELIMINARY; PRT; 671 AA.
 AC Q8EUP9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Heavy-metal transporting P-type ATPase.
 GN OrderedLocusNames=MYPE8710;
 OS Mycoplasma penetrans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=28227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HF-2;
 RX MEDLINE=22354719; PubMed=1246555; DOI=10.1093/nar/gkf667; Furuya K.,
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T.,

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RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
RT "The complete genomic sequence of Mycoplasma penetrans, an  
RT intracellular bacterial pathogen in humans.";  
RL Nucleic Acids Res. 30:5293-5300(2002).  
DR EMBL; BA000026; BAC44663.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.  
DR GO; GO:0003624; F:catalytic activity; IEA.  
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . .; IEA.  
DR GO; GO:0008152; P:metabolism; IEA.  
DR GO; GO:0030001; P:metal ion transport; IEA.  
DR InterPro; IPR006416; ATPase-IB hvj; 1.  
DR InterPro; IPR001757; ATPase-E1-E2.  
DR InterPro; IPR005834; Dehal-like hydro.  
DR InterPro; IPR008250; E1-E2 ATPase-reg.  
DR Pfam; PF00122; E1-E2 ATPase; 1.  
DR Pfam; PF00702; Hydrolase; 1.  
DR PRINTS; PR00119; CATATPASE.  
DR TIGRFAMs; TIGR01525; ATPase-IB hvj; 1.  
DR TIGRFAMs; TIGR01494; ATPase_P-type; 2.  
DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.  
KW Complete proteome.  
SQ SEQUENCE 671 AA; 75854 MW; 8EE005CA3B60671 CRC64;  
  
Query Match 78.6%; Score 33; DB 2; Length 671;  
Best Local Similarity 77.8%; Pred. No. 2.3e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 ORIKASKSF 9  
Db 551 KEIKASKSF 559  
  
RESULT 14  
Q4S703 TETNG PRELIMINARY; PRT; 1618 AA.  
AC Q4S703;  
DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)  
DE Chromosome 14 SCAF14723, whole genome shotgun sequence.  
DE (Fragment).  
GN ORFNames=GSTENG00023047001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaul S., Jaffe D., Fisher S., Lufalla G., Dossat C., Segreus B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castellino V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an
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CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAE01014723; CAG03579.1; -; Genomic_DNA.  
DR InterPro; IPR001660; SAM.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR011511; SH3_2.  
DR Pfam; PF00536; SAM_1; 2.  
DR Pfam; PF07653; SH3_2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00454; SAM; 2.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS0105; SAM_DOMAIN; 1.  
KW SH3 domain.  
FT NON TER 1618 1618  
SQ SEQUENCE 1618 AA; 177245 MW; C89436939816A448 CRC64;  
  
Query Match 78.6%; Score 33; DB 2; Length 1618;  
Best Local Similarity 77.8%; Pred. No. 5.6e+02;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ORIKASKSF 9  
Db 1192 QRTKGSKSF 1200  
  
RESULT 15  
RL10 MYCPE STANDARD; PRT; 161 AA.  
ID RL10 MYCPE  
AC Q8EVJ0;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE 50S ribosomal protein L10.  
GN Name-rplJ; OrderedLocNames=MYP5740;  
OS Mycoplasma penetrans.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI_TaxID=28227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=HF-2;  
RX MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;  
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,  
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
RT "The complete genomic sequence of Mycoplasma penetrans, an  
RT intracellular bacterial pathogen in humans.";  
RL Nucleic Acids Res. 30:5293-5300(2002).  
CC -!- SIMILARITY: Belongs to the ribosomal protein L10P family.  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; BA000026; BAC44364.1; ALT_INIT; Genomic_DNA.  
DR HAMAP; MF 00362; -; 1.  
DR InterPro; IPR001790; Ribosomal_L10.  
DR InterPro; IPR002363; Ribosomal_L10eub.  
DR Pfam; PF00466; Ribosomal_L10; 1.  
DR PROSITE; PS01109; RIBOSOMAL_L10; FALSE_NEG.  
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.  
SQ SEQUENCE 161 AA; 17949 MW; 1D95D1C29B5E87D3 CRC64;  
  
Query Match 76.2%; Score 32; DB 1; Length 161;  
Best Local Similarity 66.7%; Pred. No. 91;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ORIKASKSF 9  
Db 17 EQIKSKSF 25  
  
Search completed: March 11, 2006, 00:39:00
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Job time : 99.3333 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 00:41:16 ; Search time 21.2222 Seconds
(without alignments)
35.061 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgm2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgm2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	2	US-09-502-600-99
2	42	100.0	9	2	US-09-502-600-130
3	42	100.0	9	2	US-09-918-243-99
4	42	100.0	9	2	US-09-918-243-130
5	42	100.0	144	2	US-09-618-259-4
6	42	100.0	154	2	US-09-261-416-7
7	42	100.0	224	2	US-08-944-483-33
8	42	100.0	225	1	US-08-557-146-12
9	42	100.0	225	1	US-09-027-337-4
10	42	100.0	225	1	US-09-154-344-12
11	42	100.0	225	2	US-09-644-600-4
12	42	100.0	225	2	US-09-654-600A-4
13	42	100.0	253	1	US-08-557-146-2
14	42	100.0	253	1	US-08-824-874-3
15	42	100.0	253	1	US-09-154-344-2
16	42	100.0	253	2	US-08-930-188-2
17	42	100.0	253	2	US-09-210-084-3
18	42	100.0	253	2	US-09-764-762-3
19	42	100.0	253	4	PCT-US96-04294-2
20	42	100.0	265	2	US-09-949-016-7716
21	36	85.7	9	2	US-09-502-600-97
22	36	85.7	9	2	US-09-918-243-97
23	31	73.8	35	2	US-09-149-476-619
24	31	73.8	132	2	US-09-513-999C-5132
25	31	73.8	250	1	US-07-914-282D-6
26	31	73.8	250	1	US-08-276-887A-6
27	31	73.8	250	4	PCT-US93-02460-6

28	31	73.8	314	2	US-09-248-796A-19386	Sequence 19386, A
29	31	73.8	2317	2	US-09-949-016-10109	Sequence 10109, A
30	31	73.8	2860	1	US-08-826-267-2	Sequence 2, Appli
31	30	71.4	342	2	US-08-252-991A-18101	Sequence 18101, A
32	30	71.4	666	2	US-08-982-785A-11	Sequence 11, Appl
33	30	71.4	666	2	US-09-629-498-11	Sequence 11, Appl
34	30	71.4	726	2	US-09-949-016-5916	Sequence 5916, Ap
35	30	71.4	737	2	US-09-949-016-11607	Sequence 11607, A
36	29	69.0	73	2	US-09-248-796A-26710	Sequence 26710, A
37	29	69.0	203	2	US-09-710-279-2424	Sequence 2424, A
38	29	69.0	222	2	US-09-134-001C-3400	Sequence 3400, Ap
39	28	66.7	61	1	US-08-194-211A-3	Sequence 3, Appli
40	28	66.7	61	2	US-08-456-748B-3	Sequence 3, Appli
41	28	66.7	61	2	US-09-492-709A-357	Sequence 357, App
42	28	66.7	67	2	US-09-489-039A-10090	Sequence 10090, A
43	28	66.7	108	2	US-09-248-796A-17972	Sequence 17972, A
44	28	66.7	159	2	US-09-134-000C-4565	Sequence 4565, Ap
45	28	66.7	188	2	US-09-248-796A-27949	Sequence 27949, A

ALIGNMENTS

RESULT 1

US-09-502-600-99

; Sequence 99, Application US/09502600A

; Patent No. 6294344

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP-C

; CURRENT FILING DATE: 2000-02-11

; CURRENT APPLICATION NUMBER: US/09/502.600A

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 99

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 91-99 of the SCCE protein

US-09-502-600-99

Query Match 100.0%; Score 42; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 1 QRIKASKSF 9

RESULT 2

US-09-502-600-130

; Sequence 130, Application US/09502600A

; Patent No. 6294344

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; FILE REFERENCE: D6223CIP-C

; CURRENT FILING DATE: 2000-02-11

; CURRENT APPLICATION NUMBER: US/09/502.600A

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 130

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 91-99 of the SCE protein
US-09-502-600-130

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 3

US-09-918-243-99
; Sequence 99, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCE protein
US-09-918-243-99

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 4

US-09-918-243-130
; Sequence 130, Application US/09918243
; Patent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCE protein
US-09-918-243-130

Query Match 100.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 1 QRIKASKSF 9

RESULT 5
US-09-618-259-4
; Sequence 4, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (sece) catalytic domain
US-09-618-259-4

Query Match 100.0%; Score 42; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 28 QRIKASKSF 36

RESULT 6

US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
; FILE REFERENCE: D6192
; CURRENT APPLICATION NUMBER: US/09/261,416A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 7
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Serine protease catalytic domain of stratum corneum
; OTHER INFORMATION: chymotryptic enzyme (scce) homologous to similar
; OTHER INFORMATION: domain in TADG-12
US-09-261-416-7

Query Match 100.0%; Score 42; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 37 QRIKASKSF 45

RESULT 7

US-08-944-483-33
; Sequence 33, Application US/08944483

Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/944,483
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183-US.01
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-33

Query Match 100.0%; Score 42; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 62 QRIKASKSF 70

RESULT 8
US-08-557-146-12
Sequence 12, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hanson, Lemart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-557-146-12

Query Match 100.0%; Score 42; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 9
US-09-027-337-4
Sequence 4, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotooshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 225
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
OTHER INFORMATION: similar domain in TADG-15
US-09-027-337-4

Query Match 100.0%; Score 42; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 10
US-09-154-344-12
Sequence 12, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:

; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/154,344
; FILING DATE: 16-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-181
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8783
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; US-09-154-344-12

Query Match 100.0%; Score 42; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 11
US-09-644-600-4
; Sequence 4, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Enzyme (SCCE)
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE

US-09-644-600-4

Query Match 100.0%; Score 42; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 12
US-09-654-600A-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: SCCE
; US-09-654-600A-4

Query Match 100.0%; Score 42; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 63 QRIKASKSF 71

RESULT 13
US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; APPLICANT: Hansson, Lennart
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Enzyme (SCCE)
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,146
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.

REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-146-2

Query Match 100.0%; Score 42; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 14
US-08-824-874-3
Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
US-08-824-874-3

Query Match 100.0%; Score 42; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 91 QRIKASKSF 99

RESULT 15
US-09-154-344-2
Sequence 2, Application US/09154344
Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-154-344-2

Query Match 100.0%; Score 42; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

Search completed: March 11, 2006, 01:24:29
Job time : 22.2222 secs

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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:24:47 ; Search time 69.4444 Seconds
(without alignments)
54.151 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	3	US-09-918-243-99
2	42	100.0	9	3	US-09-918-243-130
3	42	100.0	9	3	US-09-905-083-99
4	42	100.0	9	3	US-09-905-083-130
5	42	100.0	9	4	US-10-372-521-99
6	42	100.0	9	4	US-10-372-521-130
7	42	100.0	9	5	US-10-831-075-99
8	42	100.0	9	5	US-10-831-075-130
9	42	100.0	97	4	US-10-262-511-100
10	42	100.0	144	3	US-09-796-294-4
11	42	100.0	144	4	US-10-461-787-4
12	42	100.0	181	4	US-10-262-511-98
13	42	100.0	198	4	US-10-262-511-96
14	42	100.0	224	3	US-09-789-210-33
15	42	100.0	224	4	US-10-262-511-104
16	42	100.0	225	4	US-10-600-187-4
17	42	100.0	247	4	US-10-262-511-102
18	42	100.0	250	4	US-10-262-511-92
19	42	100.0	252	4	US-10-262-511-94
20	42	100.0	253	3	US-09-888-615-98
21	42	100.0	253	3	US-09-784-762-3
22	42	100.0	253	4	US-10-071-214-2
23	42	100.0	253	4	US-10-071-214-48
24	42	100.0	253	4	US-10-264-283-90
25	42	100.0	253	4	US-10-295-027-498
26	42	100.0	253	4	US-10-173-999-48
27	42	100.0	253	4	US-10-408-765A-639

28	42	100.0	253	5	US-10-643-795A-95	Sequence 95, Appl
29	42	100.0	253	5	US-10-948-518-95	Sequence 95, Appl
30	42	100.0	253	5	US-10-868-490A-1	Sequence 1, Appl
31	42	100.0	257	4	US-10-344-394-38	Sequence 38, Appl
32	39	92.9	226	4	US-10-071-214-49	Sequence 49, Appl
33	37	88.1	136	5	US-10-450-763-53737	Sequence 53737, A
34	36	85.7	9	3	US-09-918-243-97	Sequence 97, Appl
35	36	85.7	9	3	US-09-905-083-97	Sequence 97, Appl
36	36	85.7	9	5	US-10-372-521-97	Sequence 97, Appl
37	36	85.7	9	5	US-10-831-075-97	Sequence 97, Appl
38	36	85.7	249	4	US-10-071-214-50	Sequence 50, Appl
39	33	78.6	243	4	US-10-071-214-46	Sequence 46, Appl
40	33	78.6	411	4	US-10-210-172-122	Sequence 122, App
41	33	78.6	411	4	US-10-210-172-124	Sequence 124, App
42	33	78.6	411	4	US-10-210-172-126	Sequence 126, App
43	33	78.6	411	4	US-10-210-172-128	Sequence 128, App
44	33	78.6	411	4	US-10-210-172-130	Sequence 130, App
45	33	78.6	411	4	US-10-210-172-132	Sequence 132, App

ALIGNMENTS

RESULT 1

US-09-918-243-99

; Sequence 99, Application US/09918243

; Patent NO. US20020142317A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 99

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CHAIN

; OTHER INFORMATION: Residues 91-99 of the SCCE protein

US-09-918-243-99

Query Match 100.0%; Score 42; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9

Db 1 QRIKASKSF 9

RESULT 2

US-09-918-243-130

; Sequence 130, Application US/09918243

; Patent NO. US20020142317A1

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Cannon, Martin J.

; APPLICANT: Santin, Alessandro

; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

; FILE REFERENCE: D6223CIP/C/D/CIP

; CURRENT APPLICATION NUMBER: US/09/918,243

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2001-07-13

; NUMBER OF SEQ ID NOS: 136

; SEQ ID NO 130

; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-918-243-130

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 3
US-09-905-083-99
; Sequence 99, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/DiV
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-905-083-99

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 4
US-09-905-083-130
; Sequence 130, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP/C/DiV
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/502,600
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-905-083-130

Query Match      100.0%; Score 42; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 5
US-10-372-521-99
; Sequence 99, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-372-521-99

Query Match      100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9

RESULT 6
US-10-372-521-130
; Sequence 130, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT APPLICATION NUMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-372-521-130

Query Match      100.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
   |||||
Db 1 QRIKASKSF 9
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RESULT 7

US-10-831-075-99
; Sequence 99, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 99
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-831-075-99

Query Match 100.0%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9

Db 1 QRIKASKSF 9

RESULT 8

US-10-831-075-130
; Sequence 130, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
; FILE REFERENCE: D6223CIP/C/D/CIP3
; CURRENT APPLICATION NUMBER: US/10/831,075
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/372,521
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-831-075-130

Query Match 100.0%; Score 42; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9

Db 1 QRIKASKSF 9

RESULT 9

US-10-262-511-100
; Sequence 100, Application US/10262511
; Publication No. US20040036223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle

; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSequist version 0.1
; SEQ ID NO 100
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-100

Query Match 100.0%; Score 42; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9

Db 72 QRIKASKSF 80

RESULT 10

US-09-796-294-4
; Sequence 4, Application US/09796294
; Patent No. US20020037581A1

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; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Extracellular Serine Protease
; FILE REFERENCE: D6020CIP3
; CURRENT APPLICATION NUMBER: US/09/796,294
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/618,259
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4

Query Match      100.0%; Score 42; DB 3; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ORIKASKSF 9
Db      28 ORIKASKSF 36

RESULT 11
US-10-461-787-4
; Sequence 4, Application US/10461787
; Publication No. US20030199010A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. US20030199010A1e1 Extracellular Serine Protease
; FILE REFERENCE: D6020CIP2
; CURRENT APPLICATION NUMBER: US/10/461,787
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US/09/618,259
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 09/127,444
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-10-461-787-4

Query Match      100.0%; Score 42; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ORIKASKSF 9
Db      28 ORIKASKSF 36

RESULT 12
US-10-262-511-98
; Sequence 98, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennnda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Rameah
```

```
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fatturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: Curasequidist version 0.1
; SEQ ID NO 98
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-98

Query Match      100.0%; Score 42; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ORIKASKSF 9
Db      72 ORIKASKSF 80

RESULT 13
US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennnda
```

```
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 96
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96

Query Match 100.0%; Score 42; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 14
US-09-789-210-33
; Sequence 33, Application US/09789210

; Publication No. US20040241646A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GRANADOS, EDWARD N.
; KLASS, MICHAEL R.
; RUSSELL, JOHN C.
; STEWART, KENT D.
; STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,210
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/944,483
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33

Query Match 100.0%; Score 42; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 62 QRIKASKSF 70

RESULT 15
US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
; APPLICANT: Smithson, Glennda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Ju, Jingfang
; APPLICANT: Li, Li
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Patturajan, Meera
```

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; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Ort, Tatiana
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Catterton, Elina
; APPLICANT: Ji, Weizhen
; APPLICANT: Miller, Charles E.
; APPLICANT: Rastelli, Luca
; APPLICANT: Stone, David J.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Leach, Martin D.
; APPLICANT: Agee, Michele L.
; APPLICANT: Berghs, Constance
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-462C
; CURRENT APPLICATION NUMBER: US/10/262,511
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/373,815
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,642
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 60/381,038
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/373,260
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/373,826
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/327,435
; PRIOR FILING DATE: 2001-10-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 104
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-104

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Query Match      100.0%; Score 42; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 QRIKASKSF 9
Db      77 QRIKASKSF 85

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Search completed: March 11, 2006, 01:37:26
Job time : 70.4444 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 11, 2006, 01:27:17 ; Search time 8 Seconds
(without alignments)
31.314 Million cell updates/sec

Title: US-09-905-083A-99

Perfect score: 42

Sequence: 1 QRIKASKSF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA/US:

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubppaa/PTC_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	181	6	US-10-412-748-19
2	42	100.0	253	6	US-10-412-748-11
3	42	100.0	253	6	US-10-412-748-14
4	42	100.0	253	6	US-10-412-748-17
5	42	100.0	253	7	US-11-037-243-98
6	31	73.8	352	7	US-11-036-568A-5482
7	31	73.8	356	7	US-11-036-568A-5481
8	31	73.8	386	7	US-11-036-568A-5480
9	30	71.4	299	7	US-11-087-099-3123
10	30	71.4	726	7	US-11-051-720-1604
11	30	71.4	747	7	US-11-051-720-1605
12	29	69.0	203	6	US-10-733-626-2424
13	29	69.0	277	7	US-11-036-568A-6766
14	29	69.0	294	7	US-11-036-568A-20947
15	29	69.0	296	7	US-11-036-568A-6765
16	29	69.0	328	7	US-11-036-568A-20946
17	29	69.0	355	7	US-11-087-099-8470
18	29	69.0	355	7	US-11-087-099-12111
19	29	69.0	529	7	US-11-087-099-11190
20	28	66.7	46	6	US-10-510-959-108
21	28	66.7	132	7	US-11-036-568A-15475
22	28	66.7	139	7	US-11-036-568A-15474
23	28	66.7	182	7	US-11-036-568A-15473
24	28	66.7	351	7	US-11-087-099-2242
25	28	66.7	351	7	US-11-087-099-8245

26	28	66.7	384	7	US-11-074-176-78	Sequence 78, Appl
27	28	66.7	390	6	US-11-096-568A-23573	Sequence 23573, A
28	28	66.7	469	6	US-10-510-386-14	Sequence 14, Appl
29	28	66.7	600	6	US-10-131-826A-462	Sequence 462, App
30	28	66.7	600	6	US-10-973-115B-462	Sequence 462, App
31	27	64.3	87	6	US-10-667-295-68	Sequence 68, Appl
32	27	64.3	125	6	US-10-467-557-2128	Sequence 2128, Ap
33	27	64.3	163	7	US-11-036-568A-25357	Sequence 25357, A
34	27	64.3	268	7	US-11-096-568A-25355	Sequence 25355, A
35	27	64.3	318	6	US-10-131-826A-374	Sequence 374, App
36	27	64.3	318	6	US-10-973-115B-374	Sequence 374, App
37	27	64.3	343	6	US-10-793-626-1626	Sequence 1626, Ap
38	27	64.3	343	6	US-10-793-626-1964	Sequence 1964, Ap
39	27	64.3	744	7	US-11-087-099-3289	Sequence 3289, Ap
40	27	64.3	838	7	US-11-031-737A-11	Sequence 11, Appl
41	27	64.3	838	7	US-11-031-482-11	Sequence 11, Appl
42	27	64.3	1121	7	US-11-113-751-19	Sequence 19, Appl
43	27	64.3	1248	7	US-11-096-568A-29804	Sequence 29804, A
44	27	64.3	1295	7	US-11-096-568A-29803	Sequence 29803, A
45	27	64.3	1305	7	US-11-096-568A-29802	Sequence 29802, A

ALIGNMENTS

RESULT 1

US-10-412-748-19
; Sequence 19, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PSI616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-19

Query Match 100.0%; Score 42; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
| | | | | | | | | |
Db 19 QRIKASKSF 27

RESULT 2

US-10-412-748-11
; Sequence 11, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PSI616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT

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; ORGANISM: Human
US-10-412-748-11

Query Match      100.0%; Score 42; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 3
US-10-412-748-14
; Sequence 14, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-14

Query Match      100.0%; Score 42; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 4
US-10-412-748-17
; Sequence 17, Application US/10412748
; Publication No. US20060035219A1
; GENERAL INFORMATION:
; APPLICANT: Queensland University of Technology
; APPLICANT: Clements, Judith A
; TITLE OF INVENTION: Aberrant Kallikrein Expression
; FILE REFERENCE: DAVI172.003AUS
; CURRENT APPLICATION NUMBER: US/10/412,748
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: AU PS1616/02
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Human
US-10-412-748-17

Query Match      100.0%; Score 42; DB 6; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 5
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US-11-037-243-98
; Sequence 98, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-98

Query Match      100.0%; Score 42; DB 7; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 91 QRIKASKSF 99

RESULT 6
US-11-096-568A-5482
; Sequence 5482, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5482
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(352)
; OTHER INFORMATION: Ceres Seq. ID no. 14310397
US-11-096-568A-5482

Query Match      73.8%; Score 31; DB 7; Length 352;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 176 QRLKASRAY 184

RESULT 7
US-11-096-568A-5481
; Sequence 5481, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

;; TITLE OF INVENTION: Therby
;; FILE REFERENCE: 2750-1592PUS2
;; CURRENT APPLICATION NUMBER: US/11/096.568A
;; CURRENT FILING DATE: 2005-04-01
;; NUMBER OF SEQ ID NOS: 34471
;; SEQ ID NO 5481
;; LENGTH: 356
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)..(356)
;; OTHER INFORMATION: Ceres Seq. ID no. 14310396
US-11-096-568A-5481

Query Match 73.8%; Score 31; DB 7; Length 356;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 180 QRLKASRAY 188

RESULT 8

US-11-096-568A-5480
;; Sequence 5480, Application US/11096568A
;; Publication No. US20060048240A1
;; GENERAL INFORMATION:
;; APPLICANT: Alexandrov, Nikolai et al.
;; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;; FILE REFERENCE: 2750-1592PUS2
;; CURRENT APPLICATION NUMBER: US/11/096.568A
;; CURRENT FILING DATE: 2005-04-01
;; NUMBER OF SEQ ID NOS: 34471
;; SEQ ID NO 5480
;; LENGTH: 386
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)..(386)
;; OTHER INFORMATION: Ceres Seq. ID no. 14310395
US-11-096-568A-5480

Query Match 73.8%; Score 31; DB 7; Length 386;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 210 QRLKASRAY 218

RESULT 9

US-11-087-099-3123
;; Sequence 3123, Application US/11087099
;; Publication No. US20060041961A1
;; GENERAL INFORMATION:
;; APPLICANT: Abad, Mark S. et al.
;; TITLE OF INVENTION: Genes and Uses for Plant Improvement
;; FILE REFERENCE: 38-21(53450)B EP
;; CURRENT APPLICATION NUMBER: US/11/087,099
;; CURRENT FILING DATE: 2005-03-22
;; NUMBER OF SEQ ID NOS: 12464
;; SEQ ID NO 3123
;; LENGTH: 299
;; TYPE: PRT
;; ORGANISM: Glycine max
US-11-087-099-3123

Query Match 71.4%; Score 30; DB 7; Length 299;

Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QRIKASKSF 9
Db 237 QRLKSSLSF 245

RESULT 10

US-11-051-720-1604
;; Sequence 1604, Application US/11051720
;; Publication No. US20060046257A1
;; GENERAL INFORMATION:
;; APPLICANT: Compugen Ltd
;; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;; FILE REFERENCE: 1847.1002
;; CURRENT APPLICATION NUMBER: US/11/051,720
;; CURRENT FILING DATE: 2005-01-27
;; NUMBER OF SEQ ID NOS: 1780
;; SEQ ID NO 1604
;; LENGTH: 726
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-051-720-1604

Query Match 71.4%; Score 30; DB 7; Length 726;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKS 8
Db 148 QRIKASRS 155

RESULT 11

US-11-051-720-1605
;; Sequence 1605, Application US/11051720
;; Publication No. US20060046257A1
;; GENERAL INFORMATION:
;; APPLICANT: Compugen Ltd
;; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;; FILE REFERENCE: 1847.1002
;; CURRENT APPLICATION NUMBER: US/11/051,720
;; CURRENT FILING DATE: 2005-01-27
;; NUMBER OF SEQ ID NOS: 1780
;; SEQ ID NO 1605
;; LENGTH: 747
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-051-720-1605

Query Match 71.4%; Score 30; DB 7; Length 747;
Best Local Similarity 75.0%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QRIKASKS 8
Db 148 QRIKASRS 155

RESULT 12

US-10-793-626-2424
;; Sequence 2424, Application US/10793626
;; Publication No. US20050255478A1
;; GENERAL INFORMATION:
;; APPLICANT: KIMMERLY, WILLIAM JOHN
;; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;; FILE REFERENCE: PU3480US
;; CURRENT APPLICATION NUMBER: US/10/793,626
;; CURRENT FILING DATE: 2004-03-04
;; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2424
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2424

Query Match 69.0%; Score 29; DB 6; Length 203;
Best Local Similarity 55.6%; Pred. No. 37;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 179 KRLKSDKSF 187
:|:|:|

RESULT 13
US-11-096-568A-6766
; Sequence 6766, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6766
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(277)
; OTHER INFORMATION: Ceres Seq. ID no. 14316538
US-11-096-568A-6766

Query Match 69.0%; Score 29; DB 7; Length 277;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IKASKSF 9
Db 69 IRASKSF 75
:|:|:|

RESULT 14
US-11-096-568A-20947
; Sequence 20947, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20947
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(294)
; OTHER INFORMATION: Ceres Seq. ID no. 12391401
US-11-096-568A-20947

Query Match 69.0%; Score 29; DB 7; Length 294;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRIKASKSF 9
Db 21 KRLRASESF 29
:|:|:|

RESULT 15
US-11-096-568A-6765
; Sequence 6765, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6765
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(296)
; OTHER INFORMATION: Ceres Seq. ID no. 14316537
US-11-096-568A-6765

Query Match 69.0%; Score 29; DB 7; Length 296;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IKASKSF 9
Db 88 IRASKSF 94
:|:|:|

Search completed: March 11, 2006, 01:38:44
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